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OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 19:23:49 ; Search time 90.7435 seconds
(without alignments)
8672.640 Million cell updates/sec

Title: US-09-918-568-46

Perfect score: 1783
Sequence: 1 CGCGTAGCAAAAGCAGGGGT.....ACCCCTGTTCTGCTAGCCG 1783

Scoring table: IDENTITY NUC
Gapop 10.0 ; Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCRTUS.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1783	100.0	1783	1 US-08-229-781-46	Sequence 46, Appl
2	1783	100.0	1783	1 US-08-630-918-46	Sequence 46, Appl
3	1783	100.0	1783	4 US-09-004-422-46	Sequence 46, Appl
4	1606.4	90.1	1728	1 US-08-229-781-28	Sequence 28, Appl
5	1606.4	90.1	1728	1 US-08-630-918-28	Sequence 28, Appl
6	1606.4	90.1	1728	4 US-09-004-422-28	Sequence 28, Appl
7	908.8	51.0	1135	1 US-08-229-781-49	Sequence 49, Appl
8	908.8	51.0	1135	1 US-08-630-918-49	Sequence 49, Appl
9	908.8	51.0	1135	4 US-09-004-422-49	Sequence 49, Appl
10	734	41.2	1701	3 US-09-232-468A-13	Sequence 13, Appl
11	734	41.2	1701	4 US-09-784-984B-11	Sequence 11, Appl
12	707.4	39.7	1721	3 US-08-686-968C-226	Sequence 226, Appl
13	706.2	39.6	1766	2 US-08-453-848-8	Sequence 8, Appl
14	706.2	39.6	1766	3 US-09-169-027-8	Sequence 8, Appl
15	696.4	39.1	1724	3 US-09-197-679A-1	Sequence 1, Appl
16	695.6	39.0	1754	1 US-08-229-781-27	Sequence 27, Appl
17	695.6	39.0	1754	1 US-08-630-918-27	Sequence 27, Appl
18	695.6	39.0	1754	4 US-09-004-422-27	Sequence 27, Appl
19	400	22.4	400	1 US-08-229-781-33	Sequence 33, Appl
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21	400	22.4	400	4 US-09-004-422-33	Sequence 33, Appl
22	397	22.3	405	1 US-08-229-781-34	Sequence 34, Appl
23	397	22.3	405	1 US-08-630-918-34	Sequence 34, Appl
24	397	22.3	405	4 US-09-004-422-34	Sequence 34, Appl
25	382.4	21.4	410	1 US-08-229-781-35	Sequence 35, Appl
26	382.4	21.4	410	1 US-08-630-918-35	Sequence 35, Appl
27	382.4	21.4	410	4 US-09-004-422-35	Sequence 35, Appl

28	379.6	21.3	394	1 US-08-229-781-36	Sequence 36, Appl
29	379.6	21.3	394	1 US-08-630-918-36	Sequence 36, Appl
30	379.6	21.3	394	4 US-09-004-422-36	Sequence 36, Appl
31	373	20.9	924	5 PCT-US94-01149-15	Sequence 15, Appl
32	372.6	20.9	810	5 PCT-US94-01149-19	Sequence 19, Appl
33	368.2	20.7	670	5 PCT-US94-01149-5	Sequence 5, Appl
34	361.4	20.3	912	5 PCT-US94-01149-31	Sequence 31, Appl
35	318.6	17.9	1777	1 US-08-229-781-54	Sequence 54, Appl
36	318.6	17.9	1777	1 US-08-630-918-54	Sequence 54, Appl
37	318.6	17.9	1777	4 US-09-004-422-54	Sequence 54, Appl
38	309.4	17.4	1762	1 US-08-105-483-284	Sequence 284, Appl
39	309.4	17.4	1762	1 US-08-709-209-284	Sequence 284, Appl
40	309.4	17.4	1762	1 US-08-458-101-284	Sequence 284, Appl
41	309.4	17.4	1793	2 US-08-453-848-6	Sequence 6, Appl
42	309.4	17.4	1793	3 US-09-169-027-6	Sequence 6, Appl
43	307.4	17.2	1757	2 US-08-453-848-14	Sequence 14, Appl
44	307.4	17.2	1757	3 US-09-169-027-14	Sequence 14, Appl
45	302.6	17.0	1757	2 US-08-453-848-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-229-781-46
Sequence 46, Application US/08229781
Patent No. 5589174
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,781
FILING DATE: April 19, 1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: A/Okuda/57
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:

HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-229-781-46

Query Match 100.0%; Score 1783; DB 1; Length 1783;
Best Local Similarly 100.0%; Pred. No. 0;
Matches 1783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 241 CTTGAACCTAGGGGACTGTAGCATTTGCCGATGGCTCTTGGAAATCCAAATGTGATAGC 300
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DB 1201 TTTGATGCAATCAACCAAGGTAATTTCTGTGATTGAAAAGATTAACCCCAATTTGAA 1260
QY 1261 GCTGTGGGAAAGAAATTCGTTACTTATGAGAAAAGCTGGAACACTTGACAAAGATG 1320
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DB 1741 TAAGTATTTTAAATTAATAAACACCCCTTGTCTGTACCG 1783

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RESULT 3

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US-09-004-422-46
; Sequence 46, Application US/09004422.
; Patent No. 6337070
; GENERAL INFORMATION:
; APPLICANT: Yoshinobu OKUNO et al.
; TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
; TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,422
; FILING DATE: January 8, 1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/443,862
; FILING DATE: May 22, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,781
; FILING DATE: April 19, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/054,016
; FILING DATE: April 29, 1993
; ATTORNEY/AGENT INFORMATION:

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NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: A/Okuda/57
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-09-004-422-46
Query Match 100.0%; Score 1783; DB 4; Length 1783;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 CGGCTGACAAAGCGAGGGTTATACCATAGAAACCAAGCAATGCGCATCATTT 60
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QY 121 AATTAATTCACAGAGAGGTGACACAAATTTAGAGCGGAACTGCTACTGTACTATGCC 180
DB 121 AATTAATTCACAGAGAGGTGACACAAATTTAGAGCGGAACTGCTACTGTACTATGCC 180
QY 181 AAGGACATCCTTGAGAGAGCCCATTAAGCGGAAGTTATGCAACTAAACGGGATCCCTCCA 240
DB 181 AAGGACATCCTTGAGAGAGCCCATTAAGCGGAAGTTATGCAACTAAACGGGATCCCTCCA 240

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QY 301 CTTCTAAGTGTGCCAAGAGGCTCTTATATATTTGAGAGAAAGAAACCAGAGAGCGTTTG 360
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Db 301 CTTCTAAGTGTGCCAAGAGGCTCTTATATATTTGAGAGAAAGAAACCAGAGAGCGTTTG 360
QY 361 TGTATATCAGGAGCTTCATGATATGAGAAATGGAACATCTCCAGAGCGGTAA 420
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Db 361 TGTATATCAGGAGCTTCATGATATGAGAAATGGAACATCTCCAGAGCGGTAA 420
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Db 421 CATTTGAGAGAAAGTAAAGATTCGCCCAAGATGATGACACAGCATATGACAACTGGA 480
QY 481 GGTTCACAGGCGCTGCGGGTGTCTGTGTAATCCATATTTTTCAGGAACATGGTGTGCTG 540
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Db 481 GGTTCACAGGCGCTGCGGGTGTCTGTGTAATCCATATTTTTCAGGAACATGGTGTGCTG 540
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QY 601 CAAATGCTAATTAATTTGGGGGGTGCACCATCCATTCATGATGAGACAGAGAAAGAACTTG 660
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Db 601 CAAATGCTAATTAATTTGGGGGGTGCACCATCCATTCATGATGAGACAGAGAAAGAACTTG 660
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Db 1081 GCAATAGCTGGTTTATAGAAGAGAGATGGCAAGGAATGTTGACGGTGTGATGATAC 1140
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Db 1141 CATTCACAGCAATGACGAGGATCAGGGTATGACAGACAGCAAGAAATCCACTCAAAAGCA 1200
QY 1201 TTTGATGAGATCACCACCAAGGTAAATCTGTGTTTAAAGATAAACACCAATTTGAA 1260
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Db 1201 TTTGATGAGATCACCACCAAGGTAAATCTGTGTTTAAAGATAAACACCAATTTGAA 1260
QY 1261 GCTGTTGGGAAAGATTCGGTAACTTGAAGAAAAGATGAGAACTTGGAACAAAGATG 1320
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Db 1261 GCTGTTGGGAAAGATTCGGTAACTTGAAGAAAAGATGAGAACTTGGAACAAAGATG 1320
QY 1321 GAAGACGGGTTTCTTGATGTGTGACATACAAATGCTGAGCTTTTATGATGGAATA 1380
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Db 1741 TAAGTCAATTTTATTAATTAATAAACACCTGTTTCTGCTAGCCG 1783

RESULT 4

US-08-229-781-28
Sequence 28, Application US/08229781
Patent No. 5589174
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,781
FILING DATE: April 19, 1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1728 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

Db 1501 AACGGGACGTATGATATCCCAAGTATGAGAGAACTTAACCTAAATGAAATGAAT 1560
QY 1587 CAAAGGGGTAAATATGACAGCATGGGGTTTATCAATCCTTCCATTTATGCTACAGT 1646
Db 1561 CAAAGGGGTAAATATGACAGCATGGGGTTTATCAATCCTTCCATTTATGCTACAGT 1620
QY 1647 AGCAGGTTCTATGATCTCTGGCAATCATGATGGCTGGGATCTCTTCTGGGTGCTCCAA 1706
Db 1621 TGCAGGTTCTCTGCTCTCTGGCAATCATGATGGCTGGGATCTCTTCTGGATGCTCTCAA 1680
QY 1707 CGGGTCTCTGACGTCTGAGATCTGCAATGATTAATGATTTTATA 1754
Db 1681 CGGGTCTCTGACGTCTGAGATCTGCAATGATTAATGATTTTATA 1728

RESULT 5
US-08-630-918-28
Sequence 28, Application US/08630918
Patent No. 5631350
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,918
FILING DATE: April 5, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,781
FILING DATE: April 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheel, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8150
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1728 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
ORIGINAL SOURCE:
ORGANISM: A/izumi/5/45
US-08-630-918-28

Query Match 90 18: Score 1606.4; DB 1: Length 1728;
Best Local Similarity 95 68: Pred. No. 0;
Matches 1652; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 27 ATGAGAAACCAAAATCAAAACATGCGCATTTATCTCATCTCTGTTACAGAGT 86
Db 1 ATGAGCAACCAAAATCAAAACATGCGCATTTATCTCATCTCTGTTACAGAGT 60
QY 87 GAGAGGGACCAAGATATGATTTGATTCATGCTCAATTAATTTCCAGAGAGAGTGCAGAC 146

Db 61 GAGGGGGACCAAGATATGATTCATGATACCATGCCAATAATTCACAGAGAGAGTGCAGAC 120
QY 147 AATTCGTAGAGCGGACGTCAGTCTGACTCATGCCAGAGACATCCTTGAGAGACCCATA 206
Db 121 AATTCGTAGAGCGGACGTCAGTCTGACTCATGCCAGAGACATCCTTGAGAGACCCATA 180
QY 207 CGGAAAGTTATGCAACTTAAACGGAATCCCTCCACTGAACTAGGGGAGCTGTACATTCG 266
Db 181 CGGAAAGTTATGCAACTTAAACGGAATCCCTCCACTGAACTAGGGGAGCTGTACATTCG 240
QY 267 CGGATGGCTCTCTGGAATCCAAATGATAGAGCTTCTAAGTGTCCAGAACGCTCTTA 326
Db 241 CGGATGGCTCTCTGGAATCCAGATGATAGAGCTTCTAAGGTTGCCAGATGTCTCTA 300
QY 327 TATATTGAG 386
Db 301 TATATTGAG 360
QY 387 TGAAGATTTGAAACATCTCTCAGCAGCGTGAACATTTGAGAGAGAGAGAGAGAG 446
Db 361 TGAAGATTTGAAACATCTCTCAGCAGCGTGAACATTTGAGAGAGAGAGAGAGAG 420
QY 447 CAAAGATAGATGACACAGCATACACAACTGAGAGTTCAAGGCTGCGGCTGTCTGG 506
Db 421 CAAAGATAGATGACACAGCATACACAACTGAGAGTTCAAGGCTGCGGCTGTCTGG 480
QY 507 TAATCCATCATTTTTCAGAGAACATGCTGTGGCTGACAAAGAGAGATCATTCGGGT 566
Db 481 TAAACCATCATTTTTCAGAGAACATGCTGTGGCTGACAAAGAGAGATCATTCGGGT 540
QY 567 TGCCAAAGAGATCGACAAACATACAGCGAGAGCAATGATTAATTTGGGGAGTGA 626
Db 541 TGCCAAAGAGATCGACAAACATACAGCGAGAGCAATGATTAATTTGGGGAGTGA 600
QY 627 CCATCCCATTTGATGAGACAGACAAACAAAGATTTGACAGAAATTTGGGAACTATGTTTC 686
Db 601 CCATCCCATTTGATGAGACAGACAAACAAAGATTTGACAGAAATTTGGGAACTATGTTTC 660
QY 687 CGTAGGACATCAACATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 746
Db 661 CGTAGGACATCAACATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 747 GAATGACAG 806
Db 721 GAATGACAG 780
QY 807 AAATTTTGAAGAGTACTGTAATCTAATTTGACAGAGATGATTCAAATATTCGAAAG 866
Db 781 AAATTTTGAAGAGTACTGTAATCTAATTTGACAGAGATGATTCAAATATTCGAAAG 840
QY 867 AGTAGTTCAGGGATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 926
Db 841 AGTAGTTCAGGGATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 927 AACTCCTTTGGAGCAATAATACATTAATCAATACCTTTCAATGTCCACCCAGTACAT 986
Db 901 AACTCCTTTGGAGCAATAATACATTAATCAATACCTTTCAATGTCCACCCAGTACAT 960
QY 987 AGGTAGTTCAGGGATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1046
Db 961 AGGTAGTTCAGGGATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1047 TGTTCCTCCCAATGATTAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1106
Db 1021 TGTTCCTCCCAATGATTAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1107 ATGCAAG 1166
Db 1081 ATGCAAG 1140
QY 1167 GTATGACAG 1226

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Db 1141 G7ATGACGACGACAAAGATTCACCTCAAAAAGCATTGATGGAATCCACCAAGGTAAA 1200
QY 1227 TTCTGTATGTAAGAAAGATTAACACCCCAATTTGAAGCTGTTGGAAAGAAATTCGTAAGT 1286
Db 1201 TTCTGTATGTAAGAAAGATTAACACCCCAATTTGAAGCTGTTGGAAAGAAATTCATTAATTT 1260
QY 1287 AGGAAAGACCTGGAGAACTTGAACAAAAGATGGAAGACGGGTTCTAGATGTGTGAC 1346
Db 1261 AGGAAAGACCTGGAGAACTTGAACAAAAGATGGAAGACGGGTTCTAGATGTGTGAC 1320
QY 1347 ATCAATGCTGAGCTTTTACTTTGATGAGAAATGAGAGGACCTTACTTTCTGATGATTC 1406
Db 1321 ATCAATGCTGAGCTTTTACTTTGATGAGAAATGAGAGGACCTTACTTTCTGATGATTC 1380
QY 1407 TAATGTCAGAAATCTGTATAGTAAGTCAGAAATGACAGTGAAGACACCAAGTCAAAAGACT 1466
Db 1381 TAATGTCAGAAATCTGTATAGTAAGTCAGAAATGACAGTGAAGACACCAAGTCAAAAGACT 1440
QY 1467 AGGAAATGATGTTTGAATTTTATCACAATGTGATGATGATGATGATGATGATGATGATGATG 1526
Db 1441 AGGAAATGATGTTTGAATTTTATCACAATGTGATGATGATGATGATGATGATGATGATGATG 1500
QY 1527 AAACGGGACATATGATTTATCCCAAGTATGAAAGAGTCTAACTAAATGAATGAAT 1586
Db 1501 AAACGGGACATATGATTTATCCCAAGTATGAAAGAGTCTAACTAAATGAATGAAT 1560
QY 1587 CAAAGGGGTAAATTTAGACAGCATGGGGTTTATCAAAATCCTTGCCATTATGCTACAGT 1646
Db 1561 CAAAGGGGTAAATTTAGACAGCATGGGGTTTATCAAAATCCTTGCCATTATGCTACAGT 1620
QY 1647 ACAGGTTCTATGCTCCTGCAATCATGATGCTGGGATCTCTTTCTGGGTGCTCCAA 1706
Db 1621 TCAGGTTCTGCTCCTGCAATCATGATGCTGGGATCTCTTTCTGGGTGCTCCAA 1680
QY 1707 CGGGTCTCTGACGAGCATGCTGATATGATTAAGTCTTTTATA 1754
Db 1681 CGGGTCTCTGACGAGCATGCTGATATGATTAAGTCTTTTATA 1728

```

RESULT 6
US-09-004-422-28
Sequence 28, Application US/09004422
Patent No. 6337070

GENERAL INFORMATION:

APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
NUMBER OF SEQUENCES: 58
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington

STATE: D.C.
COUNTRY: U.S.A.

ZIP: 20006
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/004,422
FILING DATE: January 8, 1998

CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993

APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250

TELEX:
INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 1728 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

MOLECULE TYPE: cdna to genomic RNA

TOPOLOGY: linear

HYPOTHETICAL:

ANTI-SENSE:

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM: A/12um1/5/65

STRAIN:

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE:

ORGANELLE:

IMMEDIATE SOURCE:

LIBRARY:

CLONE:

POSITION IN GENOME:

CHROMOSOME/SEGMENT:

MAP POSITION:

UNITS:

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

ISSUE:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-09-004-422-28

Query Match 90.1%; Score 1606.4; DB 4; Length 1728;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1652; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

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QY 27 ATAGAAAACCAAAACCAAAACCAATGCGCATCTTTATCTCATCTTCTCCGTTCACAGACAGT 86
Db 1 ATAGAACCAAAACCAAAACCAATGCGCATCTTTATCTCATCTTCTCCGTTCACAGACAGT 60
QY 87 GAGAGGGGACGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 146
Db 61 GAGGGGGGACGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
QY 147 AATCTAGAGCGGAAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 206
Db 121 AATCTAGAGCGGAAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180
QY 207 CGGAAAGTTATGCAAACTAAACGGAATCCCTCCACTTGAAGTGAAGGAGCTGATGATG 266
Db 181 CGGAAAGTTATGCAAACTAAACGGAATCCCTCCACTTGAAGTGAAGGAGCTGATGATG 240

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FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: A/Okuda/57
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-229-781-49

Query Match 51.0%; Score 908.8; DB 1; Length 1135;
Best Local Similarity 98.7%; Pred. No. 2.8e-263;
Matches 916; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 853 AAAATATCGAAAAGAGTGTTCAGGAGATCATGAAAACGAGAACACTTGAGAACTGT 912
DB 208 AAGTATGCAAACTAACCGGATCCGGATCATGAAAACGAGAACACTTGAGAACTGT 267
QY 913 GAGACCAATGCGCAACTCTTGGAGCAATTAATACAACTTACCTTTGCACATGTC 972
DB 268 GAGACCAATGCGCAACTCTTGGAGCAATTAATACAACTTACCTTTGCACATGTC 327
QY 973 CACCACGTGACAAATAGTGTGAGTCCGCCAAATATGTAAATCGGAGAGTGTGCTTAGCA 1032
DB 328 CACCACGTGACAAATAGTGTGAGTCCGCCAAATATGTAAATCGGAGAGTGTGCTTAGCA 387
QY 1033 ACAGACTAAGAAATGTTCCCAATGTGAATCAAGAGATTGTTGGGCAATAGCTGCT 1092
DB 388 ACAGACTAAGAAATGTTCCCAATGTGAATCAAGAGATTGTTGGGCAATAGCTGCT 447
QY 1093 TTTATAGAAGAGATGCGCAAGAAATGTTGACGGTGTGATGATACCATCAGACCAAT 1152
DB 448 TTTATAGAAGAGATGCGCAAGAAATGTTGACGGTGTGATGATACCATCAGACCAAT 507
QY 1153 GACCAGGATCAGGGTATGACAGACAGACAAAGAAATCCACTCAAAAGCAATTTGATGAAATC 1212
DB 508 GACCAGGATCAGGGTATGACAGACAGACAAAGAAATCCACTCAAAAGCAATTTGATGAAATC 567
QY 1213 ACCAACAAGTAAATTTCTGTGATTTGAAAAGATAAACCCCAATTTGAGCTGTGGGAAA 1272
DB 568 ACCAACAAGTAAATTTCTGTGATTTGAAAAGATAAACCCCAATTTGAGCTGTGGGAAA 627
QY 1273 GAATTCGTAAGTGAAGAAAGACTGGAAGCTGAACAAAGAGTGAAGACGGCTTT 1332
DB 628 GAATTCGTAAGTGAAGAAAGACTGGAAGCTGAACAAAGAGTGAAGACGGCTTT 687

QY 1333 CTAGATGTGACATACATGCTGAGCTTTTATGTTCTGATGAAAATGAGAGACACTT 1392
DB 688 CTAGATGTGACATACATGCTGAGCTTTTATGTTCTGATGAAAATGAGAGACACTT 747
QY 1393 GACTTTCATGATTTCTATGTCAAGAATCTGTATAGTAAAGTCAAGATGACAGTCAAGAC 1452
DB 748 GACTTTCATGATTTCTATGTCAAGAATCTGTATAGTAAAGTCAAGATGACAGTCAAGAC 807
QY 1453 AACGTCAAGAACTAGAAAATGATGTTTGAATTTTATCAAAATGATGATGAAATGC 1512
DB 808 AACGTCAAGAACTAGAAAATGATGTTTGAATTTTATCAAAATGATGATGAAATGC 867
QY 1513 ATGAATAGTGTGAAAACGGGACATATGATTTATCCCAAGTATGAAAGAGTCAACTA 1572
DB 868 ATGAATAGTGTGAAAACGGGACATATGATTTATCCCAAGTATGAAAGAGTCAACTA 927
QY 1573 AATGAATGAATCAAGGGGTAAATTTGACAGATGAGGGTTTATCAATCCTTCC 1632
DB 928 AATGAATGAATCAAGGGGTAAATTTGACAGATGAGGGTTTATCAATCCTTCC 987
QY 1633 ATTTATGCTACAGTACAGTTCTATGTCACCTGGCAATCATGAGGCTGGGATCTTTC 1692
DB 988 ATTTATGCTACAGTACAGTTCTATGTCACCTGGCAATCATGAGGCTGGGATCTTTC 1047
QY 1693 TGGGTGTGCTCCACGGGTCTCTGCAAGTGCAGATTCGATATGATTAAGTCAATTTA 1752
DB 1048 TGGGTGTGCTCCACGGGTCTCTGCAAGTGCAGATTCGATATGATTAAGTCAATTTA 1107
QY 1753 TAATTAACCAACCTGTTTCTGCTAG 1780
DB 1108 TAATTAACCAACCTGTTTCTGCTAG 1135

RESULT 8

US-08-630-918-49
Sequence 49, Application US/08630918
Patent No. 5631350
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,918
FILING DATE: April 5, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:


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?      LENGTH: 1135 base pairs
?      TYPE: nucleic acid
?      STRANDEDNESS: double
?      TOPOLOGY: linear
?      MOLECULE TYPE: cDNA to genomic RNA
?      ORIGINAL SOURCE:
?      ORGANISM: A/Okuda/57
US-08-630-918-49

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Query Match	51 0%:	Score 908.8:	DB 1	Length 1135:
Best Local Similarity	98 7%:	Pred. No. 2.8e-263:		
Matches 916, Conservative	0:	Mismatches 12:	Indels 0:	Gaps 0:

QY	853	AAAAATATCGAAAAGGAGTTCAGGGGATCTGTAAAGACAGAAAGAACCTTGAGAAACGT	912
Db	208	AAAGTTATGCAAACTTAAAGGATCCGGGATCATGAAAACAGAAAGACACTTGAGAACGT	267
QY	913	GAGACCAAAATGCCAACTCTCTTTGGGAGCAATAAATACAACTTACCTTTTCCAAATGTC	972
Db	268	GAGACCAAAATGCCAACTCTCTTTGGGAGCAATAAATACAACTTACCTTTTCCAAATGTC	327
QY	973	CACCCACTGCAATAGGTGAGGTGGCCCAAAATATGTAAATCGGAAGTGGTCTTACCA	1032
Db	328	CACCCACTGCAATAGGTGAGGTGGCCCAAAATATGTAAATCGGAAGTGGTCTTACCA	387
QY	1033	ACAGGACTAAGGAATGTTCCCAATGTAATCAAGAGGATGTTTGGGGCAATAGCTGT	1092
Db	388	ACAGGACTAAGGAATGTTCCCAATGTAATCAAGAGGATGTTTGGGGCAATAGCTGT	447
QY	1093	TTTATTAAGAGAGATGGCAAGGAATGTTGACGGTGTATGATACCATCACAGCAAT	1153
Db	448	TTTATTAAGAGAGATGGCAAGGAATGTTGACGGTGTATGATACCATCACAGCAAT	507
QY	1153	GACCAGGAGATCAGGTATGCGACGACAGCAAAATCCACTCAAAAGGCAATTGATGGAATC	1212
Db	508	GACCAGGAGATCAGGTATGCGACGACAGCAAAATCCACTCAAAAGGCAATTGATGGAATC	567
QY	1213	ACCACAAGGTAAATTTCTGTGATTTGAAAAGTTAAACACCCCAATTTGAAAGCTGTGGCAA	1272
Db	568	ACCACAAGGTAAATTTCTGTGATTTGAAAAGTTAAACACCCCAATTTGAAAGCTGTGGCAA	627
QY	1273	GAATTGCGTAACCTTGAGAAAAGACTGAGAACCTTGAAACAAAAGATGGAAGACGGGTTT	1332
Db	628	GAATTGCGTAACCTTGAGAAAAGACTGAGAACCTTGAAACAAAAGATGGAAGACGGGTTT	687
QY	1333	CTAGATGTGTGACATACAAATGCTGAGCTTTTAACTTGTATGATGAAATGAGAGACACTT	1392
Db	688	CTAGATGTGTGACATACAAATGCTGAGCTTTTAACTTGTATGATGAAATGAGAGACACTT	747
QY	1393	GACCTTCATGATTCCTATATGTCACAAATCTGTATAGTAAAGTCACAAATGACACTGAGAC	1452
Db	748	GACCTTCATGATTCCTATATGTCACAAATCTGTATAGTAAAGTCACAAATGACACTGAGAC	807
QY	1453	AACGTCAAAAGACTTGGGAAATGATGATTTTGAATTTATCCAAATGCGATGATGAATGC	1512
Db	808	AACGTCAAAAGACTTGGGAAATGATGATTTTGAATTTATCCAAATGCGATGATGAATGC	867
QY	1513	ATGATATGTGTGAATAACGGACGACATATGATTTATCCAAATATGAAAGAGAGCTTAACTA	1572
Db	868	ATGATATGTGTGAATAACGGACGACATATGATTTATCCAAATATGAAAGAGAGCTTAACTA	927
QY	1573	AATGGAATGAATAATCAAGGGGTAAATATGAGCGACATGGGGGTTTATCAATCTTGGCC	1632
Db	928	AATGGAATGAATAATCAAGGGGTAAATATGAGCGACATGGGGGTTTATCAATCTTGGCC	987
QY	1633	ATTATATGCTACAGTACGAGGTTCTATGTCACTGGCAATCATGATGCGTGGATCTCTTC	1692
Db	988	ATTATATGCTACAGTACGAGGTTCTATGTCACTGGCAATCATGATGCGTGGATCTCTTC	1047
QY	1693	TGGGTGTGTCOCATGGGGTCTCTGCAATGCGAGATTCGCAATGATATATATAGTCATTTTA	1752
Db	1048	TGGGTGTGTCOCATGGGGTCTCTGCAATGCGAGATTCGCAATGATATATATAGTCATTTTA	1107

QY	1753	TAATTAATAACACCCCTGTTTCCTAG	1780
Db	1108	TAATTAATAACACCCCTGTTTCCTAG	1135

RESULT 9
 US-09-004-422-49
 Sequence 49, Application US/090044422
 Patent No. 6337070
 GENERAL INFORMATION:
 APPLICANT: Yoshinobu OKUNO et al.
 TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
 NUMBER OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
 STREET: 2033 K Street, N.W., #800
 City: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20006
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/004,422
 FILING DATE: January 8, 1998
 CLASSIFICATION: 350
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/443,862
 FILING DATE: May 22, 1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/229,781
 FILING DATE: April 19, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/054,016
 FILING DATE: April 29, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren M. Cheek, Jr.
 REGISTRATION NUMBER: 33,367
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-721-8200
 TELEFAX: 202-721-8250
 TELEX:
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1135 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to genomic RNA
 HYPOTHEICAL:
 ANTI-SENSE:
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM: A/Okuda/57
 STRAIN:
 INDIVIDUAL ISOLATE:
 DEVELOPMENTAL STAGE:
 HAPLOTYPE:
 TISSUE TYPE:
 CELL TYPE:
 GENE LINE:
 ORGANELLE:
 IMMEDIATE SOURCE:
 LIBRARY:
 CLONE:
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT:
 MAP POSITION:

UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-09-004-422-49

Query Match 51.0%; Score 908.8; DB 4; Length 1135;
Best Local Similarity 98.7%; Pred. No. 2.8e-263;
Matches 916; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 853 AAATATCGAAAGAGGTAGTTCAGGATCATGAAACAGAGAGAACTTGAGAACTGT 912
DB 208 AAGTTATGCAAACTAAACGATCCGGATCATGAAACAGAGAGAACTTGAGAACTGT 267
QY 913 GAGACCAATGCCAACTCCTTTGGAGCAATAATCAACATTTACCTTTTCAACATGTC 972
DB 268 GAGACCAATGCCAACTCCTTTGGAGCAATAATCAACATTTACCTTTTCAACATGTC 327
QY 973 CACCCCTGACATAGTGTGATGTCGCCCAATATGTAAATGCGAGAAAGTTGGTCTAGCA 1032
DB 328 CACCCCTGACATAGTGTGATGTCGCCCAATATGTAAATGCGAGAAAGTTGGTCTAGCA 387
QY 1033 ACAGGACTAAGAAATGTTCCCGAGATTGATCAAGAGAGATTGGGGGAATTCGTGT 1092
DB 388 ACAGGACTAAGAAATGTTCCCGAGATTGATCAAGAGAGATTGGGGGAATTCGTGT 447
QY 1093 TTTTATGAAGAGAGATGCGCAAGAAATGTTGACGTTGTGTATGATACATCAGCAAT 1152
DB 448 TTTTATGAAGAGAGATGCGCAAGAAATGTTGACGTTGTGTATGATACATCAGCAAT 507
QY 1153 GACCGAGGATCGAGGATGTCAGCAGCAAAAGATCCACTCAAAAGCATTGTATGATC 1212
DB 508 GACCGAGGATCGAGGATGTCAGCAGCAAAAGATCCACTCAAAAGCATTGTATGATC 567
QY 1213 ACCAACAAGTAAATCTGTGATTGAAAGATTAACACCCATTGGAAGCTTGGGAAA 1272
DB 568 ACCAACAAGTAAATCTGTGATTGAAAGATTAACACCCATTGGAAGCTTGGGAAA 627
QY 1273 GAATTCGGTAACTTGAAGAAAGACTGGAACCTTGACAAAAGATGGAAGAGGTTT 1332
DB 628 GAATTCGGTAACTTGAAGAAAGACTGGAACCTTGACAAAAGATGGAAGAGGTTT 687
QY 1333 CTAGATGCTGACATATGACATGCTGCTGCTTTAGTTAGTTGATGAAATGAGAGACATT 1392
DB 688 CTAGATGCTGACATATGACATGCTGCTGCTTTAGTTAGTTGATGAAATGAGAGACATT 747
QY 1393 GACTTTCATGATTTATGTCAGAAATCTGTATAGTAAAGTGCAGATGCGAGAGAGC 1452
DB 748 GACTTTCATGATTTATGTCAGAAATCTGTATAGTAAAGTGCAGATGCGAGAGAGC 807
QY 1453 AAGCTCAAGAAGCTGGAAGAAATGATTTTGAATTTTATCACAATGTGATGATGATGC 1512
DB 808 AAGCTCAAGAAGCTGGAAGAAATGATTTTGAATTTTATCACAATGTGATGATGATGC 867
QY 1513 ATGATAGTGAAGAAAGGAGCATATGATTTATCCCAATATGAGAGAGAGTCTTAACCTA 1572
DB 868 ATGATAGTGAAGAAAGGAGCATATGATTTATCCCAATATGAGAGAGAGTCTTAACCTA 927
QY 1573 AATAGAAATGAATCAAGAGGAGTAAATATGACAGCATGGGGTTTATCAAAATCCTTGGC 1632

DB 928 AATAGAAATGAATCAAGAGGAGTAAATGAGCAGCATGGGGTTTATCAAAATCCTTGGC 987
QY 1633 ATTATAGTACAGAGAGGTTTATGCTGCTGACATGATGATGCTGGGATCTCTTC 1692
DB 988 ATTATAGTACAGAGAGGTTTATGCTGCTGACATGATGATGCTGGGATCTCTTC 1047
QY 1693 TGGGTGCTCCCAAGGAGTCTCTGACAGATGATGATGATGATGATGATGATGATGAT 1752
DB 1048 TGGGTGCTCCCAAGGAGTCTCTGACAGATGATGATGATGATGATGATGATGATGAT 1107
QY 1753 TAATTAACACCCCTGTTCTGCTAG 1780
DB 1108 TAATTAACACCCCTGTTCTGCTAG 1135

RESULT 10
US-09-232-468A-13
Sequence 13, Application US/09232468A
Patent No. 6207165
GENERAL INFORMATION:
APPLICANT: AUDONNET et al.
TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE FORMULA AGAINST PORCINE
FILE REFERENCE: 454313-2230
CURRENT APPLICATION NUMBER: US/09/232.468A
CURRENT FILING DATE: 1999-01-05
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 1701
TYPE: DNA
ORGANISM: Porcine Flu Virus (SIV, H1N1 "Sw" strain)
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1698)
US-09-232-468A-13

Query Match 41.2%; Score 734; DB 3; Length 1701;
Best Local Similarity 65.5%; Pred. No. 1.3e-210;
Matches 1092; Conservative 0; Mismatches 570; Indels 6; Gaps 1;
QY 76 TTCACAGCAGTGAAGAGGAGCAGATGATGATGATGATGATGATGATGATGATGATGAT 135
DB 34 TTCACAGCAGTGAAGAGGAGCAGATGATGATGATGATGATGATGATGATGATGATGAT 93
QY 136 AAGGTGACACATTTCTAGAGGAGAGCAGTGTGATGATGATGATGATGATGATGATGAT 195
DB 94 ACTGTGACACATTTCTAGAGGAGAGCAGTGTGATGATGATGATGATGATGATGATGAT 153
QY 196 AAGACCCATTAACGAAAGTTATGCAAACTAAGAGGATCCCTGCACTGAACTAGAGGAG 255
DB 154 AAGACCCATTAACGAAAGTTATGCAAACTAAGAGGATCCCTGCACTGAACTAGAGGAG 213
QY 256 TGTAGCATTCGCGAGAGGCTCTCTTGGAAATCCAAATGTGATAGGCTTCTAAGTCCCA 315
DB 214 TGTAGCATTCGCGAGAGGCTCTCTTGGAAATCCAAATGTGATAGGCTTCTAAGTCCCA 273
QY 316 GAAGGCTCTATATATGGAAGAAACCCGAGAGAGGTTTGTATTCACAGGAGC 375
DB 274 TCATGCTCTTACATATATGAGACTTCAAAATTTGAAATGCAATGCTTACCCGAGAA 333
QY 376 TTCATGATTAAGAAATTAAGATCTCTCAGCAGCGTGAACATTTTGGAGAAAGTA 435
DB 334 TTCATGATTAAGAAATTAAGATCTCTCAGCAGCGTGAACATTTTGGAGAAAGTT 393
QY 436 AAGATTTCTCCCAAGAGTA-----GATGACACAGCATTAACAACTGAGGTTCAACG 489
DB 394 AAGATTTCTCCCAAGAGTA-----GATGACACAGCATTAACAACTGAGGTTCAACG 453
QY 490 GCCTGGCGGCTGTCTGATATCCATCATTTTTCAGAGATGATGCTGCTGCTGCTGCTGCT 549
DB 454 GCATGCTCTTACTCTGAGAACCCCGAGTTTATGAGAAATTTGATGATGATGATGATGATG 513

QY 550 GGATCAGATTATCCGTTGGCCAAAGATCGTACAACTACAGCGGAGAACAAATGCTA 609
DB 514 GAAATATTCATCTCTAACTCAGCAATTCATACCAACAACAAGGAAAGAAAGTCTT 573
QY 610 ATAAATTTGGGGGGTGCACCATCCATTGATGAGACAGACAAAGAACATTTGTACCAAT 669
DB 574 ATATCTGGGGAGTGCACCACTCCCACTAACCAATGACCAACAAACCTCTATACGAAT 633
QY 670 GTGGAGACCTATGTTCCGTAGGACATCAACATTTGAACAAAGTCAACCCCAAGATA 729
DB 634 GCTGATCATATGTTTGTAGTTGGTCTCAATCAAAATACACGAAGTTTCACACAGATA 693
QY 730 GCAACAGGCTTAAATGTGATGAGACAGAGATGATGAAATTTCTGTGACCCCTTGT 789
DB 694 GCAGCTGACCTTAAATTCACAGAGACAGACGAGATGATTTATTTGTGACATTTGTA 753
QY 790 GATATGTGGACACCATTAATTTTGAAGATGATGATTAATCTAATTTGCACAGATATGA 849
DB 754 GATCAAGAGACACCATTAAGCTTTGAGCCACTGGAACTTAATAGCACCATGATGAGCC 813
QY 850 TTCAAAATATCGAAANAGTAGTTCAGGATCATGAAAACAGAGAACATTTGAGAAC 909
DB 814 TTGCAATGATTAAGGCTCTGTCTGGAATTAACGTCGATCTCGGTTCAAT 873
QY 910 TGTGAGACCAATGCTCAACTCTTTGGGAGACATTAATCAACATTTACCTTTCAAT 969
DB 874 TGTGATGCAAAAGTCCAAACCTCATGGGGCTTGAACGATGCTCTCTTTTCAGAAC 933
QY 970 GTCCACCCACTGACATAGTGTAGTGTGAGTGTGATTAATGAGAGAAATGCTGCTTA 1029
DB 934 GTACATCTCCATCTACTTTGGAGATGCCCAATATGTTAAAGACCAACCTGAGATG 993
QY 1030 GCAACAGGACTAAGGATGTTCCCAAGATGATCAAGAGATGTTGGGGAATAGCT 1089
DB 994 GCACAGGACTAAGGAGAGCTCCCTCTATTCATTCACAGAGACTTTTCGAGCAATGCT 1053
QY 1090 GGTATTAATAGAGGATGATGAGCAAGAAATGTTGAGGATGATGATTCATCAGAC 1149
DB 1054 GGAATTCATTAAGGATGATGAGCAAGAAATGATGATGATGATGATGATGATGATG 1113
QY 1150 AATGACCAAGGATGATGATGAGCAAGAAATGATGATGATGATGATGATGATGATG 1209
DB 1114 AATGAGGAGGATGATGATGAGCAAGAAATGATGATGATGATGATGATGATGATG 1173
QY 1210 ATACCAAGCAAGGATGATGATGAGCAAGAAATGATGATGATGATGATGATGATG 1269
DB 1174 ATGAGCAAGCAAGGATGATGAGCAAGAAATGATGATGATGATGATGATGATGATG 1233
QY 1270 AAGAAATTCGATTAATGAGCAAGAAATGATGATGATGATGATGATGATGATGATG 1329
DB 1234 AAGAAATTCATTAATGAGCAAGAAATGATGATGATGATGATGATGATGATGATG 1293
QY 1330 TTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1389
DB 1294 TTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1353
QY 1390 CTGACATTCATTAATGAGCAAGAAATGATGATGATGATGATGATGATGATGATG 1449
DB 1354 CTGATATTCATTAATGAGCAAGAAATGATGATGATGATGATGATGATGATGATG 1413
QY 1450 GACACGCTCAAGAAATGAGCAAGAAATGATGATGATGATGATGATGATGATGATG 1509
DB 1414 AACAAATTCGATTAATGAGCAAGAAATGATGATGATGATGATGATGATGATGATG 1473
QY 1510 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1569
DB 1474 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1533
QY 1570 CTGATATTCATTAATGAGCAAGAAATGATGATGATGATGATGATGATGATGATG 1629
DB 1534 TTGATATTCGATTAATGAGCAAGAAATGATGATGATGATGATGATGATGATGATG 1593

QY 1630 GCCATTTATGCTACAGTACAGGATTTCTATGTCATCTGCAATCATGATGATGATGATG 1689
DB 1594 GCGATTCATTCACAGTACAGGATTTCTATGTCATCTGCAATCATGATGATGATGATG 1653
QY 1690 TTTGGGTGTCTTCCAAAGGCTCTCTGATGATGATGATGATGATGATGATGATGATG 1737
DB 1654 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1701

RESULT 11
US-09-784-984B-11
: Sequence 11, Application US/09784984B
: Patent No. 6576243
: GENERAL INFORMATION:
: APPLICANT: Merit Ltd.
: APPLICANT: Audomnet, Jean-Christophe
: APPLICANT: Bouchardon, Annabelle
: APPLICANT: Baudouin, Philippe
: APPLICANT: Riviere, Michael
: TITLE OF INVENTION: Polynucleotide Vaccine Formula Against Porcine Reproductive an
: TITLE OF INVENTION: Respiratory Pathologies
: FILE REFERENCE: 454313-2230.1
: CURRENT APPLICATION NUMBER: US/09/784,984B
: PRIOR FILING DATE: 2001-02-16
: PRIOR APPLICATION NUMBER: FR 96/09338
: PRIOR FILING DATE: 1996-07-19
: PRIOR APPLICATION NUMBER: PCT/FR97/01313
: PRIOR FILING DATE: 1997-07-15
: PRIOR APPLICATION NUMBER: US 6,207,165
: PRIOR FILING DATE: 2001-03-27
: NUMBER OF SEQ ID NOS: 54
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 11
: LENGTH: 1701
: TYPE: DNA
: ORGANISM: Porcine Flu Virus (SIV, HINI "SW" Strain
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)-(1698)
: OTHER INFORMATION:
US-09-784-984B-11

Query Match 41.2%; Score 734; DB 4; Length 1701;
Best Local Similarity 65.5%; Pred. No. 1.3e-210;
Matches 1092; Conservative 0; Mismatches 570; Indels 6; Gaps 1;

QY 76 TTCACAGCAGTACAGGAGGACAGATGATGATGATGATGATGATGATGATGATGATGATG 135
DB 34 TTCACGCTGCTGAAGCTGACACCATCTGTGATGATGATGATGATGATGATGATGATG 93
QY 136 AAGTGTGACCAATTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 195
DB 94 ACTGTGACACATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 153
QY 196 AAGACCATTAACGGAAGTATGCAAACTAAAGGATCCCTCACTTGAAGTAAAGGAGG 255
DB 154 AACAGTCATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 213
QY 256 TGTAGCATTCGCGAGTGTCTTGAATTCGCAAAATGATGATGATGATGATGATGATG 315
DB 214 TGCACGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 273
QY 316 GAGCGGCTTATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 375
DB 274 TCATGCTTCAATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 333
QY 376 TTCATGATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 435
DB 334 TTCATGATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 393
QY 436 AAGATTCCTGCCAAGATA-----GATGACACAGCATTAATCAACAACTGAGGATGACGG 489
DB 394 GAAATTTTCCCAAAAGCAACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 453

QY	490	GCCTGCGCCGGGTGTGGGAATCCATCAATTTTTCAGGAACAATGGCTGGGTCAGCAAGGAA	54 98
Db	454	GCATGCTTACTCTGTGGAAACCCCGACGTTTATTATCGAAATTTGCTATGGATGTRGAAAGC	51 38
QY	550	GGATCAGATTATCCGGTGTGCCAAGATCGTACAAACAATCAAGCCGAGAACAAATGCTA	60 98
Db	514	GAATAATTCATCTTAATCTTAACCTAGCAAAATCAATACAAACAAGGAAAGAAAGTCTT	57 38
QY	610	ATAATTTGGGGGGGGCGACATGCCATTGATGAGACACAAACAAGAACATTTGTACGAAAT	66 98
Db	574	ATATATCTGGGGAATGCGACCACTCCAACTACCAATACCAACAAACCCCTCTATCGAAT	63 38
QY	670	GTEGGAAACCTATGTTTCCGTAGGCACATCAACATTTGAACAAAGGTCACCCCGAATAA	72 98
Db	634	GCATGATGCATATGTTTCAGTTGGTGTCATCAAAATACACCGAAGGTTCAACACGAAAT	69 38
QY	730	GCAACAAGGCTTAAGTGAATGGACACAAAGAGTGAATGGAATTTCTTGGACCCCTTG	78 98
Db	694	GCAGCTTAGACTTAAGTCAAAAGACAAAGCAGGAGATGAATTAATTAATGGACATTGTTA	75 38
QY	790	GATATGTGGGACACCAATAAATTTTGAGTACAGTGGTAATTAATTCACACAGATGAGA	84 98
Db	754	GATCAAGGAGACACCAATTAAGTTTGAAGCCACTGGGAACCTTAATAGCACCATGTCGCC	81 38
QY	850	TTCAAAATATCGAAAAGAGTACTTCAGCGATCATGAAAACAGAAAGAACCTTGGAAAC	90 98
Db	814	TTTGCATTTGAATTAAGGCTCTCGTGTGGAATTAATTAACGTCGATCTCCGGTTCAAT	87 38
QY	910	TGTGAGCCCAATAGCCAACTCCTTTGGGACAAATAATACACATTACTTTTCACAAT	96 98
Db	874	TGTGATACAAAGTGCACCAACCCCTCATGGGGCCTTAACACGTAATGTTCTCTTTTCGAAC	93 38
QY	970	GTCACCCCACTGACAAATAGTGAAGTCCCCCAATATGTAATAATCGAGAAGTTGGCTTA	102 98
Db	934	GTACATCCCATCCTACTTTGAGAAATGCCCAATATGTTAAAGCACCAACTGGAATG	99 38
QY	1030	GCAACGAGCTAAGGAATGTTCGCCGATTTGAATCAAGAGATTTGTTGGGCAATAGCT	108 98
Db	994	GCAACGAGCTAAGGAAGCTCCCTTATTAATCAACGAGAGACTTTTCGAGCAAAATGCT	105 38
QY	1090	GCTTTTATAGAAAGAGATGCGAAGGAATGTTGACGTTGGATGATACCATCAGAC	114 98
Db	1054	GGATTCATTGAAGAGAGATGCAAGGAATGATAGATGGGTGGTATGCTATCACCATGAC	111 38
QY	1150	AATGACACAGGATCAAGGATGATGACAGACACAAGAAATCCACTCAAAAAGCAATTTGATGA	120 98
Db	1114	AATGACACAGGATCTGGTTACGACGCTGATCAAGAAAGCACAAATTTGCAATTAACGGG	117 38
QY	1210	ATCACCACACAGGTAATCTGTGATGTAAGATTAACACCCAAATTTGAACCTGTGGG	126 98
Db	1174	ATCAGCAACAAGTGACTCACTAATTTGAGAAATGAACACTCAATTCACCTGACGTGGCC	123 38
QY	1270	AAAGATTTGGTAACTTGAGAAAAAGCTGGAGAACTTGAAACAAAAGATGGAACAGGG	132 98
Db	1234	AAGGAATTCAGATCTAGAAAAAAGAGATTGAGAAATTTGAATAAGAAAGTGCATGATGG	129 38
QY	1330	TTTTCAGATGTGTGACATACATACATCTGAGCTTTAGTTCTGTATGGAATAATGAGACACA	138 98
Db	1294	TTTTTGGATGTTTGAACATTAATATCTGATGTCGCTTTTGGCTCGAACAACGAAGGACT	135 38
QY	1390	CTTGACTTTCATGATTTCAATGTCAAAGATCTGATAGTAAAGTGCAGAAATGCAGCTGACA	144 98
Db	1354	CTAGATTTCCATGACTTTTAACTTAAGAAATTTATTTGAAAAGGTCAAGTCACAATTTGAGA	141 38
QY	1450	GACAACTGCAAGAACTAGAAATGAGATTTTGAATTTTATCAACAAATGTGATGATGAA	150 98
Db	1414	AACATGTCCAAGAAATGCGGAATGTTGTTTGGATTCTATCACAAAATGTGATGACGAA	147 38
QY	1510	TGCATGATAGTGGTAAAAAGGGGACATATGATTAATCCCAAGTATGAAGAAAGCTTAA	156 98
Db	1474	TGCATGAAAGACGTTAAAGAAATGGCACATATTAATCAACCCCAATATTCAGAGAAATCCAA	153 38

QY 1570 CTAATAAGAAATCAATCAAAAGGGTAAATTTGACGACGATGGGGGTTATCAAAATCCT 162

Db 1534 TTCAATATGACAGGAAATATACGGTGTGAACCTAGCAATCAATGGAGCTTTTACCAAGATTTTG 1593

QY 1630 GCCATTATAGCTACAGTATGACAGCTCTCATGTCACTGGCAATCAATGATGGCTGGAGATCTT 1689

Db 1594 GCATCTACTCCACAGTGCGCCAGTTCCCTGGTCTTGTATGCTTCCTCGGGGCAATCAAGC 1653

QY 1690 TTCTGGGATGCTCCCAAGGGGCTCTCGCAGTGCAGATTCGATATGA 1737

Db 1654 TTCTGGATGTGTTAATAGGCGCATTCGAATGCAGATATGCATTTAA 1701

```

RESULT 12
US-08-686-968C-226
: Sequence 226, Application US/08686968C
: Patent No. 6221361
:
: GENERAL INFORMATION:
: APPLICANT: Cochran, Mark D.
: APPLICANT: Cochran, David E.
: TITLE OF INVENTION: Recombinant Swinepox Virus
: FILE REFERENCE: 39119-H/JML
: CURRENT APPLICATION NUMBER: US/08/686, 968C
: CURRENT FILING DATE: 1996-07-25
: NUMBER OF SEQ ID NOS: 231
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 226
: LENGTH: 1721
: TYPE: DNA
: ORGANISM: Swinepox virus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1707)
:
: (S-08-686-968C-226

```

Query Match	39.7%;	Score 707.4;	DB 3;	Length 1721;
Best Local Similarity	64.4%;	Pred. No. 1.3e-202;		
Matches 1078;	Conservative	0;	Mismatches 591;	Indels 6;
				Gaps 1

QY	1	TTTACAGCAGTGTGGAGGGGACAGATATCCATTGCGATGGATTTACCATGCCAATATATTCACAGAG	13
Db	43	TTTACAAACGCAATATCAGACACATATATGATAGTTTACCATGCAAAATATATTCAACTGAC	10
QY	136	AAGCTGACACAAATTCTAGAGCGGAACGTCATCTGTACTCATGCCAAAGCACAATCCTTGAG	19
Db	103	ACTGTTGACACAACTACTGTAGAAAAAGATGTACAGTAACACACTCTGTTAACCTTACAGAA	16
QY	196	AAGACCCATTAACGGAAGTTATGCAAACTAAACGGATCCCTCCCACTTGAACCTAGGGGAC	25
Db	163	GACAGACATTAACGGGAACCACTATGTATTAAGAGGGGTATGCCCCATTGCATTGGGTAAA	22
QY	256	TGTAGCATTTGCCGATGGCTCCTTGGAAATCCCAAAATGTATAGGCTTTCTAAGTGTGCA	31
Db	223	TCTAACATTGTGGATGGCTCCTGGGAAACCAAGGTGTGATTTACTATTCACACAGAC	28
QY	316	GAAAGCTCCTATATATTTGGAGAAGAAAACCCGAAGACGGTTTGTGTTATTCAGGACGC	37
Db	283	TCATGTCTTACATTTCTGGAAACATCTAATTCAGACAAATGGACATGTTTACCAGAGAT	34
QY	376	TTTCATGATTTGAAGAATTGAAACATCTCCCTACAGACGTGAACATTTGGAGAACTA	43
Db	343	TTTCATCAATTAAGAAGAGCTAAGAGACGTTGACCTCAGTGTCTCATTTTGAAAGATTT	40
QY	436	AAGATTTCTGCCCAAGATAGAT-----GACACACGATATCAACCAACAGGAGGTTTCACGG	48
Db	403	GAGATATTTCCCAAGGCAAGTTCATGCGCCCATCTGTAACAGCAATATAGTGTGACGCCA	46
QY	490	GCTTCGCGGTGTCTGCTAATTCATCATTTTTCAGGAACATGTGTGCTGTACAAAGGAA	54
Db	463	GCATGCTCTTAATGAGCAACACAGTCTTACAGAAACTTAATATGCTGTGTAAGAAAA	52
QY	550	GGATAGATTTATCCGGTTGCCAAAGATTCGTACAACTATACAGCGGAGAACTAATCTTA	60

Db 523 GGAATTCATACCCCAAGCTCAGCAAAATCCATATATTAACATTAAGAGAAAGATCCTC 582
QY 610 ATATTTGGGGGGTCCACCATCCATGATGAGACAGACAAAGAACATTTTACCAGAT 669
Db 583 GTGCTATGGGGGCTCACCATCCACCTACAGTACTGACCAACAAAGCTCTCTACAGAT 642
QY 670 GTGGAACTATGTTTCCGTAGGACATCAACATTTGAACAAAGTCAACCCAGAAATA 729
Db 643 GCATATGCCCTATGTTTGTGGGGTCAATCAAAATACAAAGAAATTCAGCCAGAAATA 702
QY 730 GCAACAAAGCCCTAAATGATATGCAAGAGAGTGAATGAATTCCTTGGACCCCTCTG 789
Db 703 GCAACAGACCCCAAGTGAAGAGTCAAGAGGAGAAATGAATCTTACTGACCTAGTA 762
QY 790 GATATGGGACATTAATTTAGAGTACTGTATCTAATTTGACCCAGATTAAGA 849
Db 763 AAGCTGAGACACATATACATTTGAGCAACTGAAATCTAGGTGTCAGAAATATGCC 822
QY 850 TTCAAAATATCGAAAGAGGTAGTTCAAGGATCATGAACAGAAAGACACTTGAGAAC 909
Db 823 TTCCCATGAAAGAGGTTCGATCTGATTTATTCATTTTCAGATACACAGTCCAGAT 882
QY 910 TGTAGACCAATATCAAACTCTTTGGAGCAATTAATACACATTACCTTTTCAAT 969
Db 883 TGTATATGAGCTTGTCAACACCCCAAGGTCTTATTAACACACCTCTTCATTCAGAA 942
QY 970 GTCCACCACCTGACAAATAGGTGAGTGGCCCAATATGTAATGGAAGTGTCTTA 1029
Db 943 ATATATCCAGTCAATTTGAGAAATGTCCAAATATGTCAAAACACAAATTTAGATG 1002
QY 1030 GCAACAGGACTAGAAATGTTCCCAATGTAATCAAGAGATGTTTGGGGCAATAGCT 1089
Db 1003 GCTACAGAGATTAAATATATCCCTATATCAATCTAGAGCCCTGTTTGGAGCATTTGCT 1062
QY 1090 GGTTTTATAGAGAGAGATGCAAGAGATGTTACGTTGTTTGTATTCATCAACAGC 1149
Db 1063 GGCCTTTATGAGGGTGAAGAGATGAGATGATGCTGCTGCTTATCACCATCAG 1122
QY 1150 AATGACAGGAGATGAGGATATGACAGACAAAGATCCACTCAAAAGGCAATTGATGGA 1209
Db 1123 AATAGAGAGGATGAGATATGACGCCAGCCGAAAGAGCACACAAATGCAATTTGACGG 1182
QY 1210 ATCACCAACAGGTTAAATTTCTGATGTAAGAAAGATAACACCCATTTGAAGCTTTGG 1269
Db 1183 ATCACTAACAAAGTAACTCTGTTATGAAAGATGAACACACATTCACACGAGTGGT 1242
QY 1270 AAAAATTCGGTAATTAGAGAAAGAGCTGAGACATTTGAACAAAGAGTGAAGACGG 1329
Db 1243 AAAAATTTCAACCCCTGGAAGAAAGAAATGAGAAATTTAAACAAAGGTTGATGATGCT 1302
QY 1330 TTTCTAGATGTTGATGATCAATGCTGAGCTTTTACTGATGGAAGAAATGAGAGACA 1389
Db 1303 TTTCTGATGTTTGSACTTACAAATGCCAGCTGTTGGTTCTATTTGAAAGAAAGAACT 1362
QY 1390 CTGACTTTGATGTTCTAATGTCAGAAATCTGTAAGTAAAGTCAGAAATGCACCTGAGA 1449
Db 1363 TTGATTTATCAGCTTCAAAATGTGAAGACCTATATGAGAAAGTAAAGACACTAAA 1422
QY 1450 GACACGTCAAAGTACTAGAGAAATGATGTTTCAATTTTATCAAAATGATGATGAA 1509
Db 1423 AACATGCCAAGGTAATGGAAGGCTGCTTGAATTTTACCCAATATGATGAGACGC 1482
QY 1510 TGCATGATAGTGTGAAAGACGGCATATGATTTCCCAAGTGTGAAGAAAGATCTAAA 1569
Db 1483 TGCATGAGAGCGCTCAAAATGAGACTTATGATTTACCCAAATATCTAGAGAGAAAGAAA 1542
QY 1570 CTAATATGAATGTAATCAAGGGGTAAATTTGAGACGATGGGGGTTTATCAAAATCCT 1629
Db 1543 CTAACAGAGAGGATGATAGATGGGTTAAGCTGGAATCAACAAAGATTTTACCAATTTG 1602
QY 1630 GCCATTTATGCTAATAGTAGAGGTTCTATGTCATGCGCAATCATGATGGCTGGATCTCT 1669
Db 1603 GCGATTTATTCATTTGCGCAGTTTCATTTGCTACTGTTAGTCTCCCTGGGGGCAATCAGT 1662

QY 1690 TTCTGGGTCGTCACAGGGCTCTGCGAGTCAGAGATTCGATATGATTATAG 1744
Db 1663 TTCTGATGTGCTCAATGGGTCTTTACAGTCAGAAATGTATTTAAATTAG 1717

US-08-453-848-B
Sequence 8, Application US/08453848
Patent No. 5853368
GENERAL INFORMATION:
APPLICANT: Smith, Gale Eugene
APPLICANT: Volovitz, Franklin
APPLICANT: Wilkinson, Bethanie Elident
APPLICANT: Voznesensky, Andrei I.
APPLICANT: Hackett, Craig Stanway
TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,848
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/120,607
FILING DATE: 13-SEPT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MGS101CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1766 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Influenza virus
INDIVIDUAL ISOLATE: A/Texas/36/91 rHA
FEATURE:
NAME/KEY: polyhedrin mRNA leader (partial)
LOCATION: 1 to 18
FEATURE:
NAME/KEY: coding region for AcNPV 61k protein signal
NAME/KEY: peptide
LOCATION: 19 to 72
FEATURE:
NAME/KEY: SmaI restriction site
LOCATION: 76 to 81
FEATURE:
NAME/KEY: KpnI restriction site
LOCATION: 82 to 87
FEATURE:

	CORRESPONDENCE ADDRESS:	
	ADDRESSEE: Patricia L. Pabst	
	STREET: 2800 One Atlantic Center	
	STREET: 1201 West Peachtree Street	
	CITY: Atlanta	
	STATE: GA	
	COUNTRY: USA	
	ZIP: 30309-3450	
	COMPUTER READABLE FORM:	
	MEDIUM TYPE: Floppy disk	
	COMPUTER: IBM PC compatible	
	OPERATING SYSTEM: PC-DOS/MS-DOS	
	SOFTWARE: PatentIn Release #1.0, Version #1.25	
	CURRENT APPLICATION DATE:	
	APPLICATION NUMBER: US/09/169,027	
	FILING DATE:	
	CLASSIFICATION:	
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER: US/08/453,848	
	FILING DATE: 30-MAY-1995	
	APPLICATION NUMBER: 08/120,607	
	FILING DATE: 13-SEPT-1993	
	ATTORNEY/AGENT INFORMATION:	
	NAME: Pabst, Patricia I.	
	REGISTRATION NUMBER: 31,284	
	REFERENCE/DOCKET NUMBER: MGS10JCIP	
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: (404)-873-8794	
	TELEFAX: (404)-873-8795	
	INFORMATION FOR SEQ ID NO: 8:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 1766 base pairs	
	TYPE: nucleic acid	
	STRANDEDNESS: single	
	TOPOLOGY: linear	
	MOLECULE TYPE: DNA (genomic)	
	HYPOTHETICAL: NO	
	ANTI-SENSE: NO	
	ORIGINAL SOURCE:	
	ORGANISM: Influenza virus	
	INDIVIDUAL ISOLATE: A/Texas/36/91 rHA	
	FEATURE:	
	NAME/KEY: polyhedrin mRNA leader (partial)	
	LOCATION: 1 to 18	
	FEATURE:	
	NAME/KEY: coding region for AcNPV 61k protein signal peptide	
	NAME/KEY: 19 to 72	
	LOCATION: 19 to 72	
	FEATURE:	
	NAME/KEY: SmaI restriction site	
	NAME/KEY: 76 to 81	
	LOCATION: 76 to 81	
	FEATURE:	
	NAME/KEY: KpnI restriction site	
	NAME/KEY: 82 to 87	
	LOCATION: 82 to 87	
	FEATURE:	
	NAME/KEY: SmaI restriction site	
	NAME/KEY: 88 to 93	
	LOCATION: 88 to 93	
	FEATURE:	
	NAME/KEY: coding region for mature rHA	
	NAME/KEY: 73 to 1734	
	LOCATION: 73 to 1734	
	FEATURE:	
	NAME/KEY: KpnI restriction site	
	NAME/KEY: 1744 to 1749	
	LOCATION: 1744 to 1749	
	FEATURE:	
	NAME/KEY: BglII restriction site	
	NAME/KEY: 1750 to 1755	
	LOCATION: 1750 to 1755	
	FEATURE:	
	NAME/KEY: universal translation termination signal	
	NAME/KEY: 1756 to 1766	
	LOCATION: 1756 to 1766	
	US-09-169-027-8	

	Matches	1069:	Conservative	0:	Mismatches	578:	Indels	6:	Gaps	1:	
QY	91	GGGACCAAGATATG	ATGATTGATG	ATCATCGCAT	GCCTAATTA	TTCCACAGAGAGAGG	TCGACACA	ATT	150		
Db	91	GGGACCAAGATATG	ATGATTGATG	ATCATCGCAT	GCCTAATTA	TTCCACAGAGAGAGG	TCGACACA	ATT	150		
QY	151	CTGAGAGGGAACG	TCATGCTG	CTCATG	CCAAAGGACAT	CCCTTG	GACAAACCCAT	TTAAGCA	210		
Db	151	CTTGGAGAAACG	TGACAGTAC	GCACAC	TCCTGTGCA	ACCTACTT	GAGAGACAGT	CTACACGA	210		
QY	211	AAGTTAAACAACT	TAACGGAAT	CCCTCC	CTACTT	GAAGTAC	AGGAGG	AGTATGAC	ATTCGCA	270	
Db	211	AAACATATGCG	ATTAAGGAA	TATACCC	CCACTAC	ATGATTTGG	GAATTTG	GACGCTT	CCCGCA	270	
QY	271	TGGCTCTTGG	AAATCAAT	CAAAATG	TGATAG	CGCTTCT	TAAGTGTG	CCGAAAGCT	CTATAT	330	
Db	271	TGGATCTTGA	AAACCCAA	AAATGCG	CAATCAG	CTGTTTCT	TAAGAGAT	CTATGCTT	CTACAT	330	
QY	331	TTGAGAAAGAA	AACCCGAG	AGCGGTT	TGGTTAT	TCAGCAG	CGCTTCA	ATATGAT	TTATGA	390	
Db	331	GCAGAAACCA	CAACCCG	AGATGAA	CAATGTTAT	CCAGGAT	TTATTTG	CCGACAT	ATAG	390	
QY	391	GAATTTGA	AAACATCT	CTCAG	AGCGCT	GAACATTT	CGAGAA	AGTTAA	GATTTCTG	450	
Db	391	GAATTTGA	AAACATCT	CTCAG	AGCGCT	GAACATTT	CGAGAA	AGTTAA	GATTTCTG	450	
QY	451	GATAGAT	-----	GGACAC	ACCATTA	CAACA	CTGAGG	TTGCA	CGGGCC	TCGCGGT	504
Db	451	GAAACCTCAT	GAGCCAC	CAACCG	CTACCA	AAAGAG	TTAAGAGAT	CTATGCT	CCCAT	ATAT	510
QY	505	GGTATTCAT	ATTTT	TTCAG	AGACAT	TGCTTG	CGTAC	AAAGGA	AGGAT	TCAGAT	564
Db	511	GGGAAAGAC	AGTTT	TTAC	AGAAATTT	TCGATG	CGAGG	AGAA	AAATG	CGCTTG	570
QY	565	GTTGGCA	AAGAGT	CGTAC	CAACA	ATATTC	CAAGCG	AGACAA	CAATGCT	TAATTT	624
Db	571	AATCGAC	AGCAAGT	CTTAT	GTAAAC	CACAA	AGAAAG	AAAGT	CTTGT	ACTAT	630
QY	625	CACCATCC	CAATGAT	GAGAC	AGAAC	CAAGAA	CAATTTG	TACAGAA	TGTGGA	CACTAT	684
Db	631	CATCAC	CCGCTTA	CAATTA	AGGAG	ACCAT	CTATCT	ATAC	AGAAAT	AGCTTAT	690
QY	665	TCCGTAG	GCACAT	CAACAT	TTGAC	ACAAAG	GTCAAC	CCCGA	AAATG	CAACA	744
Db	691	TCTGTAG	TGCTT	CACTAT	TATAG	CGAAG	ATTTAC	CCCGA	AAATG	CAACA	750
QY	745	GTAATG	AGCAG	AGG	GTGAT	GAATG	AAATTC	TCTG	TGACCC	TCCTG	804
Db	751	GTAAAG	ATCA	AGAG	GAAG	AAATTA	CTACT	AGGACT	TGCTG	TGGAAC	810
QY	805	ATAAATTT	TGAG	AGTACT	GTATAT	CTAATTT	CCAC	AGATAT	TGATTC	CAAAAT	864
Db	811	ATAATAT	TTTGA	GGCAAT	TGAAAT	CTATAT	TAG	CGCAT	TGATTC	TGCACT	870
QY	865	AGAGT	ATGTTA	GGGAT	CTATG	AAAC	CAGAG	AGAACT	TGGAAC	CTGTG	924
Db	871	GCGTTT	GGGTG	CAGAT	CACTAC	CTCAAC	CCCAAT	CAATG	ATGATG	AGCAGCA	930
QY	925	CAACCTC	CTTTGG	GGCAAT	AAATAT	CAACA	CAATTTAC	CTTTTC	ACAN	TGCTCC	984
Db	931	CAAAAC	CCCCAG	GGGAG	GTATTA	AAAC	GTATG	CTTCTT	CTTCA	GAATG	990
QY	985	ATAGT	AGTAC	CCCCCA	AAATAT	GTAAAT	CGAG	AGAGT	GTGCTT	AGCAAC	1044
Db	991	ATAGAG	AGTGTCC	CAAA	ATATG	TCAG	CGAGT	ACAAA	ATTA	AAGAT	1050
QY	1045	AATGTT	CCCCAG	ATTTGA	ATCAAG	AGATTT	GTGG	GGCAAT	ATAGCT	GTTTTAT	1104
Db	1051	AAACAT	CCCCAT	CAATTC	ATCCAG	AGGTTT	GTGG	AGCCAT	TGCGG	TTTCA	1110
QY	1105	GGAGT	GCAG	AAAGAT	GTTCAG	CGTTG	GTATG	ATACAT	TCAC	AGCAAT	1164
Db	1111	GGGTG	AGCAT	GAATG	ATGAT	GTATG	ATGAT	GTAT	ATC	ATGCA	1170

QY	1165	GGGATGACGAGACGAAGAAGTCCACCTCCTCAAAAGCATTTGATGTGATACCAACAAGSTA	1224
Db	1171	GGCTATGCTGGCGACCAAAAAGCCACACAAATGCAATTAACGGGATTACAAACAAGGTG	1230
QY	1225	AATTCGTGATGTGAAGAAGATTAACACCCCAATTTGAGACTGTGGGAAAGAATTCGTAAAC	1284
Db	1231	AATTCGTGAATCGAAGAAATATGACACTCAATTCACAGCTGTGGGCAAGAATTCACAAA	1290
QY	1285	TTAGAGAAAACACTGGAGAACTTGACACAAAAGATGAGAAGCGGGTTCTTGATGTGTGG	1344
Db	1291	TTAGAAAACAAAGATGGAAGAACTTAAATAAAAAGTTGATGTGATTTCTGACATTTGG	1350
QY	1345	ACATACAACTGCTGAGACCTTTTGTGTTCTGATGGAAAAATGAGAGACACTTGACATCATGAT	1404
Db	1351	ACATTAATATCGACAAATTTTGTGTTCTACTGGAATAATGGAAGGACTTTGGATTTTCATGAC	1410
QY	1405	TCTAATGTCAAGAACTCTGTATAGTAAGTAAGTCAAGATGCAGCTGAGAGACAACGTCACAA	1464
Db	1411	TCAATATGGAAGAAATCTGTATGAGAAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG	1470
QY	1465	CTAGAAATGATGATGTTTGGATTTTATACAAATGTGATGATGATGATGATGATGATGATG	1524
Db	1471	ATAGGGAAGGGGTGTTTGAATTTATATCACAAGGTAAACAATGATGATGATGATGATGATG	1530
QY	1525	AAAAACGGACATATGATTTATTTCCCAAGTATCAAGATCAAGATCAAGATCAAGATCAAG	1584
Db	1531	AAAAATGCACTTATGACTATATCCAAAATATTCGACAGATCAAAAGTTAAACAGGGGAAA	1590
QY	1585	ATCAAGGGGTAAATATGAGCAGCATGGGGGTTTATCAAACTCTTGCCATTTATGCTACA	1644
Db	1591	ATTATGAGAGCAATGGAATGCAATGAGGAGTCAATGATGATGATGATGATGATGATGATG	1650
QY	1645	GTACAGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1704
Db	1651	GTCCGCACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1710
QY	1705	AACGGGCTCTGTCAGTGCAGGATCTGCATATGA	1737
Db	1711	AATGGCTCTTGCAGTGCAGGAATGATGATCTGA	1743

RESULT 15

US-09-197-679A-1

Sequence 1, Application US/09197679A

Patent No. 6287570

GENERAL INFORMATION:

APPLICANT: Foley, Patricia L

TITLE OF INVENTION: Vaccine Against Swine Influenza

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hendricks and Associates

STREET: P.O. Box 2509

CITY: Fairfax

STATE: Virginia

COUNTRY: USA

ZIP: 22031

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/197, 679A

FILING DATE: 23-NO. 6287570-1998

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hendricks, Glenna

REFERENCE/DOCKET NUMBER: foley

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 425-8405

TELEFAX: (703) 425-8406

INFORMATION FOR SEQ ID NO: 1:

Query Match	39.1%	Score 696.4	DB 3	Length 1724
Best Local Similarity	64.3%	Pred. No. 2.6e-199		
Matches 1078	Conservative 0	Mismatches 591	Indels 7	Gaps 2
SEQUENCE CHARACTERISTICS: LENGTH: 1724 base pairs Type: nucleic acid STRANDEDNESS: unknown TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: NO SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-197-679A-1				
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QY	136	AAGGTGACACATCTCTAGAGGGAGCGCTGACTGTGACTGATGCGACGACATCTCTGAG	195	
DB	94	ACGTGTGATACAGTACTAGAAAGAAATGTAACAGTAACACAGCTGTGTAACCTTTAGAA	153	
QY	196	AAGACCCATACAGGAAAGTTATGCAACTAAACGAAATCCCTCCACTTGAAGTAGGGAC	255	
DB	154	GATAGACATACAGGAAACATATGTAACATAAGGGGGGTACCCCATGTGCAATTTGGTTAA	213	
QY	256	TGTAGCATTTGCCGATGGCTCTCTGGAATCCAAATGTGATAGCGCTTCAATGTGACCA	315	
DB	214	TGTAAATTTGCTGATAGGCTCTCTGGAACCCAGAAATGTGATTAATTCATTCACAGAAC	273	
QY	316	GAACGCTCTATATATTGGAGAAAGAAACCCGAGACGGTTTGTTATTCAGGCGAC	375	
DB	274	TCAATGCTTCAATTTGTGAAACATCTTAACCTCAACAAATGGGACATGTTAACCGAGAGAT	333	
QY	376	TTCAATGATTAGAGAAATTTGAACATCTCTCAGACGCGTGAACATTTTCGGAAGTA	435	
DB	334	TTTATCAATTTAGAAAGACTAAGAGAGAGCTTGAAGCTGTCATCATTTTGAAGGTTT	393	
QY	436	AAGATTCTGCCCAAGATAGAT-----GGACACAGCATCAACCACTGGAGTTACGG	489	
DB	394	GAGATTTTCCCAAGCAAGTTCAATGGCCCAACCATGAAGAAAGAGGTGACGCA	453	
QY	490	GGCTGGGGGGTCTGCGTAATCATCATTTTTCAGAAACATGCTGCGCTGACAAAGAA	549	
DB	454	GCATGCTCTTATGCTGAGACAAACGCTTCTACGAAATTTAATATATGCTGTAAAGAAA	513	
QY	550	GGATCAGATTATCCGGTTGCCAAAGAGATCGTACAAACATCAAGCGGAGAACAAATGCTA	609	
DB	514	GGAAATTTATACCCAAAGCTCAGCAAAATTCGATATGTTAACATTAAGAGAAAGAGTCTC	573	
QY	610	ATATATTTGGGGGGTCCACCATTCCTATGATGAGACAGACAAAGAAACATTTGACAGAAAT	669	
DB	574	GTCGATATGGGCGATTTCACCATTCACATACAGTACTGACCAACAAAGTCTTACAGAAAT	633	
QY	670	GTGGGACCTATGTTTCGCTAGGAGCAATCAACATTTGAACAAAGAGTCAACCCAGAAATA	729	
DB	634	GCAGATGCTATATGTTTTTGTGGGGTCAATCAAGTACACAAAGAAATTTCAAGCGAGAAATA	693	
QY	730	GCACAGAGCCCTAAAGTGAATGGAACAGAGAGGTAGATGGAAATCTTTGGAACCTCTTG	789	
DB	694	GCACAAAGACCCAAAGGTGAGAGGTCAAGCAGGGAGATGAATCACTATTAAGTACACTAGTT	753	
QY	790	GATATGTGGGACACCATTAATTTTGAAGATGCTGATATCTAATTTGACACAGATATGGA	849	
DB	754	GAGCCTGGAGACACATTAATTTGGAAGCACTGGAAATCTATGCTGATCAAGATATATCC	813	
QY	850	TTCAAAATATGAAAGAGTAGTTTCAAGGATATGAAACAGAAAGACACTTATAGAAC	909	
DB	814	TTTCGCAATGAAAGAGGTTCTGATCTGATATTAATCATTTTCAGATTAACACAGATCCAGAT	873	
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/product= Stem region of C-terminal domain

EP621339-A2.
26-OCT-1994.
20-APR-1994; 94EP-0302819.
20-APR-1993; 93JP-0115216.
16-MAR-1994; 94JP-0070194.
(TAKI) TAKARA SHUZO CO LTD.
Isegawa Y, Okuno Y, Sasao F, Ueda S;
WPI: 1994-325949/41.
P-PSDB: AAR63588.
Human influenza-A virus haemagglutinin polypeptide(s) - useful in
Influenza-A vaccine composition
Example 1; Page 45-49; 68pp; English.
This sequence was amplified using the primer sequences given in
AA072845:47 and it encodes the hemagglutinin (HA) gene of the H2N2
subtype of human influenza A virus from A/Okuda/57. The protein encoded
by the amplified cDNA contains two conserved regions, the A region, TGLRN
and the B region, GTRNVNVIETK. These regions are close to each other in
the stem of the HA molecule and they represent epitopes which are
recognised by the antibody C179. C179 binds to the stem region of the HA
molecule and thus inhibits the membrane fusion action of the HA molecule
and neutralises the virus. Polypeptide molecules which contain the
conserved peptide regions, A and B, esp. HA molecules lacking the
globular head region, are antigenically equivalent to the stem region
of the HA molecule of influenza A virus. These artificial peptides may
be used as vaccines for prophylaxis of influenza A virus infection.
(Updated on 25-MAR-2003 to correct PN field.)
Sequence 1783 BP; 610 A; 323 C; 424 G; 426 T; 0 other;

Query Match 100.0%; Score 1783; DB 15; Length 1783;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGGCTGACAAAGACAGGGGTTATACCTAGAAAACCAAGCAAAACCAATGCCATCATTT 60
1 CGGCTGACAAAGACAGGGGTTATACCTAGAAAACCAAGCAAAACCAATGCCATCATTT 60
61 TATCTCATTTCTCTGTTACAGAGAGTGAAGGGAGCCAGATATGCAATGGATACATGCC 120
61 TATCTCATTTCTCTGTTACAGAGAGTGAAGGGAGCCAGATATGCAATGGATACATGCC 120
121 AATTAATTCACAGAGAGAGTGCACAAATTTAGAGGGGAAAGCTGACTGACTATGCC 180
121 AATTAATTCACAGAGAGAGTGCACAAATTTAGAGGGGAAAGCTGACTGACTATGCC 180
181 AAGGACATCTTGAGAGAGACCCATTAAGGAAAGTTATGCAAACTAAAGGAATCCCTCCA 240
181 AAGGACATCTTGAGAGAGACCCATTAAGGAAAGTTATGCAAACTAAAGGAATCCCTCCA 240
241 CTTGAACATGAGGAGCTGTAGCATTTGCCGATGGCTCTTGGAAATCCAAATGTGATAGG 300
241 CTTGAACATGAGGAGCTGTAGCATTTGCCGATGGCTCTTGGAAATCCAAATGTGATAGG 300
301 CTTCTAAGTGTGCCAGAACGGTCTATATATTTGGAGAAAGAAAACCCGAGAGAGGTTTG 360
301 CTTCTAAGTGTGCCAGAACGGTCTATATATTTGGAGAAAGAAAACCCGAGAGAGGTTTG 360
361 TGTATCCAGAGGAGCTTCATATGATTAATGAAGAAATGAAACATCTCTCAGACGCTGAAA 420
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421 CATTTGAGAAAGTAAGAATTTCTGCCAAAGATAGATGAGACAGCATACAACTGGA 480
421 CATTTGAGAAAGTAAGAATTTCTGCCAAAGATAGATGAGACAGCATACAACTGGA 480
481 GGTTCACGGGCTGCGGGGTGTCTGTAATCATCATTTTTCAGGAACATGTCGCTG 540
481 GGTTCACGGGCTGCGGGGTGTCTGTAATCATCATTTTTCAGGAACATGTCGCTG 540
541 ACAAGGAAGATCAGATTTATCCGTTGCCAAAGATGTCACCAATTAACAGGGGAA 600
541 ACAAGGAAGATCAGATTTATCCGTTGCCAAAGATGTCACCAATTAACAGGGGAA 600
601 CAATGCTAATTAATTTGGGGGGTGCACCATTCATATGAGACAGAAACAAATG 660
601 CAATGCTAATTAATTTGGGGGGTGCACCATTCATATGAGACAGAAACAAATG 660
661 TACCAAGATGTGGGAGCTATGTTCCGTAGGCATCATACATTGAAACAAAGTCAAC 720
661 TACCAAGATGTGGGAGCTATGTTCCGTAGGCATCATACATTGAAACAAAGTCAAC 720
721 CCAGAAATAGCAAGAGCTTAAGTGAATGACAGAGGTAGAAATGGAATTCCTTGG 780
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781 ACCCTTTGATATGTGGGACACCATTAATTTGAGAGTACTGTAATCTAATTCAGCA 840
781 ACCCTTTGATATGTGGGACACCATTAATTTGAGAGTACTGTAATCTAATTCAGCA 840
841 GAGTATGATCAAAATATGGAAGAGTGTCCAGGATTCATGAAACAGAGAAACA 900
841 GAGTATGATCAAAATATGGAAGAGTGTCCAGGATTCATGAAACAGAGAAACA 900
901 CTTGAGAACTGTGAGACCAATGCCAAATCCTTTGGAGCAATTAATCAACATTAAC 960
901 CTTGAGAACTGTGAGACCAATGCCAAATCCTTTGGAGCAATTAATCAACATTAAC 960
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961 TTTACAGATGTCCCAACAGCAGCAATATGAGTGTGACCCCAATATATGTAATTCGAGAG 1020
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1021 TTGGCTTTACCAAGAGACTAAGAAATGTTCCCAAGTGAATCAAGAGATTTGTTGG 1080
1081 GCAATAGCTGTTTATAGAAGAGATGAGCAAGATGTTGACGTTGATGATGATAC 1140
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1141 CATCAGAGCAATGACAGGGATGAGGTATGACGACAGACAAAGAAATCCACTCAAAAGGCA 1200
1141 CATCAGAGCAATGACAGGGATGAGGTATGACGACAGACAAAGAAATCCACTCAAAAGGCA 1200
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1261 GCTGTTGGCAAGAAATTCGTTAAGTGAAGAAAGACTGGAGACCTTGAAACAAAGATG 1320
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1321 GAAGAGGGGTTCTAATATGTGTGACATCATGCTGACCTTTTGTCTGATGGAAT 1380
1321 GAAGAGGGGTTCTAATATGTGTGACATCATGCTGACCTTTTGTCTGATGGAAT 1380
1381 GAGAGGACACTTGACTTATCATGATTTATGTCAGAAATCTGTATAGTAAGTCAATG 1440
1381 GAGAGGACACTTGACTTATCATGATTTATGTCAGAAATCTGTATAGTAAGTCAATG 1440
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1501 GATGATGAATGATGATATGTTGTAAGAAAGGGGACATATGATTTATCCCAAGTATGAAGA 1560


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DB 961 CAATGTCACACCACTGACATAGTGTAGTCCCAATATGTAAATCGSAGAAGTTGCT 1020
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DB 1021 CTTAGCAACAGAGCTAGGAATGTTCCCAAGATTGATCAAGAGATGTTTGGGCAAT 1080
QY 1086 AGCTGCTTTTATAGAGAGAGATGGCAAGAAATGTTGAGGTTGATGATACCATCA 1145
DB 1081 AGCTGCTTTTATAGAGAGAGATGGCAAGAAATGTTGAGGTTGATGATACCATCA 1140
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DB 1141 CAGCAATGACACAGGATGACAGGATGACAGACAAAGAAATCCACTCAAAAGGCATTGA 1200
QY 1206 TGGAAATCACCACCAAGTAAATCTGTAATGTAAGAAATTAACACCAATTTAACTGCT 1265
DB 1201 TGGAAATCACCACCAAGTAAATCTGTAATGTAAGAAATTAACACCAATTTAACTGCT 1260
QY 1266 TGGGAAAGAAATTCGTAATGTAAGAAAGACTGAGAACTTGAACAAAAGATGAGAGA 1325
DB 1261 TGGGAAAGAAATTCGTAATGTAAGAAAGACTGAGAACTTGAACAAAAGATGAGAGA 1320
QY 1326 CCGGTTTCTAGATGTTGACATACATGCTGACCTTTTATGTTCTGATGGAATGAGAG 1385
DB 1321 CCGGTTTCTAGATGTTGACATACATGCTGACCTTTTATGTTCTGATGGAATGAGAG 1380
QY 1386 GACACTTGACTTTCATGATTTCAATGTCAGAAATCTGTATAGTAAGTCAGATGAGCT 1445
DB 1381 GACACTTGACTTTCATGATTTCAATGTCAGAAATCTGTATAGTAAGTCAGATGAGCT 1440
QY 1446 GAGACACAACTGCAAGAACTAGAGAAATGATGTTTGAATTTATCACAATGTGATGA 1505
DB 1441 GAGACACAACTGCAAGAACTAGAGAAATGATGTTTGAATTTATCACAATGTGATGA 1500
QY 1506 TGAATGCAATGATGATGTAAGAAAGGAGCATATGTTATCCCAATGATGAGAGAGTC 1565
DB 1501 TGAATGCAATGATGTAAGAAAGGAGCATATGTTATCCCAATGATGAGAGAGTC 1560
QY 1566 TAAATTAATAGAAATGAAATCAAGGGGTAAATATGACAGCATGGGGTTTATCAAT 1625
DB 1561 TAAATTAATAGAAATGAAATCAAGGGGTAAATATGACAGCATGGGGTTTATCAAT 1620
QY 1626 CTTTCCCATTTATGCTACAGTAGACAGTCTATGTCACATGCAATCATGATGAGTGGAT 1685
DB 1621 CTTTCCCATTTATGCTACAGTAGACAGTCTCTGTCACATGCAATCATGATGAGTGGAT 1680
QY 1686 CTTTTCGCGGTGCTCCACAGGGTCTGTGACAGTCAGATCTGATATGATTAAGT 1745
DB 1681 CTTTTCGCGGTGCTCCACAGGGTCTGTGACAGTCAGATCTGATATGATTAAGT 1740
QY 1746 CATTTTATTAATTAATAAACACCTTGTCTGCT 1778
DB 1741 CATTTTATTAATTAATAAACACCTTGTCTGCT 1773

```

RESULT 3
AA064452
ID AA064452 standard; cDNA to mRNA; 1728 BP.

AC AA064452;
DT 11-JAN-1995 (first entry)
DE A/Tzumi/5/65 human influenza A type virus plasmid fragment.
XX
KW Antigens: main region; hemagglutinin; H1N1; H2N2; subtype: human;
KW Influenza A type virus; H3N2; anti-human influenza virus antibody;
KW diagnosis: prevention; treatment; vaccine; ss.
OS Synthetic.
XX
PN JF06100594-A.

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XX 12-APR-1994.
PD 17-SEP-1992: 92JP-0272538.
PF 17-SEP-1992: 92JP-0272538.
PR 17-SEP-1992: 92JP-0272538.
XX (TAKI) TAKARA SHUZO CO LTD.
PA WPI; 1994-156655/19.
XX
XX Anti human influenza virus antibody - for diagnosis and treatment
PT of influenza type A virus
XX
XX Disclosure: page 14; 18pp; Japanese.
PS
CC The sequences given in AA064451-65 represent fragments of plasmids which
CC encode antigenic peptides from the H1N1, H2N2 or H3N2 subtypes of human
CC influenza A type virus. These sequences were derived by PCR using the
CC primer sequences given in AA062141-50 and AA064439-50. The amplified
CC sequence encode at least one antigen which is derived from the main
CC region of hemagglutinin of the H1N1, H2N2, or H3N2 subtype of human
CC influenza A type virus. The anti-human influenza virus antibody of the
CC invention, is reactive against antigens derived from the H1N1 and H2N2
CC subtypes but not against H3N2 subtype derived peptides. This antibody
CC is useful for diagnosis, prevention and treatment of human influenza A
CC type virus. The antigenic peptides are important in vaccine production.
XX
SQ Sequence 1728 BP; 599 A; 318 C; 407 G; 404 T; 0 other:

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Query Match 90.1%; Score 1606.4; DB 15; Length 1728;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 1652; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

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QY 27 ATGAAACCAACCAACCAACCAATGCGCATATTTATCTCTCTGTTACAGACAT 86
DB 1 ATGAAACCAACCAACCAACCAATGCGCATATTTATCTCTCTGTTACAGACAT 60
QY 87 GAGAGGGGACGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 146
DB 61 GAGGGGGGACGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 147 AATCTAGACGCGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 206
DB 121 AATCTAGACGCGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 207 CGGAAAGTTATGCAACCACTAAACGGAATCCCTCCACTGTAATAGGGAGCTGACATTC 266
DB 181 CGGAAAGTTATGCAACCACTAAACGGAATCCCTCCACTGTAATAGGGAGCTGACATTC 240
QY 267 CGGATGGCTCTTGGAAATCCCAATGATGATGATGATGATGATGATGATGATGATGAT 326
DB 241 CGGATGGCTCTTGGAAATCCCAATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 327 TATATTTGAGAAAGAAACCCGAGAGAGCGTTTGTGTTATCCAGGACGCTTCAATGATTA 386
DB 301 TATATTTGAGAAAGAAACCCGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 387 TGAAGAAATTTGAACATCTCTCTGACAGCGTGAACATTTTGAAGAAATGATTTGCTGCC 446
DB 361 TGAAGAAATTTGAACATCTCTCTGACAGCGTGAACATTTTGAAGAAATGATTTGCTGCC 420
QY 447 CAAGATAGATGAGACACAGCATACAACTGAGAGGTTTCAAGGCGCGCGCGGTGCTGG 506
DB 421 CAAGATAGATGAGACACAGCATACAACTGAGAGGTTTCAAGGCGCGCGCGGTGCTGG 480
QY 507 TAATTCATCATTTTTCAGAAACATGTTGCTGCTGCAAAAGAAAGATACATTTATCCGCT 566
DB 481 TAATTCATCATTTTTCAGAAACATGTTGCTGCTGCAAAAGAAAGATACATTTATCCGCT 540
QY 567 TGCCAAAGAGATCGTACAAACATTAACAGCGAGAAACAAATGCTATATTTGGGGGCTGCA 626
DB 541 TGCCAAAGAGATCGTACAAACATTAACAGCGAGAAACAAATGCTATATTTGGGGGCTGCA 600

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Oy	07	ATGCGAAGAAATGGTTGACGGTGGTAGATGCCATCACAGCAATGACGAGGA
Dd	1081	ATGGCAAAGAATGTGGTAGTGCTATGATACCATCACAACATGACCAAGGA
Oy	1167	GTAATGAGAGACAAAGATCCACTAAAAGCATTTGATGGAAATCCAAACAG
Dd	1141	GTAATGAGAGACAAAGATCCACTAAAAGCATTTGATGGAAATCCAAACAG
Oy	1227	TTCCTGATTTGAAAAAGATAAACACCCAAATTGAAAGCTTTGGGAAAGATTGGGT
Dd	1201	TTCTGTGATTTGAAAAAGATGAACACCCAAATTTGAAGCTGTGGGAAAGATTCAATP
Oy	1287	AGAGAAAAGACTGAGAGAACTTGAACAAAAGATGGAAACGGGTTTTCAATGTGT
Dd	1261	AAGAGAAAAGACTGAGAGAACTTGAACAAAAGATGGAAACGGGTTTTCAATGTGT
Oy	1347	ATACAACTCTAGCTTTTAACTTGATGGAAATGAGAGACACTTACTTTGATG
Dd	1321	ATACAACTCTAGCTTTTAACTTGATGGAAATGAGAGACACTTACTTTGATG
Oy	1407	TAAATGCAGAAATGCTATAGTAATGAATCGAAATGACGTGAGACACAACGTCAAAG
Dd	1381	TAAATGCAGAACTGATGATATAAAGTCAGAAATGACGTGAGAGACAACGTCAAAG
Oy	1467	AGGAAATGATGTTTGAATTTATACAAATGTGATGAAATGCAATGAATATGTG
Dd	1441	AGGAAATGATGTTTGAATTTATACCAATGTGACATGAAATGCAATGAATATGTG
Oy	1527	AAAGGGACATATGATTTATCCAGATGTAAGCAAGAGCTTAACTAAATAGAAATG
Dd	1501	AAAGGGACATATGATTTATCCCAAGATGTAAGCAAGAGCTTAACTAAATAGAAATG
Oy	1587	CAAGGGGTAAATTTAGCAGCATGGGGTTTATCAAAATGCTGCCATTAATGCTAA
Dd	1561	CAAGGGGTAAATTTAGCAGCATGGGGTTTATCAAAATGCTGCCATTAATGCTAA
Oy	1647	AGCAGGTTCTATATGTCACCTGGCAATCATGATGSGCTGGGATCTTTCTGGGTGCT
Dd	1621	TGCAGGTTCTCTCTCACTGCAATCATGATGSGCTGGGATCTTTCTGGATGCTCT
Oy	1707	CGGGTCTCTCAGTGCAGAGATCGCATATGATTTAATGATCATTTTATA 1754
Dd	1681	CGGGTCTCTCAGTGCAGAGATCGCATATGATTTAATGATTTTATATA 1728
RESULT 5		
AAQ72806		
ID	AAQ72806	standard; cdna: 1135 BP.
XX	AAQ72806;	
AC	AAQ72806;	
XX	25-MAR-2003	(updated)
DT	22-JUN-1995	(first entry)
DE	DNA encoding stem region of A/Oxuda/57 influenza virus.	
XX	Conserved peptide: stem region: hemagglutinin: HA; H1N1; H2N2;	
KM	subtype: human; Influenza A virus; immunogenic artificial peptide:	
KW	antigen; vaccine; infection; ss.	
XX	Human influenza A virus.	
OS		
XX		
FH	Key	Location/Qualifiers
FT	CDS	46..1092
FT		/tag= a
XX	EP621339-A2.	
PN	26-OCT-1994.	
PD		
XX	20-APR-1994;	94EP-0302819.
PF		
PR	20-APR-1993;	93JP-0115216.

PR 16-MAR-1994; 94JP-00701194.
 XX (TAKI) TAKARA SHUZO CO LTD.
 PA
 XX Isegawa Y, Okuno Y, Sabsao F, Ueda S;
 PI WPI: 1994-325949/41.
 XX P-PSDB: AAR63589.
 DR
 XX Human influenza A virus haemagglutinin polypeptide(s) - useful in
 PT influenza A vaccine composition
 PS
 XX Claim 17: Page 50; 68pp; English.
 PS
 XX This sequence encodes the stem region of the haemagglutinin (HA) molecule
 CC of the A/Osaka/57 strain of human influenza A virus. This antigenic
 CC molecule contains the conserved peptides derived from the stem region
 CC of the H1N1 and H2N2 subtypes of human influenza A virus. Immunogenic
 CC polypeptides such as this are antigenically equivalent to the stem region
 CC of the HA molecule of influenza A virus. This artificial peptide may be
 CC used as a vaccine for prophylaxis of influenza A virus infection.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX Sequence 1135 BP; 395 A; 197 C; 265 G; 278 T; 0 other;

Query Match 51.8%; Score 908.8; DB 15; Length 1135;
 Best Local Similarity 98.7%; Pred. No. 2.8e-232;
 Matches 916; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 853 AAATATCGAAGAAGAGTACTTCAGGATCATGAAAACAGAGAGACACTTGAGACTGT 912
 DB 208 AAGTTAAGCAACTTAAACGGATCCGGGATCATGAAAACAGAGAGACACTTGAGACTGT 267
 OY 913 GAGACCAAAATGCCAACTCTCTTGGGAGCAATAAATCAACATTAACCTTTTCAAAATGTC 972
 DB 268 GAGACCAAAATGCCAACTCTCTTGGGAGCAATAAATCAACATTAACCTTTTCAAAATGTC 327
 OY 973 CACCCACTGCAATATGTGAGTGGCCCCCAATATGTAATAATCGGAGAGTGGCTTACGA 1032
 DB 328 CACCCACTGCAATATGTGAGTGGCCCCCAATATGTAATAATCGGAGAGTGGCTTACGA 387
 OY 1033 ACAGGACTAAGGAAATTTTCCCGAGATTGAATCAAGAGATGTTTGGGCAATAGCTGCT 1092
 DB 388 ACAGGACTAAGGAAATTTTCCCGAGATTGAATCAAGAGATGTTTGGGCAATAGCTGCT 447
 OY 1093 TTTATAGAAGGAGAAAGGCAAGATGTTGAGCGTTGATGATCCATCAGCAAT 1152
 DB 448 TTTATAGAAGGAGAAAGGCAAGATGTTGAGCGTTGATGATCCATCAGCAAT 507
 OY 1153 GACCCAGGATCAGGATATGAGAGACAAAGAAATCCACTCAAAAGGCAATTTGATGAAATC 1212
 DB 508 GACCCAGGATCAGGATATGAGAGACAAAGAAATCCACTCAAAAGGCAATTTGATGAAATC 567
 OY 1213 ACCAACAAGTAAATTTCTGTGATTGAAAAGATTAACCCCAATTTGAAGCTTTGGGAAA 1272
 DB 568 ACCAACAAGTAAATTTCTGTGATTGAAAAGATTAACCCCAATTTGAAGCTTTGGGAAA 627
 OY 1273 GAATTCGGTAACTTAAGAAAAGACCTGAGAGACTTGAACAAAAGATGGAAGCGGGTTT 1332
 DB 628 GAATTCGGTAACTTAAGAAAAGACCTGAGAGACTTGAACAAAAGATGGAAGCGGGTTT 687
 OY 1333 CTAGATGTGTGACAAATCAATGCTGAGCTTTTGAATCTGATGAAAATGAGAGACACTT 1392
 DB 688 CTAGATGTGTGACAAATCAATGCTGAGCTTTTGAATCTGATGAAAATGAGAGACACTT 747
 OY 1393 GACTTTCATGATTTCTATGTCAAGAAATCTGTATAGTAAGTCAAGTGCAGCTGAGAGAC 1452
 DB 748 GACTTTCATGATTTCTATGTCAAGAAATCTGTATAGTAAGTCAAGTGCAGCTGAGAGAC 807
 OY 1453 AAGCTCAAGAAGACTAGAAATGATGTTTGAATTTATCACAATGTGATGATGATGC 1512
 DB 808 AAGCTCAAGAAGACTAGAAATGATGTTTGAATTTATCACAATGTGATGATGATGC 867

OY 1513 ATGAATAGTGTGAAAACGGGACATATGATTATCCAAAGTATGAAGAAGACTTAACCTA 1572
 DB 868 ATGAATAGTGTGAAAACGGGACATATGATTATCCAAAGTATGAAGAAGACTTAACCTA 927
 OY 1573 AATGAAATGAAATCAAGGGGTAAATATGAGCAGCATGGGGTTTATCAAAATCCTTGCC 1632
 DB 928 AATGAAATGAAATCAAGGGGTAAATATGAGCAGCATGGGGTTTATCAAAATCCTTGCC 987
 OY 1633 ATTTATGCTACAGTAGAGGTTCTATATGCTACATGCGCATATGATGATTAAGTATTTTA 1692
 DB 988 ATTTATGCTACAGTAGAGGTTCTATATGCTACATGCGCATATGATGATTAAGTATTTTA 1047
 OY 1693 TGGGTGTGCTCCAAAGGGTCTGTCAGTGCAGATGTCATGATGATTAAGTATTTTA 1752
 DB 1048 TGGGTGTGCTCCAAAGGGTCTGTCAGTGCAGATGTCATGATGATTAAGTATTTTA 1107
 OY 1753 TAATTAATAACACCTTTGTTCTGCTAG 1780
 DB 1108 TAATTAATAACACCTTTGTTCTGCTAG 1135

RESULT 6

AAC64297
 ID AAC64297 standard; cDNA; 1770 BP.

AC AAC64297;

DT 23-FEB-2001 (first entry)

DE Influenza virus haemagglutinin (HA) gene.

KW Influenza virus: haemagglutinin; HA; Sendai virus vector;

KW recombinant protein expression; Influenza vaccine; Immunogen;

KS immunoassay; ss.

OS Influenza virus.

PN JP2000253876-A.

PD 19-SEP-2000.

PE 08-MAR-1999; 99JP-0060918.

PR 08-MAR-1999; 99JP-0060918.

PA (DINA-) DINABEKU KENKYUSHO KK.

DR WPI: 2000-624368/60.

DR P-PSDB: AAR29746.

PT A vaccine and a vaccine protein using Sendai virus vector

PS Example 2: Page 17-19; 28pp; Japanese.

XX The invention relates to a Sendai virus vector expressing an influenza
 CC virus protein or a fragment thereof. The invention also relates to
 CC an influenza vaccine comprising the Sendai virus vector of the
 CC invention or a purified influenza virus protein obtained from the Sendai
 CC virus vector; and a method for vaccination against influenza in which
 CC the vaccine is administered to an intermediate non-human animal host of
 CC influenza virus. The invention additionally encompasses a Sendai virus
 CC vector comprising a gene from a pathogenic organism in an expressible
 CC form, the preparation of the expressed protein from the Sendai virus
 CC vector, and the use of the expressed protein as an immunogen or in
 CC immunoassays. The present sequence represents an influenza virus
 CC haemagglutinin (HA) cDNA used in an exemplification of the invention.
 XX

Query Match 47.3%; Score 843; DB 21; Length 1770;
 Best Local Similarity 69.3%; Pred. No. 1.2e-214;
 Matches 1181; Conservative 0; Mismatches 515; Indels 9; Gaps 2;

QY	42	CAAAACAATGGGCATCATTTATCTCAATCTCCGTTTCCAGACAGAGTAGAGGGGACACAGAT	101
Db	16	CAAAATGGAGAAATATAGTCTCTTTTTCCAATAGTCACTCTTGTCTAGAGATGACAGAT	75
QY	102	ATGCATTGGATACCATGTCGAATTAATTCACAGAGAAGGTGACACAAATTCAGAGCGAA	161
Db	76	TTGCATTGGTTTACATATGCAAAACACCAACAAACAGGTGACACAAATTAATGGAAAGAA	135
QY	162	CGTCACCTGGACTCATGCCCAAGAGACATCTCTTGAGAAGACCCATAGCGAAAGTTATGCA	221
Db	136	TTCTTACTGTCACACATATGCCCAAGACACTACTTTAAAAAACACACACGGGAACCTCGCAG	195
QY	222	ACTAAACGGGAATCCCTCCACTTGAACCTAGGAGACTGTAGCATTTGGCGATGGCTCTTG	281
Db	196	CCTAATATGGAGTAGAGCCCTCATTTTGGAGGATGTACTGTAGCTGATGGCTCTCTCG	255
QY	282	AAATCCAAATATGTATAGCTTCTAAGTGTGCCAGACAGGTCTTATATATGTGAGANA	341
Db	256	AAATCCTATGTATGACGAATTCCTTAATGTGGCAGAGTGCTTCACTAGTGAAGAAAGCA	315
QY	342	AAACCCGAGAGACGGTTTGTGTATTCACAGCGAGCTTCAATGATTAATGAAGATTTGAACA	401
Db	316	TATTCAGATCATTTGGCTTTGCTTACCAGAGGATTTCAACGACTAGGAAGACTGAAACA	375
QY	402	TCTCCTCAGCACGCGTGAACATTTTGAGCAAGTAAAGATTTCCCAAGATATGATGAC	461
Db	376	TCTATTAAGTTTACGAAACATTTTGGAGAAATTTGGAATCAATCCCGAGATTTCCGTGCC	435
QY	462	ACAGATATCAACATCTGACGTTCACGG---CCCTGGCGGGTGCTGGGAATTCATCAT	518
Db	436	CAACCATGAGAGCTCATTAGAGTAGCTCTGACTATGCTCATCAATGGAGGTCTTCTT	495
QY	519	TTTCAAGAACATGTCCTGGCTGACAAAGAGATCAGATTATTCGGTTCCTCAAGATC	578
Db	496	TTTTCAGGATGTGATGCTATGCTTATCAAAAAGAACATGATCCCAACATTAAGAGAG	555
QY	579	GTACACACATACAACGGGAGAACAAATGCTAATTTTGGGGGGTGACACATCCCATTTGA	638
Db	556	TTTACGCAATCTAATTAAGAAAGATCTTCTAATCTGTGGGGAATTTACACATCTTAATGA	615
QY	639	TGAGACAGAACAAAGACATTTGTACAGAAATGTGGGAACCTATTTGCCGTAGGCACATC	698
Db	616	TGCACAGAGCAACCAAGCTCTATCAAAACCAACCACTTATGTCTCGCTGGAAACATC	675
QY	699	AACATTTGAACAAAGGTCAACCCCAAAATTAGCAACAAGGCTTAAGTGAATGACACAAG	758
Db	676	AACCTGTGATCCAAATATTCACAAATATCCAAATATCCCTAGGCCCAATTAATGAAGGCAAG	735
QY	759	AGGTGATGATGGAATCTCTGTGAGACCTCTGGATATGTGGGACACATTAATTTGAGAG	818
Db	736	TGGAAGATTTGGAATCTTTTGGACAGATTTTGAAGCAAGTATACCATCAATTTTGAAG	795
QY	819	TACTGGTATCTAATTTGACACAGAGATGATTCAAATATTCGAAAGAGGTAGTTTCAGG	878
Db	796	TAAATGGAACCTCATTTCTCCAGAGATAGCCATTAATTAATTTGCAAGAAGGGGACATCAGC	855
QY	879	GATCATGAAACAGAGAGACACTTGAGACATGTGAGACCAATAGCCAAATCTCTTGGG	938
Db	856	AATCATGAGAAAGTGGATTGGATATGTATACATGCAATACTAATGTCTAAATCCCAATAGG	915
QY	939	AGCAATTAATACAACTTACCTTTTCCACAAATGTCCACCACCTGACAAATAGGTGATGCC	998
Db	916	TGCGATTAATTTCCACATGATCCATTCACAAATATACATCTCTTACATTTGGAGATGGCC	975
QY	999	CAATATATTAATATCGAGAAAGTTGCTTACCAACAGAGACTAAGGAATGTTCCCCAGAT	1058
Db	976	CAAAATACGTAAATTCAGATAGATTTGCTCTTGCACCACTGACAGTCAAGAACACCCCTCAAG	1035
QY	1059	TGAATCA-----AGAGATGTTTGGGGCAATAGCTGGTTTATAGAAAGAGATGAGCA	1112
Db	1036	AAAAAGAAAAAGAGAGGTCTATTTTGGAGCTATGGCAGGCTTCATAGAGGGGGGATGGCA	1095
QY	1113	AGGAATGGTTAGCGTTTGGTATGATATACATCACAGCAATACAGAGGATCAGGTTATGC	1172

Db	1096	GGGAATGTAAGCAGGTTGATAGTTACCACTATAGCAACGACGAGGGAATGCATATGC	1155
QY	1173	ACGACAGCAAGAATCCACTCAAAAAGGCAATTTGATGAAATCACCAACAAGTAAATCTGT	1232
Db	1156	TGCAGACAAAGAATCCACCCAAAAGGCAATAGATGAAATCAACCAATAAAGTCACATCAAT	1215
QY	1233	GATTGAAAAAGATAAACACCCCAATTTGAGAGCTGTTGGGAAABAATTTCCGTAACTTAGGAA	1292
Db	1216	CAATTACAAAATGAACACCCAGTTTGAAGGCAAGTTGGGAAAGAAATTAATTAACCTTAGAGAG	1275
QY	1293	AAGACTGAGAACTTGAACAAAAGAAGATGGAAGAGGGTTTCTAGATGTTGACATACAA	1352
Db	1276	AAGAATAGAAAATTTGAACAAGATTTTGGAAAGACGGTTTCTAGATGTTTGGACTTAATA	1335
QY	1353	TGCTAGACTTTTAGTTTGATGATGGAATAGAGAGCACTTACTTTCAATGATTAATGT	1412
Db	1336	TGCTTAACCTTCTAGTTCTCATGGAATAAGAAAGAACTCTAGATTTTCATGACGCAACGT	1395
QY	1413	CAGAATCTGPTTAGTAAGATGACAAATGCAGTGCAGTGCAGACAAAGCTCAAGAATAGGAA	1472
Db	1396	AAAGAGCCTTTACGACAAAGGTTTCGACTACACTTAAGATTAATGCAAGGAACTGGGTA	1455
QY	1473	TGGAATGTTTGAATTTATVCACAAAATGTGATGATGATGATGAAATAGTGTGAAAAACGG	1532
Db	1456	TGGTTGTTTCGAGTTCTACCAATAAATGTGACAATGATGATGGAAGACATCAAAAAACGG	1515
QY	1533	GACATATGTAATTTCCCAAGPTATGAAGAAGAGAGCTTAACATAATGAATGAATCAAAAGG	1592
Db	1516	AACATATTAACATATCCACAGATATTCGAAGAGAGCAAGACTTAACAGGGAAAGAAATAGTCG	1575
QY	1593	GCTAAATTTGAGCAGCAGATGGGGGTTTATCAAACTCTTGCCATTTATGCTACAGTAGAGG	1652
Db	1576	GATCAAAATTTGCAATCAATGGGAATTTATCAAAATCTGCAATTAATTCACACAGTGGCGAG	1635
QY	1653	TTCTATGTACATGGGAATCATGATGGCTGGGATCTCTTTGGGGTGTGCTCCACAGGGTC	1712
Db	1636	TTCCCTACACTGGGAATCATGATGCTGCTATCTTTCTGGAAATGTCCTCAATGGATC	1695
QY	1713	TCTGCAGTGCAGAGATCTGCAATATGA	1737
Db	1696	ATTGCAGTGCAGAAATTTGCATTAA	1720
RESULT 7			
AAL39863			
ID	AAL39863	standard; DNA; 1773 BP.	
XX	AAL39863;		
XX	AC		
XX	AA		
XX	13-SEP-2002	(first entry)	
XX	DE		
XX	DNA of HA hologene.		
XX	Transgenic crop: fowl virus; avian influenza; Newcastle disease; chicken;		
XX	infective cloacal bursa disease; hologene; plant; feed; HA; ds.		
XX	OS	Unidentified.	
XX	PN	CN1333370-A.	
XX	PD	30-JAN-2002.	
XX	PF	16-AUG-2001; 2001CN-0125352.	
XX	PR	16-AUG-2001; 2001CN-0125352.	
XX	PA	(SHEN-) SHENZHEN SANFANGYUAN INFORMATION TECHNOL.	
XX	PI	Zhong A, Qin Z;	
XX	WP1	2002-292920/34.	

PT Crops capable of resisting virus diseases of poultry and production
PT method thereof -
XX
PS Claim 1; Page 1-2 (Claims); 22pp; Chinese.
XX
CC The invention relates to a transgenic crop capable of simultaneously
CC resisting up to three kinds of fowl viruses of avian influenza, Newcastle
CC disease and infective bursal disease. The invention also relates
CC to the production method of the crop. The method of the invention
CC includes the following processes: insertion of HA, F and VP2 hologene
CC into a plasmid vector; expression of the recombinant plasmid transferred
CC into the plant; pairwise hybridisation of the plants which respectively
CC possess the action of resisting the above-mentioned three viruses or
CC simultaneous hybridisation of three plants. The transgenic seeds can be
CC planted into soil to obtain crops for use as a raw material of feed for
CC poultry with the feed containing a recombinant active protein. This
CC polynucleotide sequence represents the 1773 nucleotide DNA of the HA
CC hologene relating to the invention.
CC
XX
SQ Sequence 1773 BP; 605 A; 336 C; 403 G; 429 T; 0 other;

Query Match 46 48; Score 834.4; DB 24; Length 1773;
Best Local Similarity 69.48; Pred. No. 2.4e-212;
Matches 1183; Conservative 0; Mismatches 501; Indels 18; Gaps 3;

QY 85 GTGAGAGGGAGCCAGTATGCTATTGATACCATTAATATCCACAGAGAGGTGCAC 144
DB 56 GTTAAAGATGATCAGTTTCATTTGGTTACCATGCACACACTGCAGACAGGTTGAC 115
QY 145 ACAATTTCTAGAGGGGAAAGCTGACTGACTCATGCCAAGGACATCCTTGAGAGACCCAT 204
DB 116 ACAATATGAGAAAGATGTTACTTACATGCCACAGACATACCTGAGAAAGACACAC 175
QY 205 AAGGAAAGATTATGCTAACAAACGAAATCCCTCCACTTAATAGAGGACTATGATAT 264
DB 176 AAGGGAGAGCTGCTGCATCTAAATGAGAGGAGCTCTCTATTGAGGGATTGTAGTGA 235
QY 265 GCCGATGAGCTCTCTTGAATCCAAATGATAGGCTTGAAGTGCAGACAGGCTGC 324
DB 236 GCTGATGAGCTCTCTGAAACCTATGTGTGACGAAATTCATCATGTGCCGGAATGTC 235
QY 325 TATATATTGAGAAAGAAAACCCGAGAGCGTTTGTGTTATCCAGGACCTTCATGAT 384
DB 296 TACATAGTGTGAGAGAGCCAGTCCAGCAATGACCTGTATTCAGGGAATTTCAACGAC 355
QY 385 TATGAGAAATTTGAAATATCTCTCAGAGCGTGAATTCGAGAAAGTAAAGATTCTG 444
DB 356 TATGAGAAATCTGAATACCTATTGAGCAGATTAACCAATTTGAGAAATTCATGATC 415
QY 445 CCCAAAGATGATG--ACACAGCATACAACTGAGAGGTTCCAGGCGCTCCGCGGTG 501
DB 416 CCCAAAGTCTTGGTCCATCATGATGCTCATCAAGGGGTGAGCTCAGCATGCTCATC 475
QY 502 TCTGTGTAATCATCATTTTTCAGGAACATGCTGCTGCTGACAAAGAGATGATAT 561
DB 476 CTTCGAGAGGTCTCTCTTTTTCAGAAATGTGTGTATGCTTATCAAAAGAACAGTGCAT 535
QY 562 CGGTTGCCAAAGAGATCGTACACATACAAAGGCGGAACAATGCTAATATTTGGGGG 621
DB 536 CCACACATTAAGAGGAGCTACATTAATTAACCAACCAAGAGATCTTTTGTACTGTGGGG 595
QY 622 GTGCACCATCCCATTTATGAGACAGAAACAAGACATTTGACCAAGATGTGGGACCTAT 681
DB 596 GTTCACCATCTAATATGCGGCGACAGACAAAGCTATCAAAATCCACACACCTAC 655
QY 682 GTTCCGTGAGCCATCAACATTAAGAAAGGTCAACCCAGAGATAGCAACAGGCTT 741
DB 656 ATTTCGTTGGAACATCAACACTGAAACAGAGATGTGTTCCAGAAATAGCTACTAGACC 715
QY 742 AAGTGAATGAGCAAGGAGGTAGATGGAATTTCTTGGACCCCTTGATATGATGTGGAC 801
DB 716 AAGTGAACGGGCAAGGTGAGAAAGATGAGTCTTCTGACAAATTTTAAAGCCGAAATGAT 775

QY 802 ACCATAATTTTGAGAGTACTGCTAATCTAATTGACACAGAGATGATGATCAAAATATGC 861
DB 776 GCCATCAATTTTGAGAGTATGAAATTTTCATTTGCTCCTCAATATGATGATCAAAATGTC 835
QY 862 AAAAGAGTATGTTTCAGGGATCATGAAACAAAGAGAACTTGTGAACTGTGACCAAA 921
DB 836 AAGAAAGGGGAGCTCAACCAATTAATGAAAGAAATTTGAAATGTAACTCAACACCAAG 895
QY 922 TGCCAAACCTCTTTGGGAGCAATTAATACAACTATACCTTTGCAATGTGCCACCCCTG 981
DB 896 TGTCAAACTTCATGAGGGGCGATTAACCTATGATGATGATGATGATGATGATGATGATG 955
QY 982 ACAATAGTATGTCCTCCCAATATGTAATTCGAGAGTGTGCTTTCAGCAACAGACTA 1041
DB 956 ACCATGGGAGATGCTCCCAATATGTAATTCAGAGATGATGATGATGATGATGATGATG 1015
QY 1042 AGCAATGTTCCCAAGATTG-----AATCAAGAGATGTTTGGGCGAATGCT 1089
DB 1016 AGAAATACCCCTCAAG 1075
QY 1090 GGTATTATAG 1149
DB 1076 GGTATTATAG 1135
QY 1150 AATGACGAGGATCAGGGTATGACAGAGACAAAGAAATCCACTCAAAAGGCAATTTGATGA 1209
DB 1136 AATGACGAGGAG 1195
QY 1210 ATCAACCAAGGTAATTTCTGATGTAAGATTAACACCAATTTGAGCTGTTGG 1269
DB 1196 GTCAACCAATTAAGGTAACCTGATCATTAACCAATTAAGGTAACCTGATTTGAGGCG 1255
QY 1270 AAGAAATGCTGATTAAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1329
DB 1256 AGGAAATTAATTAAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1315
QY 1330 TTTCTAGATGTTGAGACATCAATGCTGAGCTTTTATGTTCTGATGAGAAATGAGAGACA 1389
DB 1316 TTTCTAGATGTTGAGACATCAATGCTGAGCTTTTATGTTCTGATGAGAAATGAGAGACT 1375
QY 1390 CTTCGATTTATGATTTATATGTCAGAGATCTGATATGTAAGTCAAGATGACGCTGAGA 1449
DB 1376 CTGACCTTTATGATTTATCAATTAAGTCAAGACCTTTAGCAAGAGTCCGACTACAGCT 1435
QY 1450 GACAGCTCAAAACATGAGAAATGATGTTTGAATTTATCAAAATGATGATGAA 1509
DB 1436 GATATGCAAAAGAGAGCTGGGTATGTTGTTTGAATTTATCAAAATGATGATGAA 1495
QY 1510 TGCATGATATGTTGAAAGAGGAGATATGATTTATCCAAATGAGAGAGAGCTTAA 1569
DB 1496 TGTATGAAAGTGTAAAG 1555
QY 1570 CTAAATGAAATGAAATCAAGGGGTAAATTTGAGCAGCATGAGGGGTTTATCAATCTT 1629
DB 1556 CTAAACGAGAGAGAGAAATTAAGTGAATTTGAAATCAATGAGGAACTTCAAAATCTG 1615
QY 1630 GCAATTTATGCTCAGTAGAGGTTTATGATGCTATGCAATCAATGAGGAGATGCT 1689
DB 1616 TCAATTTATCAACAGTGGGAGATTTCCCTTGCACATGCAATCAATGAGGAGATGCT 1675
QY 1690 TTTCTGAGTGTCTCAACAGGAGCTCTTCAGCTGAGAGATGCAATGATGATTTAT 1746
DB 1676 TTTATGATGTTGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1735
QY 1747 ATTTTATTAATTAAGACCCCT 1768
DB 1736 AGATTTGATTAAGACCCCT 1757

RESULT 8
AAV49294
ID AAV49294 standard; DNA: 1701 BP.
XX

Db 1354 CTAGATTTCATGACTTTAAAGTAAAGATTTATATGAAAGGTCACAGTCACATTCAGA 1413
Oy 1450 GACACAGTCAAGAACTAGAGAAATGATGTTTAAATTTATTCACAAATGATGATGAA 1509
Db 1414 AACATGCCAAGAAATACGGAAATGTTGTTTGTAGTTTCAATCAATGATGATGAGAA 1473
Oy 1510 TGCATGATAGTGTGTAAGAAACGGAGCATATGATATCCAAATGATGAAAGATCTTAA 1569
Db 1474 TGCATGAAAGCCGTAAGAAATGGACATATACACCCCAATATTCAGAAAGATCCAAA 1533
Oy 1570 CTAAATGAAATGAAATATCAAAAGGGTAAATTTAGACAGATGGGGGTTTATCAATCCTT 1629
Db 1534 TTGAATAGAGAGAAATATAGACGGGTGTAAGTAATCAATCAATGAGAGTTTACAGATTTTG 1593
Oy 1630 CCCATTATATGCTATGATAGAGATTTCTATGCTACTGCAATCATGATGCTGGATCTCT 1689
Db 1594 GCGATCTACTCCACATGTCGCCAGTTCCCTGCTTGTAGTCTCCCTGGGGGCAATCAGC 1653
Oy 1690 TTCGGGTGTGCTCAACGGGTCTCTGACGTGACAGATGTCATATGA 1737
Db 1654 TTCGATGTGTCTCAATGGGTCTATTCATTCAGATGATGATTTAA 1701

RESULT 9
AAQ06842 ID AAQ06842 standard; RNA; 1777 BP.
XX
AC AAQ06842:
XX
DT 05-MAR-1991 (first entry)
XX
DE RNA segment 4 coding for HA.
XX
KW Influenza: haemagglutinin; HA: ribosomal frameshift signal sequence;
KW membrane anchor; RFS; S:
XX
OS Influenza virus A/PR8/3:
XX
FH Key Location/Qualifiers
FT CDS 33..1733
FT sig_peptide /*tag= a
FT 33..82 /*tag= b
FT mat_peptide 83..106
FT /*tag= c
FT mat_peptide /*product= HA1
FT 1064..1730
FT misc_RNA /*tag= d
FT 1632..1692 /*product= HA2
FT 1692..1692 /*tag= e
FT /label= insertion site for RFS
XX
XX W09014422-A.
XX
XX 29-NOV-1990.
XX
XX 21-MAY-1990; 90MO-GB00791.
XX
XX 19-MAY-1989; 89GB-0011555.
XX
XX (LYNX-) LYNXVALE LTD.
XX
XX Inglis SC, Brierley I:
XX
XX WPI; 1990-375989/50.
XX
XX Ribosomal frame shifting signal sequences - isolated from
XX PT Infectious bronchitis virus genomic RNA and used in protein
XX PT prodn.
XX
XX PS Disclosure; Fig 19; 55pp; English.

XX The HA gene encodes a spike-like protein which is embedded in the
CC membrane via a hydrophobic anchor sequence. A portion of this
CC anchor sequence may be replaced with a ribosomal frame shift signal
CC sequence (RFS), in such a way that ribosomes translating the new
CC HA sequence will usually terminate before the hydrophobic sequence
CC is encountered, leading to the prodn. of a secreted form of the HA.
CC It has been found that the primary sequence of the RFS can be rad-
CC ically altered as long as the the secondary and tertiary structures
CC are preserved, so it is possible to design an RFS which encodes
CC hydrophobic amino acids, and therefore preserves the integrity of
CC the anchor.
XX See also AAQ06841 and AAQ07007.
SO Sequence 1777 BP; 621 A; 331 C; 408 G; 417 U; 0 other;

Query Match 40.8%; Score 728.2; DB 11; Length 1777;
Best Local Similarity 48.9%; Pred. No. 5.4e-184;
Matches 835; Conservative 276; Mismatches 588; Indels 10; Gaps 2;
Oy 80 CAGCAGTGAAGGGGACCAATATGCAATTTGATACCTGCCATTAATTCACAGAGAG 139
Db CAGCUGCAGAUAGCAGACACAAUUAUAGGCUACUAGCGAACAUAUACAACGACACUG 128
Oy 140 TCACACAAATTTAGACGAGACGTCATGATGATGCAAGGACATCTTGAGAGA 199
Db UUGACACAGUGUCUGAAGAAUAUUGACUGACACACUCUUAUACUCUGCAGACACA 188
Oy 200 CCCATTAAGSAAAGTATGCAAACTAAAGSAAATCCCTCCACTTGAAGGAGCTGA 259
Db GCCACAAAGGAAACUUAUUAAGAAUAGCCCAUACUUAUAGGGAUUAU 248
Oy 260 GCAATGGCGATGGCTGCTGGAATGCAAAATGCTATAGCTTCTAAGTGGCAAC 319
Db ACATGCCGGAUUGUCUUAUAGAAACCCAGAAUAGCCACACUUCUCCAGUGAUAU 308
Oy 320 GATCTATATATTGAGAAAGAAACCAGAGAGGTTGTGTATTCAGAGCACTTCA 379
Db GGUCCUACUUAUUGUAAACACCAACUCUGAAGAAUUAUUAUUAUUAUUAUUAUUA 368
Oy 380 ATGATTATGAGAAATTAACATCTCTCAGACGCTGAAACATTTGAGAAAGTAAGA 439
Db UCGACUUAUAGAGAGCUGAGGAGAGCAUUGAGUCUUAUUAUUAUUAUUAUUAUUA 428
Oy 440 TTCGCCCCAAAGATAGAT-----GACACAGCATCAACACGAGGTTTACGCGCCT 493
Db UAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 488
Oy 494 GCGCGGTGTCTGTATTCATCTATTTTCAGAGAAATGCTGTGCTGACAAAGAGAT 553
Db GCUCCAUUGGGGGAAGACAGUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 548
Oy 554 CAGATTATCGGTTGCCAAAGATGTAACAATACACAGCGGAGAAATGCTAATA 613
Db GCUCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 608
Oy 614 TTGGGGGGGTGACCATCCATGATGAGACAGACAAAGACATCTTACCAAGATG 673
Db UGUUGGUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 668
Oy 674 GAACCTATGTTTCCGTAGGACATCAATTTGAACAAGAGTCAACCCAGAAATAGCAA 733
Db AUGCUUAUUGUCUGUAGUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 728
Oy 734 CAAGCCTTAAGTATGACAAAGAGTGAATGCAATTTCTTGAGACCTCTTGAGATA 793
Db AAAGACCCAAAGUUAAGAUCAAGCUGGGAGUUAUUAUUAUUAUUAUUAUUAUUAU 788
Oy 794 TGTGGACACCAATAATTTAGAGTACGTGATATCAATTTGACAGAGATGATGAT 853
Db CCGGAGACACAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAU 848
Oy 854 AATATGAAAGAGTAGTTTCAAGGATCAATGAAGAGAGACACTTGAGAACTGTG 913

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Db      849 CACUGAGUGAGGCUUUGGUCGCGAUCACCCUCAAACGCAUACUACUAGAGUGUA
Qy      914 AGACCAATGCGCAATCTCTGGGAGCATTAATACATATACCTTTTACAAATGCC
Db      909 ACACGGAAGGUCACAAACCCCGGAGCUDUAAACACGACUCCUCCUUCAGAUUAC
Qy      974 ACCCACTGCAATAGGTGAGTGCCTCCCAATATGTAAATGAGAAAGTTGCTTAGCAA
Db      969 ACCGAGUCACAAUAGAGAGUGGCCAAAUACGUCAGAGUCCGCAAUUAGAGUGUUA
Qy      1034 CAGGACTAAGATGTTCCCGAGATTGATCAGAGAGATTGTTGGGGCAATAGCTGTT
Db      1029 CAGGACUAAAGCAACAUCCGCUCAUUCACAGAGUCUUAUUGGAGCCUCCGCU
Qy      1094 TTAATGAAAGAGAGATGAGCAAGATGTTGACGTTGATGATACACAGCAATG
Db      1089 UUAUUGAAGGAGAGUAGACUGAUAUAGAUAGUAGUGUACGUAUACUACAGAUUG
Qy      1154 ACCAGGATCAGGAGTATGACGACGACAAAGATCCACTCAAAAGCATTTGATGAAATCA
Db      1149 AACGGGAGUACGCGCUUAGCAGCGAUCAAAAAGACACACAAAUCCAUUACGCGAUUA
Qy      1214 CCAACAGGTAATCTGTGATGTAAGATTAACACCCCAATTTGAAGCTGTTGGGAAG
Db      1209 CAACAGAGUGAUCUCUGUUAUCGAGAAAUAUGAAUACAUUCACAGCUGUGUAAAG
Qy      1274 AATTCGCTAATCTAGAGAAAGACAGCAATCTTGAACAAAAGATGAGAGAGCGGTTG
Db      1269 AAUUCACAAAUUAGAAAAAGAGAUAGAAAUUUAAAUAAAAGUUGAUGAUGAUUUC
Qy      1334 TAGATGTGACATCAATCAATGCTGAGCTTTTACTTGTGATGAAATGAGAGACACTTG
Db      1329 UGAGACAUUUGGACAUUAUUGCAGAUUUGUUAUCUGGAAAUAUGAAGGACUCUG
Qy      1394 ACTTCATGATCTATGTCAGAAATCTGTATAGTAAAGTCAGAAATGCTAGAGACA
Db      1389 AUUUCACAUACUCCAAUUGGAAAGAAUUCUUAUGAAGAAUAAAACCAUUAAGAAUA
Qy      1454 ACCTCAAGAACTAGGAATGATGTTTGAATTTATCAATGATGATGATGATGCA
Db      1449 AUGCCAAAGAAUUGGAAUUGAUUGUUAUGUUCACCAAGUUCUUGACAUAGAUUGCA
Qy      1514 TGAATAGTGTGAAAAAGGACATATGATTATCCCAAGTATGAGAAGTCTAAACTAA
Db      1509 UGGAAGUGUAAAGAAUUGGACUUAUAGUUAUCCCAAUUAUUCAGAAUGUCA
Qy      1574 ATAGAATGAAATCAAGAGGCTAAATTTGAGCAGCATGGGGGTTTCAATCTTGCCA
Db      1569 ACAGGGAAGAGUAGUAGAGUAGAAUUGAAUUAUUGGAGUUCUACAGUUCUGCGCA
Qy      1634 TTTATGCTACAGTACAGCTTCTATGTCACAGCAATGATGAGCTGGGATCTTTCT
Db      1629 UCUACUCAACUGUCCGCAAGUCACUGGUCUUGUUCUCCCGGGGCAUACGUAUUCU
Qy      1694 GGGTGTGCTCCCAAGGCTCTGCACTGCAAGATGCTGATATGATATAGTCAT---T
Db      1689 GAUUDUGUUCUUAUUGGACUUCUUGCAGUUCGAAUUAUGCAUUCGAGUUAUUCAGAA
Qy      1750 TTATATTTAAACACACCTTGTTCGCT 1778
Db      1749 AUUAGAGAAAAACACCCUUGUUCUACU 1777

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XX      Swinepox virus; SPV; recombinant; vaccine; immunisation; diagnosis;
KW      pseudorabies virus; feline immunodeficiency virus; FIV; heartworm;
KW      Dirofilaria immitis; ss.
OS      Unidentified.
XX      Key
FH      CDS      Location/Qualifiers
FT      1..1721
FT      /tag- a
FT      /note- "encodes protein given in AAM55997; stop codons
FT      are given in between amino acids at the end of
FT      the protein"
XX      MO9804684-A1.
XX      05-FEB-1998.
XX      25-JUL-1997; 97WO-0512212.
XX      25-JUL-1996; 96US-0686968.
XX      (SYTR ) SYNPRO CORP.
XX      Cochran MD, Junker DE;
XX      WPI: 1998-130677/12.
XX      P-PSDB; AAM55997.
XX      Recombinant swine pox virus - useful in vaccine for immunising
XX      animal against swine pox virus
XX      Disclosure; Page 398-400; 473pp; English.
XX      PS
XX      The present sequence represents SEQ ID NO:226 from the present invention,
XX      this sequence is only given in the sequence listing and is not mentioned
XX      further in the specification. The present invention specifically
XX      describes recombinant swinepox virus (SPV) comprising a foreign DNA (1)
XX      inserted into a SPV CC genome which is capable of being expressed in a
XX      host cell into which the virus is introduced, where (1) is inserted into:
XX      (a) an EcoRI site within a region corresponding to a 3.2 kb subfragment
XX      of the HindIII K fragment which contains both a HindIII and an EcoRI
XX      site, of the SPV genome, and optionally (b) an AclI site within a region
XX      corresponding to a 3.6 kb HindIII to BglII subfragment of the HindIII M
XX      fragment. The recombinant SPV can be used in a vaccine for immunising an
XX      animal against SPV. The invention also provides a method for testing a
XX      swine to determine whether the swine has been vaccinated with the
XX      vaccine, particularly containing S-SPV-008, or is infected with a
XX      naturally occurring wild-type pseudorabies virus. Also (1) inserted into
XX      recombinant SPV can be used in a diagnostic assay, e.g. feline
XX      immunodeficiency virus (FIV) env and gag genes and Dirofilaria immitis
XX      p39 and 22kd are used to detect feline immunodeficiency caused by FIV
XX      and to detect heartworm caused by D. immitis respectively.
XX      Sequence 1721 BP; 602 A; 322 C; 377 G; 420 T; 0 other:
XX      Query Match      39.7%; Score 707.4; DB 19; Length 1721;
XX      Best Local Similarity 64.4%; Pred. No. 1.9e-178;
XX      Matches 1078; Conservative 0; Mismatches 591; Indels 6; Gaps 1;

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RESULT 10
 AAV26247
 ID AAV26247 standard; DNA; 1721 BP.
 XX AAV26247;
 AC 24-JUL-1998 (first entry)
 DT Genomic DNA SEQ ID NO:226 from WO9804684 encoding SEQ ID NO:227.
 DE

XX	AA00774;		
AC	13-APR-1999 (first entry)		
XX	Influenza virus A/Texas/86/91 recombinant HA gene.		
DT			
XX			
XX			
DE			
XX			
KW	Recombinant; glycosylation; influenza virus; haemagglutinin; baculovirus;		
KM	fusion protein; expression system; insect cell; immunogen; vaccine;		
RW	immune response; primer; PCR; amplification; reverse transcription;		
KV	human; bird; ss.		
XX			
OS	Synthetic.		
XX	Influenza virus.		
FH	Key	Location/Qualifiers	
FT	5'UTR	1..18	
FT		/tag=	A
FT		/note=	"polyhedrin mRNA leader sequence"
FT	CDS	19..1737	
FT		/tag=	B
FT	sig_peptide	19..72	
FT		/tag=	C
FT	mat_peptide	73..1734	
FT		/note=	"AcNPV 61K signal peptide"
FT		/tag=	D
FT		/note=	"mature haemagglutinin"
FT	terminator	1756..1766	
XX		/tag=	E
PX	US5858368-A.		
PD	12-JAN-1999.		
XX			
PF	30-MAY-1995;	95US-0453848.	
XX			
PR	30-MAY-1995;	95US-0453848.	
PR	13-SEP-1993;	93US-0120607.	
XX			
PA	(PROT-) PROTEIN SCI CORE.		
PI	Hackett CS, Smith GE,	Molvovitz F, Voznesensky AI;	
PI	Wilkinson BE;		
DR	WPI; 1999-119782/10.		
XX			
PT	Recombinant influenza virus haemagglutinin fusion protein - for use		
PT	in vaccines against influenza		
XX			
PS	Example 3; Column 41-44;	50pp; English.	
CC	The invention relates to the production of a recombinant glycosylated		
CC	influenza virus haemagglutinin fusion protein by a baculovirus expression		
CC	system in cultured insect cells, where the protein is at least 95% pure,		
CC	is immunogenic, induces a protective immune response when used as a		
CC	vaccine, and comprises a second protein fused to the haemagglutinin.		
CC	This sequence represents the recombinant haemagglutinin gene from the		
CC	influenza virus type A strain Texas/36/91 linked to the baculovirus		
CC	Autographa californica nuclear polyhedrosis virus (AcNPV) 61K protein		
CC	gene signal sequence. The vaccine is used for vaccinating animals		
CC	(including humans) or birds against influenza.		
XX			
SO	Sequence 1766 BP; 604 A;	331 C; 403 G; 428 T; 0 other;	
Query Match	39.6%; Score 706.2; DB 20; Length 1766;		
Best Local Similarity	64.7%; Pred. No. 4e-178;		
Matches 1069; Conservative	0; Mismatches 578; Indels 6; Gaps 1		
OY	91 GGAGCACGATATGC	ATTGGATCATCCTCCCAATTAATTCACAGAGAGTTGACACATTT	150
DB	91 GGGGACACAATATG	ATAGGCGTACCATCGAACAACACTCAACCGACACTGTTCACACAGTA	150
OY	151 CTAGAGCGGAACGT	ACTGTGACATCATGCCAAGGACATCTTGAGAGAAGCCATAACGA	210

Db	151	CTTGGAAGAAACCGTACAGTACACACTCTGTCAACTTACTTTGAGAGACATGCACACCGA	210
Qy	211	AAGTTATGCAACTAAACGGAATCCCTCCACTTGTGAACTAGGAGCACTTGTAGCATTCGCGA	270
Db	211	AAAGTATGTGACTAAAGGAAATAGCCCACTACAAATTTGGGTAAATTGCAAGCGTTGCCGA	270
Qy	271	TGCTCTCTGGAATCCAAATTTGATAGGCTTCTAACTGTGCCAAGAACGTCCTATATA	330
Db	271	TGGATCTTGGAAAGCCCAAAATGCGAACTAGTTTCTTAAGGAATCATGTGCTTACAT	330
Qy	331	TTGGGAAGAAACCCGAGAGAGCGTTTGTGTTATCCAGGACGCTTCAATGATTTATGAA	390
Db	331	CGAGAAACCAACACCTTGAGAAATGGAACATGTTACCCAGGCTATTTGCCGACATGAG	390
Qy	391	GAATTTGAACATCTCCTCAGCAGCGTGAACATTTTCGAGAAAGTAAAGATTCTGCCAAA	450
Db	391	GACTGAGAGGAGCAATTAGTTCAGTATCATTCATTTCGAGACATTTGCAATATTTCCCAA	450
Qy	451	GATAGAT-----GGACACAGCATTAACAACAATCGAGGTTACCGGGCTCGCGGCTGCT	504
Db	451	GAAAGCTCATGGCCCAACCCAGCTTACCAAGAGGTAAAGAGATCATCTCCCATAT	510
Qy	505	GGTATTCATATTTTTAGAGACATGTCGTGCTGACAAAGGAAGATTCAGATTATCCG	564
Db	511	GGGAAAGCACTTTTACAGAAATTTGCTATGAGCTGACGAGGAAGAAATGCGTTGTACCA	570
Qy	565	GTTGCCAAGAGATCGTACACAAATTAACAAGCGAGAACAAATGCTAATTAATTTGGGCGTG	624
Db	571	AATCGACACAGTCTCTATGTAAACACAAAGAAAGAAAGTCTTGTACTATGGGTGTT	630
Qy	625	CACCATCCATTGATGAGACAGAACAAAGAAATTTTACAGAAATGTGGAACTATGTT	684
Db	631	CATCACCCGCTTAACATFAGGAGACCAGAGGCCATCTCATFACAGAAATGCTTATGTC	690
Qy	685	TCCGTAGGCATCAACATTTGAACAAAGGTCAACCCAGAAATTAAGCAACAAGGCTATAA	744
Db	691	TCTGTAGTGTTCACATTTATGACGAAGATTCAACCCAGAAATTAAGCAAAAGACCCAAA	750
Qy	745	GTGATGAGACAGAGGTAGATGAATTTCTTTGACCCTCTTGGAATGTGGAGACC	804
Db	751	GTAGAGATCAAGAAGGAAGATTACTACTAGTGCATCTGTCTGGAACCCGGGACACA	810
Qy	805	ATAAATTTTGAAGACTGTGTAATCTAATTCACACCAGATAGTGAATTCAAATATCGAA	864
Db	811	ATAATATTTGAGCCAAATGTAAATTAATAGCCCATGTAATGCTTTCGACTGTAGTA	870
Qy	865	AGAGGTACTTAGGATCATGAAAAAGAGAACACTTGGAACTGTGAACCAATATGC	924
Db	871	GGCTTTGGGTAGGAAATCATCACTCAAAACCATCAATGAGATGATGACGCGAAGGT	930
Qy	925	CAACCTCCTTTGGGCAATAAATACAACTATACCTTTTCAGATGTGCCACCACACTGCA	984
Db	931	CAACACCCCAAGGGAGCTAATACAGTATGTTCTCTTCCGAATGTACACCACGATCA	990
Qy	985	ATAGTGAATGCCCAAAATATGTAAATCGGAGAAGTTGGTCTTAGCAACAAGCACTAAG	1044
Db	991	ATAGAGAGTGTCCAAATATGTGACGAGTACAAATTAAGGATGTTCACGAGCTAAG	1050
Qy	1045	AATGTTCCCAAGATTGAATCAAGAGATGTTTGGGGCAATAGCTGTTTATAGAAAG	1104
Db	1051	AACATCCCATCATTCATCCAGAGGTTGTTTGGAGCCATTTGCCGGTTTCATTGAAGG	1110
Qy	1105	GGATGGCAAGAAATGTTGAGCGTTGGTATGGAATACATCAACAGACATGACAGGAGTCA	1164
Db	1111	GGGTGAGCTGAATGATGATGATGATGATGCTTATCATCAACAAATGAACAAGATCT	1170
Qy	1165	GGGTATGACAGACAAAGAAATTCACACTCAAAAGGCATTTGATGGAATTCACCAACAAGTA	1224
Db	1171	GGCTATGTGGCGAACAAGAAAGCAACAATGTGCTTAACGGGATTTACAAACAAGTGT	1230
Qy	1225	AATTCGTGATGTAAGAAATTAACACCCATTTGAGCTGTTGGGAAAGAAATTCGGTAA	1284

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Db 1231 AATCTGTAATCGAAAAATGACACTCATTCACAGCTGTGGCAAAAGATTACACAA 1290
Oy 1285 TTAGAGAAAAGACCTGGAGAACTTGAACAAAAGATGACAGCGGTTCTAGAGTGTGG 1344
Db 1291 TTGGAAGAAAGAGAAAAATTAATAAAGATGATGATGATGATGATGATGATGATGATG 1350
Oy 1345 ACATACAAATGCTGAGCTTTAGTCTGTGATGAGAAATGAGAGACCTGACCTTCATCAT 1404
Db 1351 ACATATATGACAGATTTGTTGCTCTACTGSAAAATGAGAGACTTTGATTTTCATGAC 1410
Oy 1405 TCTAATGTCAGAACTCTGTATAGTAAGTCGAATGACAGCTGAGAGACAGCTCAAGAA 1464
Db 1411 TCAAAATGTAAGATCTGTATGAGAAAGTAAAGCCAAATGGAAGAAATGCAAGAA 1470
Oy 1465 CTTGGAATGATGTTTGAATTTATACAAATGATGATGATGATGATGATGATGATGATG 1524
Db 1471 ATAGGAGACGGGTGTTTGAATTTCTATACAAAGTAAACATGATGATGATGATGATGATG 1530
Oy 1525 AAAAGCGGACATATGATATCCCAAGTATGAGAGAGAGTAACTAATAGAAATGAA 1584
Db 1531 AAAAATGGAACCTATGATCCAAATATTCGAAAGATCAAAAGTTAAACAGGGGAAAA 1590
Oy 1585 ATCAAAAGGCTAAATTTGACAGCAGCAGGCGGTTTATCAAAATCCTTGCCATTATGCTACA 1644
Db 1591 ATTGATGAGATGAAATGGAATGGAATGAGAGTCTATCAGATTTGGGATCTACTCACT 1650
Oy 1645 GTAGAGGTTCTATGTCACAGGCAATGATGATGATGATGATGATGATGATGATGATG 1704
Db 1651 GTCCGCAAGTTACTGCTGCTTTGGTCTCCCTGGGGCAATCAGCTTCTGATGCTTCT 1710
Oy 1705 AACGGGCTCTGACAGTGCAGATCTGCATATGA 1737
Db 1711 AATGGCTCTTTCGAGTGCAAGAAATATGATGATGA 1743

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RESULT 13

AAD09587 standard; DNA; 1766 BP.

AAD09587;

10-SEP-2001 (first entry)

Influenza virus A/Texas/36/91 recombinant haemagglutinin (rHA) DNA.

Multivalent influenza vaccine; recombinant haemagglutinin; rHA;

61K protein; ds.

Chimeric - Autographa californica nuclear polyhedrosis virus.

Chimeric - Influenza virus type A.

Key promoter 1.18 Location/Qualifiers

/*tag= a (note= "Autographa californica Nuclear Polyhedrosis Virus (AcNPV) Polyhedrin promoter"

CDS

/*tag= b (note= "AcNPV 61K protein signal peptide- Influenza virus A/Texas/36/91 mature HA fusion protein"

sig_peptide

mat_peptide

misc_signal

/*tag= e (note= "Universal translation termination signal"

US6245532-B1.

12-JUN-2001.

09-OCT-1998; 98US-0169027.

30-MAY-1995; 95US-0453848.

13-SEP-1993; 93US-0120607.

(PROT-) PROTEIN SCI CORP.

Smith GE, Volovitz F, Wilkinson BE, Voznesensky AI, Hackett CS; WPI: 2001.407272/43.

P-PSDB: AAE04952.

Expressing a protein e.g. recombinant influenza virus hemagglutinin comprising using a vector encoding a polypeptide comprising a baculovirus signal peptide and a baculovirus expression system is useful as a multivalent Influenza vaccine -

Claim 5; Column 41-44; 51pp; English.

The present invention relates to a method for expressing an exogenous protein in a baculovirus expression system which comprises using a vector encoding a polypeptide comprising a baculovirus signal peptide operably linked to a heterologous amino acid sequence. The method is especially useful for preparing a protein which may be used to make a multivalent influenza vaccine based on a mixture of recombinant haemagglutinin (HA) antigens cloned from influenza viruses having epidemic potential. The recombinant haemagglutinin proteins are full length, uncleaved (HA0) glycoproteins including both the HA1 and HA2 subunits (HA0) purified under non-denaturing conditions. The use of recombinant DNA (rDNA) technology to produce influenza vaccine offers several advantages, e.g., a recombinant DNA influenza vaccine can be produced under safer and more stringently controlled conditions; propagation with infectious influenza in eggs is not required; recombinant haemagglutinin (rHA) protein can be more highly purified; purification procedures for rHA do not have to include virus inactivation or organic extraction of viral membrane components; production of HA via rDNA technology provides an opportunity to avoid the genetic heterogeneity which occurs during the adaptation and passage through eggs, which should make it possible to better match vaccine strains with influenza epidemic strains, resulting in improved efficacy. The present sequence is recombinant haemagglutinin (rHA) DNA comprising Autographa californica Nuclear Polyhedrosis Virus (AcNPV) 61K gene partial polyhedrin promoter and signal sequence linked to Influenza virus A/Texas/36/91 mature HA coding region.

Sequence 1766 BP; 604 A; 331 C; 403 G; 428 T; 0 other;

Query Match 39.6%; Score 706.2; DB 22; Length 1766;

Best Local Similarity 64.7%; Pred. No. 46-178;

Matches 1069; Conservative 0; Mismatches 578; Indels 6; Gaps 1;

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Oy 91 GGGAGCAATATGCTTTGATACATGCAATTAATCCACAGAGAGTGCACAAATT 150
Db 91 GGGAGCAATATGATAGTACATGCAATGCAACCACTGACACTGTGACACACTA 150
Oy 151 CTAGAGCGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 210
Db 151 CTGAGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 210
Oy 211 AAGTTATGCAAACTAAGGAATCCCTCCACTTGAAGTAGGAGGAGTGTAGCATTTGCCGA 270
Db 211 AACTATGCTGCACTAAGGAATAGCCCACTACATATTGGTAATTGAGGCTTCCCGGA 270
Oy 271 TGGCTCTTGGAAATCCAAATGTATAGGCTTCTAAGTGTGCCAGAGGTCCTATATA 330
Db 271 TGGATCTTGAAGAAACCAAAATGCAATCACTGTTTCTAAGATCAATCATGCTCTCAATT 330
Oy 331 TTGAGAAAGAAACCCAGAGAGCGTTTGGTATTCAGGACGACCTCATGATTAAGA 390
Db 331 GCAGAAACACCAACCCGAGAGATGGAACATGTTACCGAGGTAATTTCGCCGACTAGAG 390

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QY 391 GAATTTGAACATCTCTCAGCAGCGGTGAACATTTGAGAAAGTAAGATTCTCCCAA 450
 Db 391 GAACTGAGGGAGCAATTTGAGTTAGTATCATCTATTCAGAGATTCGAATATTCGCCAAA 450
 QY 451 GATGAT-----GACACAGCATACAACTGAGGTTACGGCCCTGGCGGTCT 504
 Db 451 GAAAGCTCATGCGCCCAACCCACCCGTAAACCAAGATACGAGATCATGCTCCATAT 510
 QY 505 GGTAATCATCATTTTTCAGGAACATGTCGGTGCAGAAAGAGATGATGATATCCG 564
 Db 511 GGGAAAAGCAGTTTTCAGAAATTTCTATGCTGACGGAGAAATGCGTTTACCCA 570
 QY 565 GTTCCCAAGAGATCGTACAAATATCAAGCGAGAGAAATGCTAATATTTGGGGGTG 624
 Db 571 AATCTGAGCAAGTCCATGTAACACAAAGAGAAAGATGCTTACTTGGGGTCT 630
 QY 625 CACCATCCATGATTTAGACAGAAAGAAACATTTACAGAAATGTTGGAACTATGTT 684
 Db 631 CATCACCCGCTTACATAGAGGACCAAGGCCATCTATCATACAGAAATGCTTATGTC 690
 QY 685 TCCGTAGGACATCAACATTGAACAAAGGTCAACCCAGAAATAGCAACAGGCCATAA 744
 Db 691 TCTTATCTGCTTCAATTATAGCAGAAATTCACCCAGAAATAGCAACAGGCCATAA 750
 QY 745 GTGATGAGCAAGATTTAGAAATGGAATTTCTTGGACCCCTTGGATATGTTGGACACC 804
 Db 751 GTAGAGATCAAGAAATGAGAAATTAATCTACTACTGCACTGCTGGAAACCCGGGACACA 810
 QY 805 ATAAATTTGAGAGTCTGCTATCTAATTCACACAGATGATGATTCAAATATTCGAAA 864
 Db 811 ATATATTTAGAGCAATGGAATCTAATAGCCGCAATGATGCTTCCGACTGATAGA 870
 QY 865 AGAGGTGTTGAGGCTCATGAGAAACAGAGGAACACTGAGAACTGTGAGACCAATGTC 924
 Db 871 GCGTTTGGTCAGATTCATCACTCAAGCAAGATGATGATGATGATGATGATGATGAT 930
 QY 925 CAAATCTCTTTGGATCAATTAATATACAACTTACCTTTTCAATGTCACCCACTGACA 984
 Db 931 CAAACACCCAGGAGCATTAACAGTATGCTTCTTCCAGATGATACCCAGCTGACA 990
 QY 985 ATAGGTAGTCCCTCAATATGTAAATGCGAGAGTTGCTTTAGCAAGAGACTAAGG 1044
 Db 991 ATAGAGAGTGTCCAAAGTATGTCAGAGATCAAAATTAAGATGTTACAGAGCTAAGG 1050
 QY 1045 AATGTGCCAGATGATCAAGAGATGTTTGGGCAATGCTGCTTTATAGAGGA 1104
 Db 1051 AACATCCATCCATCATCATCCAGAGGTTTGTGGAGCCATGCGGTTTCATTGAAGGG 1110
 QY 1105 GGATGGCAAGATGCTTGGAGGTTGATGATGATGATGATGATGATGATGATGATGATGAT 1164
 Db 1111 GGGGAGCTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1170
 QY 1165 GGGATGACAGACAAAGATCCACTCAAAAGGCAATTTGATGATGATGATGATGATGAT 1224
 Db 1171 GGGATGCTGCTGAGCAAAAGACACAAAGATGATGATGATGATGATGATGATGATGATGAT 1230
 QY 1225 AATTCGTGATGAAAGATTAACACCAATTTGAGCTGTTGGAGAAAGATTCGGTAAAC 1284
 Db 1231 AATTCGTGATGAAAGATTAACACCAATTTGAGCTGTTGGAGAAAGATTCGGTAAAC 1290
 QY 1285 TTGAGAAAGAGCTGGTGAACCTTGAACAAAGATGAGAGCGGTTTCTAGATGTTG 1344
 Db 1291 TTGAGAAAGAGATGGAACCTTAATTAAGATGATGATGATGATGATGATGATGATGATGAT 1350
 QY 1345 ACATCAATCTGAGCTTTTATGTTGATGAGAAATGAGAGCACTTGCATTCATGAT 1404
 Db 1351 ACATCAATCTGAGCTTTTATGTTGATGAGAAATGAGAGCACTTGCATTCATGAT 1410
 QY 1405 TCTAATGTCAGAGATCTGATAGTAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1464
 Db 1411 TCAATGTCAGAGATCTGATAGTAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1470

QY 1465 CTAGAAATGAGTCTTTGAAATTTATCACAATGTGATGATGATGATGATGATGATGATGATGAT 1524
 Db 1471 ATAGGAGAGCGGCTGTTTGAATTCATCAAGTATGATGATGATGATGATGATGATGATGATGAT 1530
 QY 1525 AAAACGGGACATTTGATTTCCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1584
 Db 1531 AAAATGGAATTTGATTTATCCAAATATTCAGAGATGATGATGATGATGATGATGATGATGAT 1590
 QY 1585 ATCAAGGCGTAAATTTGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1644
 Db 1591 ATGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1650
 QY 1645 GTACAGGTTCTATCTACTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1704
 Db 1651 GTGCGCAGTTTACAGGCTGTTTGGTCTCCCTGGGGCAATCAGCTCTGATGATGATGATGAT 1710
 QY 1705 AACGGTCTGCTGAGTGCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1737
 Db 1711 AATGGTCTTTGACAGTGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1743

RESULT 14

AAAT6188

ID AAAT6188 standard; DNA; 1724 BP.

AC AAAT6188;

DT 15-DEC-2000 (first entry)

DE Swine influenza virus haemagglutinin gene SIV-HA.

KW Swine; haemagglutinin; nucleoprotein; SIV; HA; NP; vaccine;

KM immunisation; ss.

OS Swine influenza virus.

PN CA2290197-A1.

PD 23-MAY-2000.

XX 23-NOV-1999; 99CA-2290197.

PR 23-NOV-1998; 98US-0197679.

PA (FOLE/) FOLEY P. L.

PI FOLEY PL.

DR WPI: 2000-524822/48.

PT Novel recombinant vaccinia virus for immunizing swine against
 PT Influenza, contains inserts of hemagglutinin and nucleoprotein genes
 PT from swine influenza virus

PS Disclosure: Page 12; 27pp; English.

CC The present sequence is swine influenza virus (SIV) haemagglutinin (HA)
 CC gene. This sequence was used to produce a recombinant vaccinia virus
 CC containing as inserts the present sequence and the swine influenza virus
 CC nucleoprotein (NP) gene (see AAA76189). The present sequence was
 CC amplified by RT-PCR and cloned, and then subsequently subcloned into a
 CC transfection vector that allowed insertion of the SIV-HA sequence into
 CC the genome of the modified vaccinia virus Ankara (MVA) strain of vaccinia
 CC virus. The recombinant vaccinia virus is useful as a vaccine for
 CC immunizing a swine against influenza. In addition, by protecting pigs
 CC from influenza infection, the human population would be protected from
 CC transfer of infection from swine to the human population.

SQ Sequence 1724 BP; 607 A; 316 C; 377 G; 424 T; 0 other;

Query Match 39.18; Score 696.4; DB 21; Length 1724;

Best Local Similarly 64.3%; Pred. No. 1.7e-175;

Matches 1078; Conservative 0; Mismatches 591; Indels 7; Gaps 2;

Accession	Source	Strain	Length (bp)	Sequence
U01501	GenBank	Human influenza A virus	1709	1150 NATGACCGAGGATCGGGTATGACGACACAAAGATCTACTCCAAAGCGCATTTGATGGA
U01502	GenBank	Human influenza A virus	1709	1114 AATGAGCAGGGATCGAGTATGCAAGCCAGCCGAAAGAGCACACAGAAATGCCATTGACGGG
U01503	GenBank	Human influenza A virus	1709	1210 ATCACCACAAGATTAATCTGTGATGTAAGAAAGATAAACACCACAAATTTGAAGCTGTGGG
U01504	GenBank	Human influenza A virus	1709	1174 ATCATATAACAAGTAAACCTGTTATTGTAAGAAAGATAAACACAAATTCACAGCAAGTGGGT
U01505	GenBank	Human influenza A virus	1709	1270 AAAGATTCGGTAACCTTGAGAAAAAGCTGAGAACTGAGCAAAAGAAAGATGAGACGGG
U01506	GenBank	Human influenza A virus	1709	1234 AAAGATTCACACCTCTGGAATAAAGATTAAGATTTAAATTAAGAGTTGATGATGTT
U01507	GenBank	Human influenza A virus	1709	1330 TTTCTAGATGTTGGACATACAAATGCTGAGCTTTTAACTTGATGGAAGAAATGAGAGACA
U01508	GenBank	Human influenza A virus	1709	1294 TTTCTGATGTTGGACTTACCAATGCCAATTTGTTGTTATGTAAGAAAGAAAGAACT
U01509	GenBank	Human influenza A virus	1709	1390 CTGACTTCAATGATTTCAATGTCAGAAATGCTGATAGTAAGTCAGAAATGACACTGAGA
U01510	GenBank	Human influenza A virus	1709	1354 TTGGATTACCAATGACTCAAAATGTGAAGAACTATATGAGAAAGTAAGACCACTTAATA
U01511	GenBank	Human influenza A virus	1709	1450 GACAACTCAAGAACTAGAAATGATGTTGAATTTATCAAAATGATGATGATA
U01512	GenBank	Human influenza A virus	1709	1414 AACATGCGCAAGAAATGGAATAGTGCGCTTTGATTTTACCAAAATGATGATGACAAAG
U01513	GenBank	Human influenza A virus	1709	1510 TGCATGATAGTGTGAAAAACGGACATATGATTTCCCAAGTATGAAGAGACTTA
U01514	GenBank	Human influenza A virus	1709	1474 TGCATGAGAGACGTTAAAAATGAGACATATATATACCACAAATCTAGAAAGATCA
U01515	GenBank	Human influenza A virus	1709	1570 CTAATATGAATGAATCAAAAGGGGTGTAATTTGAGCAGACTGAGGGGTTTATCAATCTT
U01516	GenBank	Human influenza A virus	1709	1534 CTAACACAGAGGAGATATGATGAGTAAAGCTGGAATCAACAGAAATTTACCAATTTTG
U01517	GenBank	Human influenza A virus	1709	1630 GCCATTTATGCTACAGTAGCAGGTTCTATGTAC - TGGAATCATATGATGCTGGATCTC
U01518	GenBank	Human influenza A virus	1709	1594 GCGATATATTTCAACTGTGCGCAGATTCATTTGTTAGTCTCCCTGGAGCAATCAG
U01519	GenBank	Human influenza A virus	1709	1689 TTTCTGGTGTGCTCAAGGGGTCTCGAGTGCAGATCGCATATGATTTATAG
U01520	GenBank	Human influenza A virus	1709	1654 TTTCTGGTGTGCTCAAGGGGTCTTTACAGTGCAGATATATGATTTATTAATTTAGG

XX The sequences given in A064451-65 represent fragments of plasmids which
 CC encode antigenic peptides from the H1N1, H2N2 or H3N2 subtypes of human
 CC influenza A type virus. These sequences were derived by PCR using the
 CC primer sequences given in A062141-50 and A064439-50. The amplified
 CC sequence encode at least one antigen which is derived from the main
 CC region of hemagglutinin of the H1N1, H2N2, or H3N2 subtype of human
 CC influenza A type virus. The anti-human influenza virus antibody of the
 CC invention, is reactive against antigens derived from the H1N1 and H2N2
 CC subtypes but not against H3N2 subtype derived peptides. This antibody
 CC is useful for diagnosis, prevention and treatment of human influenza A
 CC type virus. The antigenic peptides are important in vaccine production.

XX Sequence 1754 BP; 615 A; 327 C; 394 G; 418 T; 0 other;

Query Match 39.8%; Score 695.6; DB 15; Length 1754;

Best Local Similarity 64.8%; Pred. No. 2.7e-175;

Matches 1068; Conservative 0; Mismatches 594; Indels 6; Gaps 1;

QY	76	TTACAGCAGTGAAGAGGAGACAGATATGATGGATACATGCGCAATTAATCCACAG	135
DB	54	TTTACAGCTACAGATTCAGACACAAATATGTATAGCTACCATGCGAACACTCAACGAC	113
QY	136	AAGTGCACACAAATTTAGAGCGGAGCTGCTGCTATGCCAAGGACATCTTGAG	195
DB	114	ACTGTTGACACAGTATTTGAGAACAGTACAGTACACACTCTGCAACTCTTGAG	173
QY	196	AAGACCCATACGAAAGTATGCAAACTAACGATCCCTCCTGCTGCACTGAGGAGAC	255
DB	174	GACAGTACACAGGAAACTATGCTGCTAAGAGGATAGCCCTGCTACATTTGGTAT	233
QY	256	TGATGCTTCCGCGAGGCTCTCTGGAATCCAAATGTATAGCTTCTAAGTGTCCA	315
DB	234	TGACAGCTTCCGCGAGGCTCTCTGGAATCCAAATGTATAGCTTCTAAGTGTCCA	293
QY	316	GAGGCTCTATATATGAGAGAAAGAAACCCGAGACAGGTTTGTGTATCCAGGAC	375
DB	294	TCAATGCTCTACATTTGAGAAACCCAACTCCGAGATGGAATCTTACCCGAGTAT	353
QY	376	TTCAATGATTAATGAATGAAACATCTCTCAGACGCGTGAACATTTTCGAAAGTA	435
DB	354	TTCCCGCACTATGAGAACTGAGGAGCAATGTAGTTCAATATATTCGAGAGATTC	413
QY	436	AAGATTCGCCCAAGATAGAT-----GACACAGCATACAACTGAGGTTACGG	489
DB	414	GAAATATTTCCCAAGAACTCATGSCCAACCAACCGTAACCAAGAGTAAACGCA	473
QY	490	GCTTCCCGGCTCTGCTATCCATCTTTTTCAGAAACATGCTGCTGACAAAGAA	549
DB	474	TCATGCTCCCAATATGAGAAAGCAATTTTACGAAATTTGCTATGCTGACGGGAG	533
QY	550	GATATGATTAATGCGCTTGCCTGCAAGAGTGTACAACTACAGCGAGACAAATGCTA	609
DB	534	AATGCTGTTATCCCAATCTGAGCAAGTCTATCTGAAACAAAGAAAGAAAGTCTT	593
QY	610	ATAATTTGGGGGTGACCATCCCATGATGAGACAGACAAAGACATTTGACAGAT	669
DB	594	GTAATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	653
QY	670	GTTGGGAACTATGCTTCCGATGAGCATCAATGAAACAAAGTAAACCCCAAGATA	729
DB	654	GAAATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	713
QY	730	GCAACAGGCTTAAGATGATGAGCAAGAGTATGATGAATTTCTTGACCTCTG	789
DB	714	GCAAAAGAGCCCAAGTAAGAGTCAAGAGAAAGATTAATTAATTAATTAATTAAT	773
QY	790	GATATGAGGACACAAATTTTGAAGTACTGCTATTAATTTGACCAAGATATGA	849
DB	774	GAACCCGCGGACCAATTAATTTTGAAGCAATGAAATCTAATAGCGCTGATGCT	833
QY	850	TTCAAAATATGCAAAATAGTAGTTGAGGATCATGAAACAGAGAACACTTGAGAC	909

DB	834	TTCCCACTAGTAGAGCGTTGGTTCAGGAAATCATCACTCAACGCAATGATGAA	893
QY	910	TGTGAGCCCAATGCAAACTCTTTGGACCATTAATTAACATTAATCTTCCATAT	969
DB	894	TGTAGCGGAGAGTGTCAACACCCAGGAGCTTAACACATGCTCTTCCAGAT	953
QY	970	GTTCCACCACTGACAAATAGTGTAGTGTGCCCCAAATATGAAATGAGAGAGTGTG	1029
DB	954	GTAACCCAGTACAAATAGAGAGTGTGCAAAAGTATGTCAGAGTACAAATTAAGATG	1013
QY	1030	GCAACAGGACTTAAGATGTTCCCAAGATTAATCAATCAGAGATTTTGGGCAATGCT	1089
DB	1014	GTTACAGGACTTAAGAGATCCATCCATCCATCCATCCATCCATCCATCCATCCAT	1073
QY	1090	GTTTATATAGAGAGAGTGTGCAAGATGTTGAGTGTGATGATGATGATGATGATG	1149
DB	1074	GTTTATATAGAGAGAGTGTGCAAGATGTTGAGTGTGATGATGATGATGATGATG	1133
QY	1150	AATGACAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1209
DB	1134	AATGACAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1193
QY	1210	ATCACCACAAAGTAAATTTCTGTATGTAAGATTAACACCAATTTGAAGCTGTGG	1269
DB	1194	ATTCACAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1253
QY	1270	AAAGATTTGGTACTTATGAGAAAGATGAGAGAACTGGAACAAAGATGAGAGAGG	1329
DB	1254	AAAGATTTGCAAAATTTGAGAAAGATGAGAGAACTGGAACAAAGATGAGAGAGG	1313
QY	1330	TTTCTAGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG	1389
DB	1314	TTTCTAGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG	1373
QY	1390	CTTACCTTCAATGATTTAATGTAAGATGTAATGTAATGTAATGTAATGTAATG	1449
DB	1374	TTGATTTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1433
QY	1450	GACACGTCAGAGAGATGAGAAATGATGATGATGATGATGATGATGATGATGATG	1509
DB	1434	AATATGTCAGAGAGATGAGAAATGATGATGATGATGATGATGATGATGATGATG	1493
QY	1510	TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1569
DB	1494	TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1553
QY	1570	CTAATATGAAATGAAATCAAGAGGTAATGAGCAGATGAGGCTTATCAATCTT	1629
DB	1554	TTAAACAGAGGAAATTTGATGAGTGAATTTGAAATCAATCAAGGATCTATCAAT	1613
QY	1630	GCCATTTATGCTACAGTACAGTGTCTATGCTGCTGCTGCTGCTGCTGCTGCTG	1689
DB	1614	GCGATCTACATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1673
QY	1690	TTCTGGGTGCTCCAAAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1737
DB	1674	TTCTGGGTGCTCCAAAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1721

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 Job time : 347.17 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 18:20:24 ; Search time 217.814 Seconds
(without alignments)
14066.412 Million cell updates/sec

Title: US-09-918-568-49

Perfect score: 1135
Sequence: 1 CTAGCAAAAGCGGGCTAT.....AACACCCCTTGTCTCTAG 1135

Scoring table: IDENTITY_NUC
Gapop 10.0, Sapept 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfied by chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1135	100.0	1135	15	AA072806
2	908.8	80.1	1783	15	AA072849
3	884.4	77.9	1773	24	AA073057
4	838	73.8	1728	15	AA064452
5	834.8	73.6	1728	15	AA072831
6	494	43.5	1773	24	AA039863
7	491.2	43.3	1770	21	AA064297
8	466.8	41.1	1777	11	AA068442

9	461.2	40.6	1721	19	AAV26247
10	451	39.7	1766	18	AAV59213
11	451	39.7	1766	20	AAV00774
12	451	39.7	1766	22	AAV09587
13	448.6	39.5	1724	21	AAV76188
14	447.8	39.5	1754	15	AA064451
15	447.8	39.5	1754	15	AA072830
16	443	39.0	1701	19	AAV49294
17	400	35.2	400	15	AA064457
18	400	35.2	400	15	AA072836
19	397	35.0	409	15	AA064458
20	397	35.0	409	15	AA072837
21	382.4	33.7	410	15	AA064459
22	382.4	33.7	410	15	AA072838
23	379.6	33.4	394	15	AA064460
24	379.6	33.4	394	15	AA072839
25	373	32.9	924	11	AA004072
26	373	32.9	924	14	AA047364
27	373	32.9	924	15	AA070195
28	372.6	32.8	810	14	AA047366
29	372.6	32.8	810	15	AA070198
30	368.2	32.4	670	14	AA047360
31	368.2	32.4	670	15	AA070206
32	361.4	31.8	912	15	AA070202
33	356.6	25.9	1697	24	AA047370
34	293.6	25.9	1753	24	AA037088
35	293.6	25.9	1753	24	AA037087
36	293.6	25.9	1753	24	AA037089
37	280.2	24.7	1757	24	AA037090
38	263.8	23.2	729	11	AA040473
39	263.8	23.2	729	14	AA047365
40	263.8	23.2	729	15	AA070197
41	263	23.2	1777	15	AA072855
42	259.2	22.7	630	15	AA070199
43	257.6	22.7	630	14	AA047367
44	256.4	22.6	474	15	AA070203
45	254.8	22.4	474	14	AA047371

ALIGNMENTS

RESULT 1	AA072806	standard; cDNA; 1135 BP.
ID	AA072806	
AC	AA072806;	
XX		
DT	25-MAR-2003 (updated)	
DT	22-JUN-1995 (first entry)	
XX		
DE	DNA encoding stem region of A/Okuda/57 influenza virus.	
XX		
KW	Conserved peptide; stem region; hemagglutinin; HA; H1N1; H2N2;	
KW	subtype; human; influenza A virus; immunogenic artificial peptide;	
KW	antigen; vaccine; infection; ss.	
XX		
OS	Human influenza A virus.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	46..1092
XX		/*tag= a
XX		
PN	EP621339-A2.	
XX		
PD	26-OCT-1994.	
XX		
PF	20-APR-1994;	94EP-0302819.
XX		
PR	20-APR-1993;	93JP-0115216.
PR	16-MAR-1994;	94JP-0070194.
XX		
PA	(TAKI) TAKARA SHUZO CO LTD.	

Genomic DNA SEQ ID
Influenza A/Texas/
Influenza virus A/
Influenza virus A/
Swine influenza vi
A/Suited/1/89 human
HA gene of A/Suited
Siv strain H1N1 ha
A/Okuda/57 human
HA gene fragment o
A/Adachi/2/57 huma
HA gene fragment o
A/Kumamoto/1/65 hu
HA gene fragment o
A/Kaisuka/2/65 hum
HA gene fragment o
Coding region for
Sequence encoding
Sequence encoding
Sequence encoding
Sequence encoding
Sequence encoding
Influenza haemaggl
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Sequence encoding
Influenza A virus
Influenza A virus
Influenza A virus
Influenza A virus
Coding region for
Sequence encoding
Sequence encoding
Full length H3N2.1
Sequence encoding
Sequence encoding
Sequence encoding

XX Isegawa Y, Okuno Y, Sasao F, Ueda S;
 XX WPI: 1994-325949/41.
 DR P-PSDB; AAR63589.
 XX
 XX Human influenza-A virus haemagglutinin polypeptide(s) - useful in
 PT influenza-A vaccine composition
 PS Claim 17; Page 50; 68pp; English.
 CC This sequence encodes the stem region of the haemagglutinin (HA) molecule
 CC of the A/Okuda/57 strain of human influenza A virus. This antigenic
 CC molecule contains the conserved peptides derived from the stem region
 CC of the H1N1 and H2N2 subtypes of human influenza A virus. Immunogenic
 CC polypeptides such as this are antigenically equivalent to the stem region
 CC of the HA molecule of influenza A virus. This artificial peptide may be
 CC used as a vaccine for prophylaxis of influenza A virus infection.
 CC (updated on 25-MAR-2003 to correct PN field.)
 XX
 SO Sequence 1135 BP; 395 A; 197 C; 265 G; 278 T; 0 other;
 Query Match 100.0%; Score 1135; DB 15; Length 1135;
 Best Local Similarity 100.0%; Pred. No. 1.4e-290;
 Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGCAAAAGCAGGGGTTATACCATAGAAAACCAAAACCAATATGCGCATCTTTAT 60
 DB 1 CTAGCAAAAGCAGGGGTTATACCATAGAAAACCAAAACCAATATGCGCATCTTTAT 60
 QY 61 CTCATCTCCTGTTACAGAGTGAGAGGGAGCACAGATATGATGATACCATGCAAT 120
 DB 61 CTCATCTCCTGTTACAGAGTGAGAGGGAGCACAGATATGATGATACCATGCAAT 120
 QY 121 AATTCACAGAGAAGGTCGACACATTTAGAGCGGAAGCTCATCTGATCCAG 180
 DB 121 AATTCACAGAGAAGGTCGACACATTTAGAGCGGAAGCTCATCTGATCCAG 180
 QY 181 GACATCTGAGAGAAGCCATAGCGGAAGTTATGCAACTAAACGATCCGGATCATG 240
 DB 181 GACATCTGAGAGAAGCCATAGCGGAAGTTATGCAACTAAACGATCCGGATCATG 240
 QY 241 AAAACAGAGAAGACCTTGAGAACTGTGAGACCAATGCCAAATCCTTTGGAGCATA 300
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 QY 361 GTAATAATCGGAGAAGTGTGCTTACGACAGGACTAAGGAATGTTCCCGCATTTGATCA 420
 DB 361 GTAATAATCGGAGAAGTGTGCTTACGACAGGACTAAGGAATGTTCCCGCATTTGATCA 420
 QY 421 AGAGATTGTTGGGCAATAGCTGTTTTATAGAGAAGGATGGCAAGGAATGTTGAC 480
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 DB 541 TCCACTCAAAAAGGCAATTTGATGGAATCACCACAGAGTAAATTTCTGATGAAAAGATA 600
 QY 601 AACACCCATTTGAAGCTGTTGGGAAAGAAATTCGTAACCTTAGAGAAAAGCTGGGAAC 660
 DB 601 AACACCCATTTGAAGCTGTTGGGAAAGAAATTCGTAACCTTAGAGAAAAGCTGGGAAC 660
 QY 661 TTGAACAAAAGATGGAAGACGGGTTTCTAGATGTGTGACATACATCTGAGCTTTTA 720
 DB 661 TTGAACAAAAGATGGAAGACGGGTTTCTAGATGTGTGACATACATCTGAGCTTTTA 720

QY 721 GTTCTGATGAAAATGAGAGACACTTACTTTCATGATTCATATGCAAGAATCTGTAT 780
 DB 721 GTTCTGATGAAAATGAGAGACACTTACTTTCATGATTCATATGCAAGAATCTGTAT 780
 QY 781 AGTAAAGTCAGATGACAGCTGAGACACAGCTCAAGAACTAGGAAATGATGTTGAA 840
 DB 781 AGTAAAGTCAGATGACAGCTGAGACACAGCTCAAGAACTAGGAAATGATGTTGAA 840
 QY 841 TTTATACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 DB 841 TTTATACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 QY 901 CCCAAGATGAAAGAGTCTAAACCTAATAGAAATCAAAAGGGTAAATATGAGC 960
 DB 901 CCCAAGATGAAAGAGTCTAAACCTAATAGAAATCAAAAGGGTAAATATGAGC 960
 QY 961 AGCATGGGGGTTTATCAAAATCTTCCATTTATGCTACAGTACAGGTTCTATGTCAC 1020
 DB 961 AGCATGGGGGTTTATCAAAATCTTCCATTTATGCTACAGTACAGGTTCTATGTCAC 1020
 QY 1021 GCATCATGATGAGTGGGATCTCTTCTGGGTGCTCCAAAGGGTCTGCAAGTCCAG 1080
 DB 1021 GCATCATGATGAGTGGGATCTCTTCTGGGTGCTCCAAAGGGTCTGCAAGTCCAG 1080
 QY 1081 ATCTGATATGATTAATAGTCAATTTTAAATTAATTAATTAATTAATTAATTAAT 1135
 DB 1081 ATCTGATATGATTAATAGTCAATTTTAAATTAATTAATTAATTAATTAATTAAT 1135

RESULT 2
 AAQ72849
 ID AAQ72849 standard; cDNA; 1783 BP.
 XX
 AC AAQ72849;
 XX
 DT 25-MAR-2003 (updated)
 DT 23-JUN-1995 (first entry)
 XX
 DE Full length HA gene of A/Okuda/57 H2N2 Influenza A virus.
 XX
 KW Conserved peptide: stem region; haemagglutinin; HA; H1N1; H2N2; PCR;
 KW subtype; human; Influenza A virus; immunogenic artificial peptide;
 KW antigen; vaccine; infection; polymerase chain reaction; primer;
 KW amplification; C179; region A; region B; ds.
 XX
 OS Influenza A virus.
 XX
 FH Key Location/Qualifiers
 FT CDS 49..1737
 FT /*tag= a
 FT /product= Full length HA
 FT 49..93
 FT sig_peptide
 FT /*tag= b
 FT 94..231
 FT /*tag= c
 FT /product= Stem region of N-terminal domain
 FT 232..873
 FT /*tag= d
 FT /product= Globular head region
 FT 874..1734
 FT /*tag= e
 FT /product= Stem region of C-terminal domain
 EP621339-A2.
 PD 26-OCT-1994.
 XX
 PF 20-APR-1994; 94EP-0302819.
 XX
 PR 20-APR-1993; 93JP-0115216.
 PR 16-MAR-1994; 94JP-0070194.
 XX

(TAKI) TAKARA SHUZO CO LTD.
 Isegawa Y, Okuno Y, Saito F, Ueda S;
 WPI: 1994-325949/41.
 DR P-PSDB: AAR63588.
 XX Human influenza-A virus haemagglutinin polypeptide(s) - useful in
 PT Influenza-A vaccine composition
 PS Example 1: Page 45-49; 60pp; English.

This sequence was amplified using the primer sequences given in
 CC AA072845-47 and it encodes the haemagglutinin (HA) gene of the H2N2
 CC subtype of human influenza A virus from A/Osaka/57. The protein encoded
 CC by the amplified cDNA contains two conserved regions, the A region, TGLN
 CC and the B region, GTRKVSIVIRK. These regions are close to each other in
 CC the stem of the HA molecule and they represent epitopes which are
 CC recognised by the antibody C179. C179 binds to the stem region of the HA
 CC molecule and thus inhibits the membrane fusion action of the HA molecule
 CC and neutralises the virus. Polypeptide molecules which contain the
 CC conserved peptide region: A and B, esp. HA molecules lacking the
 CC globular head region, are antigenically equivalent to the stem region
 CC of the HA molecule of influenza A virus. These artificial peptides may
 CC be used as vaccines for prophylaxis of influenza A virus infection.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX

Sequence 1783 BP; 610 A; 323 C; 424 G; 426 T; 0 other;

Query Match 80.3%; Score 908.8; DB 15; Length 1783;
 Best Local Similarity 98.7%; Pred. No. 1.4e-230;
 Matches 916; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

208 AAGTATGCAACTAAGGATCCGGGATCATGATAAAGAGACACTTGAGACTGT 267
 853 AATATTCGAAAGAGATGATTCAGGATCATGATAAAGAGACACTTGAGACTGT 912
 268 GAGACCAAAATGCCAACTCCCTTTGGAGACAAATTAATACAACTTACCTTTTCAATATGC 327
 913 GAGACCAAAATGCCAACTCCCTTTGGAGACAAATTAATACAACTTACCTTTTCAATATGC 972
 328 CACCCACTGCAATATGTGAGTCCCAAAATATGTAATTCGAGAAAGTTGCTTACGA 387
 973 CACCCACTGCAATATGTGAGTCCCAAAATATGTAATTCGAGAAAGTTGCTTACGA 1032
 388 ACAGACTAAGAGATTTCCCCAGATTGATCAAGAGATTTGGGGAATAGCTGGT 447
 1033 ACAGACTAAGAGATTTCCCCAGATTGATCAAGAGATTTGGGGAATAGCTGGT 1092
 448 TTTATGAAAGAGATGGCAAGGAATGTTGACGTTGATGATACATCAGACCAAT 507
 1093 TTTATGAAAGAGATGGCAAGGAATGTTGACGTTGATGATACATCAGACCAAT 1152
 508 GACCCAGGATCAGGATATGTCAGCAGACAAAGAAATCCACTCAAAAGCATTTGATGAATC 567
 1153 GACCCAGGATCAGGATATGTCAGCAGACAAAGAAATCCACTCAAAAGCATTTGATGAATC 1212
 568 ACCAACAAGTAATTTCTGTGATTGAAAAGATTAACACCAATTTGAAGCTTTGGGAAA 627
 1213 ACCAACAAGTAATTTCTGTGATTGAAAAGATTAACACCAATTTGAAGCTTTGGGAAA 1272
 628 GAATTCGGTAACCTAGAGAAAGACTGAGAACTTGAACAAAAGATGAGAGCGGTTT 687
 1273 GAATTCGGTAACCTAGAGAAAGACTGAGAACTTGAACAAAAGATGAGAGCGGTTT 1332
 688 CTAGATGTGTGACATACATATGCTGAGCTTTTATGTTCTGTGAGAAAATGAGAGACACT 747
 1333 CTAGATGTGTGACATACATATGCTGAGCTTTTATGTTCTGTGAGAAAATGAGAGACACT 1392
 748 GACTTCATGATCTATATGTCAGAAATCTGTATAGTAAGTCAAGATGAGCTGAGAGAC 807
 1393 GACTTCATGATCTATATGTCAGAAATCTGTATAGTAAGTCAAGATGAGCTGAGAGAC 1452

QY 808 AACGTCAAGAACTAGGAAATGATGTTTGAATTTTATCACAATGTGATGATCAATGC 867
 DB 1453 AACGTCAAGAACTAGGAAATGATGTTTGAATTTTATCACAATGTGATGATCAATGC 1512
 QY 868 ATGAATATGCTGAAAACCGGACATATGATTATCCCAAGTATAGAGAGCTTAAACTA 927
 DB 1513 ATGAATATGCTGAAAACCGGACATATGATTATCCCAAGTATAGAGAGCTTAAACTA 1572
 QY 928 AATAGAAATGAATCAAAAGGGTAAATATGACAGATGGGGTTTATCAAAATCTTGGC 987
 DB 1573 AATAGAAATGAATCAAAAGGGTAAATATGACAGATGGGGTTTATCAAAATCTTGGC 1632
 QY 988 ATTATGCTACAGTACAGCTTCTATATGTCATCGCAATCATGATGCTGGATCTCTTC 1047
 DB 1633 ATTATGCTACAGTACAGCTTCTATATGTCATCGCAATCATGATGCTGGATCTCTTC 1692
 QY 1048 TGGGTGTCTCCAAACGGGCTCTGCACTGACAGATCTGCATATGATATATAGCATTTTA 1107
 DB 1693 TGGGTGTCTCCAAACGGGCTCTGCACTGACAGATCTGCATATGATATATAGCATTTTA 1752
 QY 1108 TAATTAACCAACCCCTTGTCTGCTAG 1135
 DB 1753 TAATTAACCAACCCCTTGTCTGCTAG 1780

RESULT 3

AAD37057 ID AAD37057 standard; cDNA; 1773 BP.

AC AAD37057;
 XX 21-AUG-2002 (first entry)

DE Influenza A virus/singapore/1/57/ca HA mutant cDNA.
 XX
 XX Attenuated influenza vaccine; prophylactic; therapeutic; infection;
 KW virulence; gene; HA protein; mutant; ss.
 XX
 OS Influenza A virus.
 XX
 OS Synthetic.

Key Location/Qualifiers
 FT 44..1732
 FT /*tag= a
 FT /product= "HA mutant protein"

PN W0200224876-A2.

PD 28-MAR-2002.

PF 25-SEP-2001; 2001MO-EP11087.

PR 25-SEP-2000; 2000EP-0120896.

XX (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.

PI Kallinger H, Egorov A, Feiko B, Romanova J, Kallinger D;

DR WPI: 2002-416282/44.

DR P-PSDB: AAE23111.

XX Manufacturing live vaccine, by infecting Vero cells with virus,
 PT combining cells with serum-free cell culture medium, incubating cells
 PT in presence of protease and nuclease, harvesting virus and preparing
 PT vaccine

PS Example 4: Page 41-42; 90pp; English.

XX The present invention relates to a method for isolating viruses from
 CC various sources and for producing live attenuated influenza vaccines
 CC in a serum-free African Green monkey kidney (Vero) cell culture under
 CC conditions where alterations in the surface antigens of the virus due
 CC to adaptive selection are minimised or prevented. The method is useful

CC for the manufacture of whole-virus vaccine, preferably attenuated live
CC vaccine. It is useful for prophylactic or therapeutic administration
CC against viral infection, preferably influenza virus infections. The
CC present sequence is influenza A virus/singapore/1/57/ca (cold adapted)
CC HA mutant cDNA. This sequence is used in the exemplification of the
CC invention.

XX
SO Sequence 1773 BP; 611 A; 321 C; 417 G; 424 T; 0 other:

Query Match 77.9%; Score 884.4; DB 24; Length 1773;
Best Local Similarity 97.2%; Pred. No. 4.2e-224;
Matches 900; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

```

OY 208 AAGTTATGCAAACTAAACGATCCGGATCATGAAAACAGAGACACTTGAGACTGT 267
DB 1111111111111111111111111111111111111111111111111111111
DB 848 AAAATATCGAAAAGAGTAATTCAGGGATCATGAAAACAGAGACACTTGAGACTGT 907
OY 268 GAGACCAAAATGCCAACTCTTTGGGAGCAATAATCAACATTAACCTTTTCAAAATGTC 327
DB 1111111111111111111111111111111111111111111111111111111
DB 908 GAGACCAAAATGCCAACTCTTTGGGAGCAATAATCAACATTAACCTTTTCAAAATGTC 967
OY 328 CACCACTGACAAATAGGTGAGTCCCAAAATATGTAATCGAGAGAGTTGCTTAGCA 387
DB 1111111111111111111111111111111111111111111111111111111
DB 968 CACCCACTGACAAATAGGTGAGTCCCAAAATATGTAATCGAGAGAGTTGCTTAGCA 1027
OY 388 ACAGGACTAAGGATGTTCCCAAGATTGAATCAAGAGAGTTGTTGGGCAATAGCTGT 447
DB 1111111111111111111111111111111111111111111111111111111
DB 1028 ACAGGACCAAGGATGTTCCCAAGATTGAATCAAGAGAGTTGTTGGGCAATAGCTGT 1087
OY 448 TTTATGAGAGAGATGGCAAGGATGTTGACGGTGTGATGATCCATCAGCAAT 507
DB 1111111111111111111111111111111111111111111111111111111
DB 1088 TTTATGAGAGAGATGGCAAGGATGTTGATGGTGTGATGATCCATCAGCAAT 1147
OY 508 GACCAAGGATCAAGGATGATGACAGACAAAGAAATCCACTCAAAAGCATTTGATGATC 567
DB 1111111111111111111111111111111111111111111111111111111
DB 1148 GACCAAGGATCAAGGATGATGACAGACAAAGAAATCCACTCAAAAGCATTTGATGATC 1207
OY 568 ACCACAAGGTAATTTCTGTGATTTGAAAGATTAACACCAATTTGAGCTGTTGGAAA 627
DB 1111111111111111111111111111111111111111111111111111111
DB 1208 ACCACAAGGTAATTTCTGTGATTTGAAAGATTAACACCAATTTGAGCTGTTGGAAA 1267
OY 628 GAATTCGTAATTTAGCAAAAAGATCGAGAACTTGACAAAAAAGATGCAAGCGGTTT 687
DB 1111111111111111111111111111111111111111111111111111111
DB 1268 GAATTCGTAATTTAGCAAAAAGATCGAGAACTTGACAAAAAAGATGCAAGCGGTTT 1327
OY 688 CTAGATGTGTGACATACAAATGCTGAGCTTTTATGTTCTGATGAAAAATGAGAGACTT 747
DB 1111111111111111111111111111111111111111111111111111111
DB 1328 CTAGATGTGTGACATACAAATGCTGAGCTTTTATGTTCTGATGAAAAATGAGAGACTT 1387
OY 748 GACTTCATGATTTCAATGTAAGAAATCTGTATAGTAAGTGCAGTGCAGAGAC 807
DB 1111111111111111111111111111111111111111111111111111111
DB 1388 GACTTCATGATTTCAATGTAAGAAATCTGTATAGTAAGTGCAGTGCAGAGAC 1447
OY 808 AACGTCAAAGACATGAGAAATGATGTTTGAATTTTACAAATGTGATGATG 867
DB 1111111111111111111111111111111111111111111111111111111
DB 1448 AACGTCAAAGACATGAGAAATGATGTTTGAATTTTACAAATGTGATGATG 1507
OY 868 ATGATAGTGTGAAAAACGGACATATGATATCCCAAGATGAAAGAGTGTAAACTA 927
DB 1111111111111111111111111111111111111111111111111111111
DB 1508 ATGATAGTGTGAAAAACGGACATATGATATCCCAAGATGAAAGAGTGTAAACTA 1567
OY 928 AATAAATAATGAAATGAAAGGGGTAAATATGACAGATGGGGTTTATCAAAATCCCTGGC 987
DB 1111111111111111111111111111111111111111111111111111111
DB 1568 AATAAATAATGAAATGAAAGGGGTAAATATGACAGATGGGGTTTATCAAAATCCCTGGC 1627
OY 988 ATTTATGCTACAGTACGAGGTTCTATGTCATGCGCAATCATGATGGCTGCTTTTC 1047
DB 1111111111111111111111111111111111111111111111111111111
DB 1628 ATTTATGCTACAGTACGAGGTTCTCTCTACAGTCAATATATGCTGGATCTTTTC 1687
OY 1048 TGGGTGTCTCCACAGGGTCTCTGCAAGTGCAGATCTGCATATGATTAAGTCATTTTA 1107
DB 1111111111111111111111111111111111111111111111111111111
DB 1688 TGGATGTCTCCACAGGGTCTCTGCAAGTGCAGATCTGCATATGATTAAGTCATTTTA 1747

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OY 1108 TAATTAACAAACCCCTGTTTCTGCT 1133
DB 1748 TAATTAACAAACCCCTGTTTCTGCT 1773

RESULT 4

AA064452 standard; cDNA to mRNA; 1728 BP.

AA064452:

11-JAN-1995 (first entry)

A/Tzumi/5/65 human influenza A type virus plasmid fragment.

Antigens: main region; hemagglutinin; H1N1; H2N2; subtype: human;
Influenza A type virus; H3N2; anti-human influenza virus antibody;
diagnosis; prevention; treatment; vaccine; ss.

Synthetic.

JP06100594-A.

12-APR-1994.

17-SEP-1992; 92JP-0272538.

17-SEP-1992; 92JP-0272538.

(TAKI) TAKARA SHUZO CO LTD.

WPI; 1994-156655/19.

Anti human influenza virus antibody - for diagnosis and treatment
of influenza type A virus

Disclosure; Page 14; 18pp; Japanese.

The sequences given in AA064451-65 represent fragments of plasmids which
encode antigenic peptides from the H1N1, H2N2 or H3N2 subtypes of human
influenza A type virus. These sequences were derived by PCR using the
primer sequences given in AA062141-50 and AA064139-50. The amplified
sequence encode at least one antigen which is derived from the main
region of hemagglutinin of the H1N1, H2N2, or H3N2 subtype of human
influenza A type virus. The anti-human influenza virus antibody of the
invention, is reactive against antigens derived from the H1N1 and H2N2
subtypes but not against H3N2 subtype derived peptides. This antibody
is useful for diagnosis, prevention and treatment of human influenza A
type virus. The antigenic peptides are important in vaccine production.

Sequence 1728 BP; 599 A; 318 C; 407 G; 404 T; 0 other:

Query Match 73.8%; Score 838; DB 15; Length 1728;
Best Local Similarity 95.6%; Pred. No. 8.2e-212;
Matches 862; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

```

OY 208 AAGTTATGCAAACTAAACGATCCGGATCATGAAAACAGAGACACTTGAGACTGT 267
DB 1111111111111111111111111111111111111111111111111111111
DB 827 AAAATATGCAAAAAGAGTGTTCAGGATCATGAAAGAGAGACACTTGAGACTGT 886
OY 268 GAGACCAAAATGCCAACTCTTTGGGAGCAATAATTAACATTAACCTTTTCAAAATGTC 327
DB 1111111111111111111111111111111111111111111111111111111
DB 887 GAGACCAAAATGCCAACTCTTTGGGAGCAATAATTAACATTAACCTTTTCAAAATGTC 327
OY 328 CACCACTGACAAATAGGTGAGTCCCAAAATATGTAATGCGAGAACTGCTTAGCA 387
DB 1111111111111111111111111111111111111111111111111111111
DB 947 CACCACTGACAAATAGGTGAGTCCCAAAATATGTAATGCGAGAACTGCTTAGCA 1006
OY 388 ACAGGACTAAGGATGTTCCCAAGATTGAATCAAGAGAGTTGTTGGGCAATAGCTGT 447
DB 1111111111111111111111111111111111111111111111111111111
DB 1007 ACAGGACTAAGGATGTTCCCAAGATTGAATCAAGAGAGTTGTTGGGCAATAGCTGT 447
OY 448 TTTATGAGAGAGATGGCAAGGATGTTGATGATGATGATGATGATGATGATGATGAT 507

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PA (TAKI) TAKARA SHUZO CO LTD.
 XX Isegawa Y, Okuno Y, Sasao F, Ueda S;
 XX MPI: 1994-325949/41.
 DR P-PSDB; AAR63588.
 XX
 PT Human influenza-A virus hemagglutinin polypeptide(s) - useful in
 PT influenza-A vaccine composition
 PS Example 1; Page 45-49; 68pp: English.
 XX
 CC This sequence was amplified using the primer sequences given in
 CC AA072845-47 and it encodes the hemagglutinin (HA) gene of the H2N2
 CC subtype of human influenza A virus from A/Okuda/57. The protein encoded
 CC by the amplified cDNA contains two conserved regions, the A region, TGIRN
 CC and the B region, GTRKNVYIEK. These regions are close to each other in
 CC the stem of the HA molecule and they represent epitopes which are
 CC recognised by the antibody C179. C179 binds to the stem region of the HA
 CC molecule and thus inhibits the membrane fusion action of the HA molecule
 CC and neutralises the virus. Polypeptide molecules which contain the
 CC conserved peptide regions, A and B, esp. HA molecules lacking the
 CC globular head region, are antigenically equivalent to the stem region
 CC of the HA molecule of influenza A virus. These artificial peptides may
 CC be used as vaccines for prophylaxis of influenza A virus infection.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 1783 BP: 610 A; 323 C; 424 G; 426 T; 0 other;

Query Match 80.1%; Score 908.8; DB 15; Length 1783;
 Best Local Similarity 98.7%; Pred. No. 1.4e-230;
 Matches 916; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 208 AAGTATGCAACCTAAATGCGATCCGGATCATGAAAGAGAGACACTGAGACACTGT 267
 DB 853 AAATATGAAAGAGGAGTTCAGGATCATGAAAGAGAGAGACACTGAGACACTGT 912
 QY 268 GAGACCAATGCCAATCCCTTTGGAGCAATTAATCAATTAATCAATTTTCAATGTC 327
 DB 913 GAGACCAATGCCAATCCCTTTGGAGCAATTAATCAATTAATCAATTTTCAATGTC 972
 QY 328 CACCCACTGACAAATAGTGAAGTCCCAATATGTAATGCGAGAGAGTGGCTTTAGCA 387
 DB 973 CACCCACTGACAAATAGTGAAGTCCCAATATGTAATGCGAGAGAGTGGCTTTAGCA 1032
 QY 388 ACAGGACTAAGAGATGTCGCCAGATGTAATCAAGAGATGTTGGGGCAATACCTGCT 447
 DB 1033 ACAGGACTAAGAGATGTCGCCAGATGTAATCAAGAGATGTTGGGGCAATACCTGCT 1092
 QY 448 TTTATAGAGAGAGATGTCAGAGATGTTGATGATGATGATGATGATGATGATGAT 507
 DB 1093 TTTATAGAGAGAGATGTCAGAGATGTTGATGATGATGATGATGATGATGATGAT 1152
 QY 508 GACCAAGGATGAGGATGTCAGAGAGATGATGATGATGATGATGATGATGATGATGAT 567
 DB 1153 GACCAAGGATGAGGATGTCAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1212
 QY 568 ACCAACAAGTAAATTCGTGATGTAAGATTAACCAATTTGAAGCTTTGGGAAA 627
 DB 1213 ACCAACAAGTAAATTCGTGATGTAAGATTAACCAATTTGAAGCTTTGGGAAA 1272
 QY 628 GAATTCGGTAACTAGAGAAAGAGTGGAGAACTTGAACAAAAGATGAGAGAGGTTT 687
 DB 1273 GAATTCGGTAACTAGAGAAAGAGTGGAGAACTTGAACAAAAGATGAGAGAGGTTT 1332
 QY 688 CTAGATGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 747
 DB 1333 CTAGATGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1392
 QY 748 GACTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 807
 DB 1393 GACTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1452

QY 808 AACGTCAAGAACTAGAGAAATGATGTTTGAATTTTATACAAATGTGATGATGAATGC 867
 DB 1453 AACGTCAAGAACTAGAGAAATGATGTTTGAATTTTATACAAATGTGATGATGAATGC 1512
 QY 868 ATGAATAGTGTGAAAAACGGGACATATGATTTATCCCAAGTATGAAGAAGCTTAACCTA 927
 DB 1513 ATGAATAGTGTGAAAAACGGGACATATGATTTATCCCAAGTATGAAGAAGCTTAACCTA 1572
 QY 928 AATAGAAATGAAATCAAGGGGTAAATTTGAGACACATGAGGGGTTTATCAATCTTGGC 987
 DB 1573 AATAGAAATGAAATCAAGGGGTAAATTTGAGACACATGAGGGGTTTATCAATCTTGGC 1632
 QY 988 ATTATGCTACAGTACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1047
 DB 1633 ATTATGCTACAGTACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1692
 QY 1048 TGGGTGCTCCACAGGCTCTGTCAGTGCAGAGATGATGATGATGATGATGATGATGAT 1107
 DB 1693 TGGGTGCTCCACAGGCTCTGTCAGTGCAGAGATGATGATGATGATGATGATGATGAT 1752
 QY 1108 TAATTAATAACACCTGTTCTGCTAG 1135
 DB 1753 TAATTAATAACACCTGTTCTGCTAG 1780

RESULT 3
 AAD37057
 ID AAD37057 standard; cDNA; 1773 BP.

XX AAD37057;
 XX 21-AUG-2002 (first entry)

DE Influenza A virus/singapore/1/57/ca HA mutant cDNA.
 XX
 KM Attenuated influenza vaccine; prophylactic; therapeutic; infection;
 KM virulence; gene; HA protein; mutant; ss.
 OS Influenza A virus.
 OS Synthetic.

XX Key Location/Qualifiers
 FH CDS 44..1732
 FT /tag= a
 FT /product= "HA mutant protein"

PN WO200224876-A2.
 XX
 PD 28-MAR-2002.

PF 25-SEP-2001; 2001WO-EP11087;
 XX
 PR 25-SEP-2000; 2000EP-0120896.

XX (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.

PI Kalinge H, Egorov A, Ferko B, Romanova J, Kalinge D;

XX MPI: 2002-416282/44.

DR P-PSDB; AAE23111.

XX Manufacturing live vaccine, by infecting Vero cells with virus,
 PT combining cells with serum-free cell culture medium, incubating cells
 PT in presence of protease and nuclease, harvesting virus and preparing
 PT vaccine

PS Example 4; Page 41-42; 90pp: English.

CC The present invention relates to a method for isolating viruses from
 CC various sources and for producing live attenuated influenza vaccines
 CC in a serum-free African green monkey kidney (Vero) cell culture under
 CC conditions where alterations in the surface antigens of the virus due
 CC to adaptive selection are minimised or prevented. The method is useful

OY 1048 TGGGTGTCGCCAACGGGCTCCTGCAGTCCGAGATCTCATATATTAACTCATTTTA 1107
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1688 TGCAATGTCTCCCAACGGGCTCTCTCGACTGCAGATCTGCATATATTAATGAATTTTA 1747

448 TTTATAGAAGGAGGATGCCAAGGAATGTTGACGGTTGGTATGGATACCATCACAGCAAT 507

ID	Accession	Standard	CDNA Length (BP)
D6	1067	TTTATAGAGGAGGAGJGGCAAGGAATGGTTGATGGTTGATGATACCATCACAGCATT	1126
OY	508	GACCAGGCGATCAGGG)ATGCAGCGACACAGAATCCACTCAAAGGCCATTTTGATGAATC	567
D6	1127	GACCAGGCGATCAGGG)ATGCAGCGACACAAAATACTCAAAGGCCATTTTGATGAATC	1186
OY	568	ACCAACAAGGAAATTTCTGTGATTGAAAAAAGATTAACACCAATTTGAAAGCGTTGGGAAA	627
D6	1187	ACCAACAAGGAAATTTCTGTGATTGAAAAAAGATTAACACCAATTTGAAAGCGTTGGGAAA	1246
OY	628	GAATTCGGTAACCTTAGAAAAAGACTGAGAACCTTGAAACAAAAGATGGAAGACGGGTTT	687
D6	1247	GAATTCATTAATTTTAGAAAAAGACTGAGAACCTTGAAACAAAAGATGGAAGACGGGTTT	1306
OY	688	CTAGATGCTGTGCACAAACAATGCTGAGTTTTTAATTTCTGATGGAATAATGAGAGCACTT	747
D6	1307	CTAGATGCTGTGCACAAACAATGCTGAGTTTTTAATTTCTGATGGAATAATGAGAGCACTT	1366
OY	748	GACTTTCGATTCCT)ATGTCAAAGAATCTGTATAGTAAAGTCAGAATGCAGCTGAGAGAC	807
D6	1367	GACTTTCGATTCCT)ATGTCAAAGAATCTGTATAGTAAAGTCAGAATGCAGCTGAGAGAC	1426
OY	808	AACGTCAAAGACATACGAATGATGATTTTGAATTTTATCAACAATGTGATGATGATGC	867
D6	1427	AACGTCAAAGACATACGAATGATGATTTTGAATTTTATCAACAATGTGATGATGATGC	1486
OY	868	ATGAATGCTGGAAN)ACGGGACATATGATTAATCCCAAGTATGGAAGAACATCAACTA	927
D6	1487	ATGAATGCTGGAAN)ACGGGACATATGATTAATCCCAAGTATGGAAGAACATCAACTA	1546
OY	928	AATGAATAATGAATC)AAGGGGTAAAAATTTGAGCAGCATGGGGGTTTATCAAACTCTTGCC	987
D6	1547	AATGAATAATGAATC)AAGGGGTAAAAATTTGAGCAGCATGGGGGTTTATCAAACTCTTGCC	1606
OY	988	ATTATATGCTACAGTAC)CAGGTTCTATGTCACATGGCAATCATGATGCGTCTCTTTC	1047
D6	1607	ATTATATGCTACAGTAC)CAGGTTCTCTGTGCACTGGCAATCATGATGCGTCTCTTTC	1666
OY	1048	TGGGCTGTCCTCAAC(CGGTCTCTCAGTGCAGATCTGCATATGATTTAATGATTTTAA	1107
D6	1667	TGGATGTGCTCCAAC(CGGTCTCTCAGTGCAGATCTGCATATGATTTAATGATTTTAA	1726
OY	1108	TA 1109	
D6	1727	TA 1728	
RESULT 5			
ID	AAQ72831	standard; cDNA: 1728 BP.	
XX	AAQ72831:		
XX	25-MAR-2003 (updated)		
DT	23-JUN-1995 (first entry)		
XX	HA gene of A/Tzumi/5/65 strain H2N2 subtype influenza A virus DNA.		
XX	Conserved peptide: stem region; hemagglutinin; HA; H1N1; H2N2; PCR;		
KW	subtype: human; influenza A virus; immunogenic artificial peptide;		
KW	antigen; vaccine; infection; polymerase chain reaction; primer;		
XX	amplify; C179; region A; region B; ds.		
OS	Influenza A virus.		
XX	Key	Location/Qualifiers	
FH	Misc_feature	1007..1011	
FT	/tag= ?		
FT	/note= "Incodes A region of HA stem - TGLRN"		
FT	Misc_feature	1181..1216	
FT	/tag= ?		
FT	/note= "Incodes B region of HA stem - GITKNVSVIEK"		

PX		EP621339-A2.	
XX			
ED		26-OCT-1994.	
XX			
XX		20-APR-1994;	94EP-0302819.
PF			
PR		20-APR-1993;	93JP-0115216.
PR		16-MAR-1994;	94JP-0070194.
XX			
PA		(TAKI) TAKARA SHUZO CO LTD.	
PI		Isegawa Y, Okuno Y, Sasao F, Ueda S;	
DR		WPI: 1994-325949/41.	
XX			
PT		Human influenza A virus haemagglutinin polypeptide(s) - useful in	
XX		Influenza-A vaccine composition	
PS		Example A: Page 35-36; 68pp; English.	
XX			
CC		This sequence represents the hemagglutinin (HA) molecule of the H2N2	
CC		subtype of human Influenza A virus, strain A/Izumi/5/65. This molecule	
CC		was amplified using the primers given in AAQ72808-17. The molecules	
CC		given in AAQ72836-39, represent the HA genes from various strains of	
CC		H2N2 subtype Influenza A virus. The proteins encoded by these cDNAs	
CC		contain two conserved regions, the A region, TGLRN and the B region,	
CC		GITNKVMSYIEK. These regions are close to each other in the stem of the	
CC		HA molecule and they represent epitopes which are recognised by the	
CC		antibody CI179. CI179 binds to the stem region of the HA molecule and	
CC		thus inhibits the membrane fusion action of the HA molecule and	
CC		neutralises the virus. Polypeptide molecules which contain the	
CC		conserved peptide regions, A and B, are antigenically equivalent to	
CC		the stem region of the HA molecule of Influenza A virus. These	
CC		artificial peptides may be used as vaccines for prophylaxis of	
CC		Influenza A virus infection.	
CC		(Updated on 25-MAR-2003 to correct PN field.)	
SQ		Sequence 1728 BP; 599 A; 319 C; 406 G; 404 T; 0 other:	
		Query Match 73.6%; Score 834.8; DB 15; Length 1728;	
		Best Local Similarity 95.3%; Pred. No. 5,8e-211;	
		Matches 860; Conservative 0; Mismatches 42; Indels 0; Gaps 0;	
OY	208	AAGTTATGCCAAACTTAACGCGATCCGGCATGTAGAAAACAGAAGAACACTTGACAACCTGT	267
DB	827	AAAAATATTGAAAGAGAGTAGTTCAGAGGATCATGAAAGACAGAAAGMACACTTGGGAACCTGT	886
OY	268	GAGACCATAATGCCAAACCTCTTTGGGACCAATTAATACAATATACCTTTACAAATGC	327
DB	887	GAGACCCAATCCCAACACTCTTTGGGACCAATTAATACAACTTCTTTACAAATGC	946
OY	328	CACCACATGCAATAGTGAATGCCCCCAAATGTAATATGGAAGAGTTGGTCTTAGCA	387
DB	947	CACCACATGCAATAGTGAATGCCCCCAAATATGTAATATGGAAGAGTTGGTCTTAGCA	1006
OY	388	ACAGACTAAGGAATGTTCCCACATTTGAATCAGACGATTTGTTGGGCAATAGCTGGT	447
DB	1007	ACAGACTAAGGAATGTTCCCACATTTGAATCAGAGAGATTTGTTGGGCAATAGCTGC	1066
OY	448	TTTTATAGAGAGAGTGGCAGAGGAATGTTACAGGTTGGTATGGATTACATCACAGCAAT	507
DB	1067	TTTTATAGAGAGAGTGGCAGAGGAATGTTATGGTTGGTATGGATTACATCACAGCAAT	1128
OY	508	GACCAGGATCAGGGTATGCAGCAGACAAAGAAATCCACTCAAAAGCATTTGATGAATC	567
DB	1127	GACCAGGATCAGGGTATGCAGCAGACAAAGAAATCCACTCAAAAGCATTTGATGAATC	1188
OY	568	ACCAACAAGTAAATTCGTGATTTGAANAAGTAAACACCAATTTGAAGCTTTGGGGAAA	627
DB	1187	ACCAACAAGTAAATTCGTGATTTGAANAAGTAAACACCAATTTGAAGCTTTGGGGAAA	1248
OY	628	GAATTCGGTAACTTAGAGAAAAGATCGAGAACTTGAACAAAAGATGGAAGACGGCTTT	687

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||||| 111 |||||||
Db 1247 GAATTCATTAATTTAGAGAAAGACTGGAGACTTGACAAAAAGATGAGAGCGGTTT 1306
OY 668 CTAGATGTGTGACATACATCTGTGAGCTTTAGTTCTCATGGAATATGAGAGACATT 747
Db 1307 CTAGATGTGTGACATACATCTGTGAGCTTTAGTTCTCATGGAATATGAGAGACATT 1366
OY 748 GACTTTCATGATTTCAATGTCAAGAAATCTGTATAGTAAAGTCAGATGACAGTGAAGAC 807
Db 1367 GACTTTCATGATTTCAATGTCAAGAAATCTGTATGATGAATGAAGTCAGATGACAGAC 1426
OY 808 AACGTCAAGAACTAGGAAATGAGATGTTTGAATTTTATCACAATATGATGATGATGC 867
Db 1427 AACGTCAAGAACTAGGAAATGAGATGTTTGAATTTTATCACAATATGATGATGATGC 1486
OY 868 ATGATAGTGTGAAAAACGGGACATATGATTTATCCCAATGCAAGAACAGTCAACTA 927
Db 1487 ATGATAGTGTGAAAAACGGGACATATGATTTATCCCAATGCAAGAACATCTAAGTA 1546
OY 928 AATAGAAATGAATCAAAAGGGGTAAATTTAGCAGCATGGGGTTTATCAAAATCCTTGCC 987
Db 1547 AATAGAAATGAATCAAAAGGGGTAAATTTAGCAGCATGGGGTTTATCAAAATCCTTGCC 1606
OY 988 ATTATGTCTACATGACAGGTTCTATGTCACTGGCAATCATGATGCTGGATCTCTTC 1047
Db 1607 ATTATGTCTACATGACAGGTTCTCTGTCACTGGCAATCATGATGCTGGATCTCTTC 1666
OY 1048 TGGGTGCTGCTCCAGGGGCTCTGAGTCGAGTCGAGATGTCATATGATTAAGCATTTA 1107
Db 1667 TGGATGTGCTCCAGGGGCTCTGAGTCGAGTCGAGATGTCATATGATTAAGCATTTA 1726
OY 1108 TA 1109
Db 1727 TA 1728

RESULT 6
AAL39863
ID AAL39863 standard; DNA; 1773 BP.
AC AAL39863;
XX
XX
XX 13-SEP-2002 (first entry)
XX
XX DNA of HA hologene.
XX
XX Transgenic crop: fowl virus; avian influenza; Newcastle disease; chicken;
XX KW infective cloacal bursa disease; hologene; plant; feed; HA; ds.
XX
XX unidentified.
XX OS
XX CN133370-A.
XX PN
XX 30-JAN-2002.
XX BD
XX 16-AUG-2001; 2001CN-0125352.
XX PF
XX 16-AUG-2001; 2001CN-0125352.
XX PR
XX (SHEN-) SHENZHEN SANFANGYUAN INFORMATION TECHNOL.
XX PA
XX
XX PI Zhong A, Qin Z;
XX DR WPI: 2002-292920/34.
XX
XX Crops capable of resisting virus diseases of poultry and production
XX PT method thereof.
XX
XX Claim 1; Page 1-2 (Claims); 22pp; Chinese.
XX
XX The invention relates to a transgenic crop capable of simultaneously
XX CC resisting up to three kinds of fowl viruses of avian influenza, Newcastle
XX CC disease and infective cloacal bursa disease. The invention also relates

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CC to the production method of the crop. The method of the invention
CC includes the following processes: insertion of HA, F and VP2 hologene
CC into a plasmid vector; expression of the recombinant plasmid transferred
CC into the plant; pairwise hybridisation of the plants which respectively
CC possess the action of resisting the above-mentioned three viruses or
CC simultaneous hybridisation of three plants. The transgenic seeds can be
CC planted into soil to obtain crops for use as a raw material of feed for
CC fowl with the feed containing a recombinant active protein. This
CC polynucleotide sequence represents the 1773 nucleotide DNA of the HA
CC hologene relating to the invention.
XX
XX Sequence 1773 BP; 605 A; 336 C; 403 G; 429 T; 0 other;
SQ
Query Match 43.5%; Score 494; DB 24; Length 1773;
Best local Similarity 73.5%; Pred. No. 1,1e-120;
Matches 664; Conservative 0; Mismatches 225; Indels 15; Gaps 2;
OY 235 ATCATGAAAAACGAAGAACACTTGAGAACTGTGAGACCAATATCCAAATCTCTTGGGA 294
Db 854 ATTATGAAAAAGTGAATGGAATATGTAATGCAACACCAAGTGTCAAAATCTCAATGGGG 913
OY 295 GCAATTAATACAACTTACTTTTACAAATGTCCACCCACATGACAAATAGTGAATGCC 354
Db 914 GCAATTAATACAACTTACTTTTACAAATGTCCACCAATCAATCAATGAGGGAATGCC 973
OY 355 AATATGTAATTCGAGAAAGTGTGCTTAGCAACAGCACTAAGGAATGTTCCCAAGATT 414
Db 974 AATATGTAATTCGAGAAAGTGTGCTTAGCAACAGCACTAATCAATCAATGAGGGAATGCC 1033
OY 415 G-----AATCAAGAGGATGTTTGGGGCAATAGCTGTTTATGANGAGAGA 462
Db 1034 GAGAGAGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 1093
OY 463 TGGCAAGAGATGTTGAGCGTGTGATGATGATACCAATGACCAATGACAGAGATCAAGG 522
Db 1094 TGGCAGGAGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1153
OY 523 TATGACAGCAGCAAAAGATTCACCTCAAAAGGATTTGATGATTCACCAACAGATTAAT 582
Db 1154 TACTCTGCAGCAAAAGATTCACCTCAAAAGGATTAATGATGATGATGATGATGATGATG 1213
OY 583 TCTGTGATTTGAAAAGATTAACCCCAATTTGAGCTGTGGGAAAGATTTGGTAACCTTA 642
Db 1214 TCGATCATTAACCAAAATGACACCTCAGTTGAGCGCTTGGAAAGGATTTAAATATCTTG 1273
OY 643 GAGAAAAGCTGAGAACTTGACCAAAAGATGGAAGAGCGGTTTCTAGATGTGTGACA 702
Db 1274 GAAAGAGAGATGAGAAATTTAAACAGAAATGGAAGAGCGGATTTCTAGATGTGTGACT 1333
OY 703 TACAAATGCTGAGCTTTAGTTCTGTATGGAATGGAAGAGACCTTGATTCATGATTC 762
Db 1334 TACAAATGCTGAGCTTTAGTTCTGTATGGAATGGAAGAGACCTTGATTCATGATTC 1393
OY 763 AATGTCAGAAATCTGTATGATTAAGTCAGAAATGCAAGCTGAGAGCAAACTCAAGAACTA 822
Db 1394 AATGTCAGAAATCTGTATGATTAAGTCAGAAATGCAAGCTGAGAGCAAACTCAAGAACTG 1453
OY 823 GGAATGAGATGTTTGAATTTTATCAAAATGATGATGATGATGATGATGATGATGATG 882
Db 1454 GGAATGAGATGTTTGAATTTTATCAAAATGATGATGATGATGATGATGATGATGATG 1513
OY 883 AACGGAGCAATATGATTTATCCCAATGATGATGATGATGATGATGATGATGATGATGATG 942
Db 1514 AACGGAGCAATATGATTTATCCCAATGATGATGATGATGATGATGATGATGATGATGATG 1573
OY 943 AAAGGGTAAATTTGAGCAAGATGAGGCTTTATCAATCTTGCCATTTATGCTACAGTA 1002
Db 1574 AGTGAGTAAATTTTGAATTAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATG 1633
OY 1003 GCAGGTCTATGTCCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1062
Db 1634 GCAGGTCTATGTCCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1693

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FT      /*tag= d
FT      /product= HA2
FT      misc_RNA      1632..1692.
FT      /*tag= e
FT      /label= Insertion site for RFS
XX      WO9014422-A.
XX      PD      29-NOV-1990.
XX      PF      21-MAY-1990;      90WO-GB00791.
XX      PR      19-MAY-1989;      89GB-0011555.
XX      (LYNX-) LYNXVALE LTD.
XX      Ingilis SC, Brierley I;
XX      WPI; 1990-375989/50.
XX      PT      Ribosomal frame shifting signal sequences - isolated from
XX      PT      infectious bronchitis virus genomic RNA and used in protein
XX      prodn.
XX      PS      Disclosure; Fig 19; 55pp; English.
XX      CC      The HA gene encodes a spike-like protein which is embedded in the
XX      CC      membrane via a hydrophobic anchor sequence. A portion of this
XX      CC      anchor sequence may be replaced with a ribosomal frame shift signal
XX      CC      sequence (RFS), in such a way that ribosomes translating the new
XX      CC      HA sequence will usually terminate before the hydrophobic sequence
XX      CC      is encountered, leading to the prodn. of a secreted form of the HA.
XX      CC      It has been found that the primary sequence of the RFS can be rad-
XX      CC      ically altered as long as the the secondary and tertiary structures
XX      CC      are preserved, so it is possible to design an RFS which encodes
XX      CC      hydrophobic amino acids, and therefore preserves the integrity of
XX      CC      the anchor.
XX      CC      See also AAQ06841 and AAQ07007.
XX      CC
XX      SO      Sequence 1777 BP; 621 A; 331 C; 408 G; 417 U; 0 other;

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Query Match      41.1%; Score 466.8; DB 11; Length 1777;
Best Local Similarity 51.4%; Pred. NO. 1.8e-113;
Matches 469; Conservative 172; Mismatches 267; Indels 4; Gaps 1;
XX      QY      226 GGATCCGGGATCATGAAGAAAGGAACTGAGACTGTGAGACCAATATGCCAACT 285
XX      DB      866 GGGGCCGGCAUACACCUCUCAAACGCAUAGCAUGGUGUACACAGAGUCACAA 925
XX      QY      286 CTTTGGGAGCAATTAATACAACTTACCTTTTCACAATGTCCACCCACTGCAATAGT 345
XX      DB      926 CCCCUGGAGGUAAACAGCAGUCUCCUUCAGAAUUAACACCCAGUCACAAUAGA 985
XX      QY      346 GAGTCCGCCCAATATGTAAATTCGAGAAAGTTGGCTTACGACACGAGCTAAGAAATGTT 405
XX      DB      986 GAGGCCCCCAAAUAGGUCAGAGAGGCCCAAAUAGAGAGGAGUACGACUAAAGAAACU 1045
XX      QY      406 CCCAGATTGATGAAGAGATGTTGGGCAATAGCTGTTTATAGAAAGAGATAGG 465
XX      DB      1046 CCGGCCUUAUACAAGAGGUCUUAUUGAGCCAUUCCGCUUUUUUUAAGGGGGAGUGG 1105
XX      QY      466 CAAGGAATGTTGAGGTTGGTATGATATACATCAACAGCAATGACAGGATCAAGGTAT 525
XX      DB      1106 ACUGGAUUGAUGAUGGUGAGUGGUAUUCAUCAUAGAAUAGAACAGAGAUACAGGCUAU 1165
XX      QY      526 GCAGCAGACAAAGATCCACTCAAAAGGCAATTTGATGGAATCACCACAGGTAATTTCT 585
XX      DB      1166 GCAGCGGAUACAAAAGCAGACAAAUUGCAUUAACGGGAUUAACAAAGGUGAAACUCU 1225
XX      QY      586 GTGATTAAGAAATGAACACCACTTTGAGCTGTGGGAAAGAAATGGTAAGTAACTAGAG 645
XX      DB      1226 GUUAUCGAGAAAUAGAAUUAUUCACAGCTUGGUGGUAAGAAUUAUUCACAAAUUAGAA 1285

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QY      646 AAAAGCTGAGCACTTGACAAAGAAAGATGAGAGCGGTTTCTAGATGTGTGACATAC 705
DB      1286 AAAAGAGUAGAAAUUUUAUAUAAAUAGUAGUAGUUAUUCUGGACAUUUGAGACAUU 1345
QY      706 AATGCTGAGCTTTTATGTTCTGATGGAATAAGAGAGACACTTTCATGATTCATTA 765
DB      1346 A AUGCAGAAUUGUUGUUCUACUGGAAAAUAGAAAGACUCUGAUUUUCACUACUCAAU 1405
QY      766 GTCAAGAAATCTCTATAGTAAGTGCAGATGCAGCTGAGAGACACGCTCAAGAACTAG 825
DB      1406 GUAAAGAAUUCUGUAGAGAAAGUAAAAAGCCAAUUAAGAAUUAUAGCCAAAGAAUUCGA 1465
QY      826 AATGATCTTTTATGATTTATCACAATGTGATGATGATGATGATGATGATGATGATGAT 885
DB      1466 A AUGGAAUUGUUGUAGUUCUACACAGAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1525
QY      886 GGGACATATGATTTATCCCAAGTAGAGAGAGCTTAACTAAATAGAAATGAATCAAA 945
DB      1526 GGGACUUAUAGUUAUCCCAAAUUAUUCAGAAAGUCCAAAGUUGAAGAGAAAGUAGAU 1585
QY      946 GGGTAAATTAATGAGCAGATGGGGGTTTATCAATCTTGTGCTTATGCTACAGTAGCA 1005
DB      1586 GAGUGAAAUUGGAUUAUAGGGAUUCUAGAGAUUCUGGGAUUCUACUACUGUGGCC 1645
QY      1006 GGTCTATGTCACCTGCAATCATGATGCTGGATCTTCTGCTGCTGCTGCTGCTGCTGCT 1065
DB      1646 AGUUCACUGGUGUUCUUCUCCUGGGGCAUACAGUUCUGAGUUGUUCUAAUAGGA 1705
QY      1066 TCTTCGAGTGCAGATCTGCATATGATTAATAGTCAAT---TTTATTAATTAAGAAC 1121
DB      1706 UCUUUGCAGUCAGCAAAUUAUUCAGAUUAGAAUUAUUCAGAAUUAUAGAGAAAGAAC 1765
QY      1122 CTTGTTCTGCTGCT 1133
DB      1766 CUUGUUCUACU 1777

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RESULT 9

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AAV26247
ID      AAV26247 standard; DNA; 1721 BP.
XX      AC      AAV26247;
XX      DT      24-JUL-1998 (first entry)
XX      DE      Genomic DNA SEQ ID NO:226 from WO9804684 encoding SEQ ID NO:227.
XX      KW      Swinepox virus; SPV; recombinant; vaccine; immunisation; diagnosis;
XX      KW      pseudorabies virus; feline immunodeficiency virus; FIV; heartworm;
XX      KW      Dirofilaria immitis; ss.
XX      OS      Unidentified.
XX      FH      Key
XX      FT      CDS      1..1721
XX      FT      /*tag= a
XX      FT      /note= "encodes protein given in AAW55997; stop codons
XX      FT      are given in between amino acids at the end of
XX      FT      the protein"
XX      PA      (SYTR ) SYNTRO CORP.
XX      PI      Cochran MD, Junker DE;
XX      WP      WPI; 1998-130677/12.

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DR P-PSDB; AAM55997.
 XX Recombinant swine pox virus - useful in vaccine for immunising
 PT animal against swine pox virus
 XX
 XX Disclosure: Page 398-400; 473pp; English.
 CC The present sequence represents SEQ ID NO:226 from the present invention,
 CC this sequence is only given in the sequence listing and is not mentioned
 CC further in the specification. The present invention specifically
 CC describes recombinant swinepox virus (SPV) comprising a foreign DNA (I)
 CC inserted into a SPV CC genome which is capable of being expressed in a
 CC host cell into which the virus is introduced, where (I) is inserted into:
 CC (a) an EcoRI site within a region corresponding to a 3.2 kb subfragment
 CC of the HindIII K fragment which contains both a HindIII and an EcoRI
 CC site, of the SPV genome, and optionally (b) an AccI site within a region
 CC corresponding to a 3.6 kb HindIII to BglII subfragment of the HindIII M
 CC fragment. The recombinant SPV can be used in a vaccine for immunising an
 CC animal against SPV. The invention also provides a method for testing a
 CC swine to determine whether the swine has been vaccinated with the
 CC vaccine, particularly containing S-SPV-008, or is infected with a
 CC naturally occurring wild-type pseudorabies virus. Also (I) inserted into
 CC recombinant SPV can be used in a diagnostic assay, e.g. feline
 CC immunodeficiency virus (FIV) env and gag genes and Dirofilaria immitis
 CC p39 and 22kd are useful to detect feline immunodeficiency caused by FIV
 CC and to detect heartworm caused by D. immitis respectively.

Sequence 1721 BP: 602 A; 322 C; 377 G; 420 T; 0 other;

Query Match 40.4%; Score 461.2; DB 19; Length 1721;
 Best Local Similarity 70.5%; Pred. No. 5,5e-112;
 Matches 616; Conservative 0; Mismatches 258; Indels 0; Gaps 0;

QY 226 GCATCCGATCATGCAAAACAGAGACACTTGGACACTGAGCCAAATGCCAACT 285
 DB 844 GCATCGGATATATCAATTCAGATACACGATCCAGATGTAATACGCTGTCAAACA 903
 QY 286 CCTTGGGAGCAATATATACACATTAACCTTTTACATGTCACCACTGACATAGCT 345
 DB 904 CCCAAGAGCTATATACACCAAGCTTCATTTACAGATATATCATCATCAATTCGA 963
 QY 346 GAGTGGCCCAATATGTAATCGAGAAATGGTCTTGAACAAGAGACTAAGGAATGTT 405
 DB 964 GAATGTCCAAAATATGTCACCAAAATGAGAAATGGTAAGATTAAGAAATATC 1023
 QY 406 CCCGAGATTGATCAAGAGAGATTGTTGGGCAATAGCTGGTTTATAAGAGAGATG 465
 DB 1024 CCGTCTATTCAATGACAGGCTGTTGGAGCCATTGCGCTTATTAAGGGGGATG 1083
 QY 466 CAAGGAATGGTACAGCTGTGATGATGATCAATCAAGCAATGACAGGATCAGGAT 525
 DB 1084 ACAGGAATGATGATGCTGTGATGATGATCAATCAAGCAATGATGATGATGAT 1143
 QY 526 GCAGCAGCAAAAGAAATCCACTCAAAAGGATTTGATGAATCAACCAAGGTAATTC 585
 DB 1144 GCAGCCGACGAAAGAB3CACACAGAAATGCAATGACGAGATCACTAACAAGCTCT 1203
 QY 586 GTGATTGAAAAGATATACACCAATTTGAGCTGTGGGAAGAAATTCGTAATCTAG 645
 DB 1204 GTTATTGAAAAGATATACACCAATTTGAGCTGTGGGAAGAAATTCGTAATCTAG 1263
 QY 646 AAAAGACTGAGAACTGTGAACAAAAAGATGGAAGAGGTTTCTAGATGTGTGACAT 705
 DB 1264 AAAAGATGAGAAATTTAAACAAAAAGTGTGATGATGATGATGATGATGATGAT 1323
 QY 706 AATGCTGAGCTTTAGTCTGTGATGAAAAATGAGAGACACTTGACTTTCATGATCTTA 765
 DB 1324 AATGCCGAATCTGTGTTCTATTGTAATAATGAAGAATCTTGATATATACCAATCA 1383
 QY 766 GTACAGAACTGTATATATTAAGTCAAGATGAGAGCTGAGAGCAACTCAAGACTAG 825
 DB 1384 GTGAAGAACTATATATGGAAGAAATGAGAGCACTAATAAAACAAATGCCAAGAAATTTGA 1443

QY 826 AATGATGTTTGAATTTATATCAAAATGTGATGATGAATGCATGATGTAAGTGA 885
 DB 1444 AATGCTGCTTTGAATTTATACCAAAATGTGATGATGATGATGATGATGATGAT 1503
 QY 886 GGGACATATGATTTATCCCAAGATGAGAGAGACTTAAACTAATAAGAAATCAAA 945
 DB 1504 GGGACTTATGATTTACCAAAATATCTCAGAGAGCAAACTAACAAGAGAGATGAT 1563
 QY 946 GGGGTAAATTTAGCAGCATGGGGTTTATCAAAATCTTCCCTTATGCTACAGTAC 1005
 DB 1564 GGGGTAAATCTGAAATCAACAAGATTTACCAAGATTTTGGCGATTTCAACTGTC 1623
 QY 1006 GGTTCATGTCACCTGCAATCATGATGATGATGATGATGATGATGATGATGATG 1065
 DB 1624 AGTTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1683
 QY 1066 TCTTCGACGTGACAGATGTCGATATGATTAATG 1099
 DB 1684 TCTTACAGTGCAGATATGATTAATTAATTAAG 1717

RESULT 10

AAT59213
 ID AAT59213 standard; DNA; 1766 BP.
 AC AAT59213;
 XX
 DT 25-MAR-2003 (updated)
 DT 19-AUG-1997 (first entry)
 XX
 DE Influenza A/Texas/36/91 recombinant haemagglutinin gene.
 XX
 KW primer; PCR; polymerase chain reaction; universal; amplify; HA;
 KW haemagglutinin; recombinant production; baculovirus expression system;
 KW vaccine; insect cell culture; ss.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT misc_signal 1..18
 FT CDS /note="polyhedrin mRNA leader (partial)"
 FT sig_peptide 19..1737
 FT /tag- b
 FT 19..72
 FT /tag- c
 FT /note="AcNPV 61k protein signal peptide"
 FT mat_peptide 73..1734
 FT /tag- d
 FT /note="coding region for mature rHA"
 FT misc_signal 1756..1766
 FT /tag- e
 FT /note="universal translation termination signal"
 XX
 XX MO9637624-A1.
 XX PN 28-NOV-1996.
 XX XX
 PD 26-MAY-1995; 95WO-US06750.
 PF 26-MAY-1995; 95WO-US06750.
 PR 26-MAY-1995; 95WO-US06750.
 XX
 XX (MIGR-) MICROGENESYS INC.
 PA (MGPM-) MG-PMC LLC.
 XX
 XX Smith GE, Voliovitz F, Wilkinson BE, Voznesensky AI, Hackelt CS;
 PI MPI: 1997-021228/02.
 DR P-PSDB; AAM01670.
 XX
 PT Recombinant influenza haemagglutinin produced in baculovirus system
 PT - avoids problems of growing virus in eggs and produces stable,
 PT un-cleaved protein useful in vaccines

CC (rHA) protein can be more highly purified, purification procedures for
 CC rHA do not have to include virus inactivation or organic extraction of
 CC viral membrane components, production of HA via rDNA technology provides
 CC an opportunity to avoid the genetic heterogeneity which occurs during
 CC the adaptation and passage through eggs, which should make it possible to
 CC better match vaccine strains with influenza epidemic strains, resulting in
 CC improved efficacy. The present sequence is recombinant haemagglutinin
 CC (rHA) DNA comprising Autographa californica Nuclear Polyhedrosis Virus
 CC (AcNPV) 61k gene partial polyhedrin promoter and signal sequence linked
 CC to Influenza virus A/Texas/36/91 mature HA coding region.
 CC
 XX

Sequence 1766 BP; 604 A; 331 C; 403 G; 428 T; 0 other;

Query Match 39.7%; Score 451; DB 22; Length 1766;

Best Local Similarity 70.0%; Pred. No. 2.8e-109;

Matches 607; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

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OY 226 GGATCCGGGATCATGAAAAACAGAGAACACTTGAGACTGTGACCAATGCCAACT 285
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 877 GGGTCAGGATCATCACTCAACCGCATGATGATGATGATGATGATGATGATGAT 936
OY 286 CTTTGGGAGCATATATACATATACCTTTTCCATATGTCACCCAGTACATAGGT 345
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 937 CCCCAGGAGCTATTAACAGTACTCTCTTCCAGATGTACACCCAGTACAGATAGGA 996
OY 346 GAGTCCCCCAATATGTAATCGAGAAATGGTCTTAGCAACAGGACTAAGGAATGTT 405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 997 GAGTGCACCAAGTATGTGAGAGTACAAATTAAGATGGTTACAGGACTAAGGAATC 1056
OY 406 CCCCAGATTGAATCAAGAGATTTGTTGGGCAATAGCTGTTTATAGAGAGAGATGG 465
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1057 CGATCCATTCATCCAGAGGTTGTTTGGAGCCATTGCGGTTTCAATGAGGGGGTGG 1116
OY 466 CAAGAATGGTTCAGCGTGTATGATGATCATCAGAGATGACCAAGGATCAGGATAT 525
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1117 ACTGATATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1176
OY 526 GCAGAGACAAAGAAATCCACTCAAAAGGATTTGATGATGATGATGATGATGATGAT 585
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1177 GCTGCGGACCAAAAAAGCACCAAAATGCCATTAAAGGATTTACAAAGGATGATTC 1236
OY 586 GTGATGAAAAAGATTAACCCCAATTTGAAGCTGTGGGAAAGATTCGTAACTTAGAG 645
DB 1237 GTAATCGAAAAATATAGACACTCAATTCACAGCTGTGGGCAAAAGAAATTTCAACAAATTTAGAA 1296
OY 646 AAAAGACTGAGAACTTGAACAAAGAAAGATGAGAAAGCGTTTCTAGATGTGTGACATAC 705
DB 1297 AGAAGATGAGAAATCTTAATAAATAAAGTTGATGATGATGATGATGATGATGATGAT 1356
OY 706 AATGCTGAGCTTTAGTTCTGATGAGAAATGAGAGACACTTGACTTTGATGATGAT 765
DB 1357 AATGAGAAATTTGTTGTTCTACTGTAAGAAATGAGAGACTTTGATTTCTATGACTCAAT 1416
OY 766 GTCAAGAAATCTGTATAGTAAGTCAAGATGACAGCTGAGAGACAACTCAAAAGACTAGGA 825
DB 1417 GTGAAGAAATCTGTATAGTAAGTCAAAAGCCCAATTTGAAGAAATTAATGCAAAAGAAATGAGG 1476
OY 826 AATGATGTTTGAATTTTATCACAATGTGATGATGATGATGATGATGATGATGATGAT 885
DB 1477 AACGGGTGTTTGAATTTTATCACAAGTATACATGATGATGATGATGATGATGATGAT 1536
OY 886 GGGACATATGATTTATCCCAAGTATGAGAGACTTAACATAATAGAAATGAAATCAAA 945
DB 1537 GGAATTTATGACTATCCAAATATTCGGAAGATCAAAAGTAAACAGGGGAAAAATGAT 1596
OY 946 GGGGTAATTTGAGAGACATGGGGTTTATCAAAATCTTGCATTTATCTCAGATAGGA 1005
DB 1397 GGAGTGAATTTGAAATCAATGGAGCTATATCAAGATTTGGCGATCTACTCAACTGCGCC 1656
OY 1006 GGTTCATATGCTACGCAATCATGATGGCTGGGATCTCTTCTGGGTGTCTCAACGGG 1065
DB 1657 AGTTCACAGGAGCTTTTGGTCTCCCTGGGGGCAATCAGCTTGTGATGTGTTCTAATGGG 1716
  
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OY 1066 TCTCTCAGTGCAGAGATCTGCATATGA 1092
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1717 TCTTTCAGTGCAGAGATATGAATCTGGA 1743
  
```

RESULT 13

AAA76188 standard; DNA: 1724 BP.

AAA76188:

15-DEC-2000 (first entry)

Swine Influenza virus haemagglutinin gene SIV-HA.

Swine: haemagglutinin; nucleoprotein; SIV; HA; NP; vaccine;

immunisation; ss.

Swine Influenza virus.

CA2290197 -A1.

23-MAY-2000.

23-NOV-1999; 99CA-2290197.

23-NOV-1998; 98US-0197679.

(FOLE/) FOLEY P. L.

Foley PL.

WPI; 2000-52482/48.

Novel recombinant vaccinia virus for immunizing swine against

Influenza, contains inserts of haemagglutinin and nucleoprotein genes

from swine Influenza virus

Disclosure; Page 12; 27pp; English.

The present sequence is swine influenza virus (SIV) haemagglutinin (HA) gene. This sequence was used to produce a recombinant vaccinia virus containing as inserts the present sequence and the swine influenza virus nucleoprotein (NP) gene (see AAA76188). The present sequence was amplified by RT-PCR and cloned, and then subsequently subcloned into a transfection vector that allowed insertion of the SIV-HA sequence into the genome of the modified vaccinia virus Ankara (MVA) strain of vaccinia virus. The recombinant vaccinia virus is useful as a vaccine for immunising a swine against influenza. In addition, by protecting pigs from influenza infection, the human population would be protected from transfer of infection from swine to the human population.

Sequence 1724 BP; 607 A; 316 C; 377 G; 424 T; 0 other;

Query Match 39.5%; Score 448.6; DB 21; Length 1724;

Best Local Similarity 70.3%; Pred. No. 1.2e-108;

Matches 615; Conservative 0; Mismatches 259; Indels 1; Gaps 1;

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OY 226 GGATCCGGGATCATGAAAAACAGAGAACACTTGAGAACTGTGACCAATGCCAACT 285
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 835 GGAATCTGATATATATATTTTCAATACACAGTCCAGATGTATATAGACCTGTCAACA 894
OY 286 CTTTGGGAGCAATTAATCAACATATACCTTTTCAATGTCCACCACTGACAAATAGT 345
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 895 CCCAAGAGTGTATTAACACAGCGCTCCATTTTCAATATATACATCCAGTACAAATGGA 954
OY 346 GAGTCCCCCAATATATTAATCGAGAAATGGTCTTAGCAACAGACTAAGCAATGTT 405
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 955 GAATCTCCAAATATATGTAACAAAGTAAATTTGAGAAATGCTACAGGATTAAGGAATATC 1014
OY 406 CCCCAGATTGAATCAAGAGATTTGTTGGGCAATAGCTGTTTATAGAAAGAGATGG 465
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1015 CCGTCTATTCATCTAAGGGGCTGTTTGGAGCCATTGCTGGCTTTATTGAGGGGGGTGG 1074
  
```



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DB      1575 GGAGTGAATTCATGCAATGGAGTCTATCAGATTCTGCGATCTACTCACTGCGCC 1634
OY      1006 GGTTCATGTCACATGTCATCATGATGGGATGCTCTTCGGGTCGTCACACGGG 1065
DB      1635 AGTTCACGTGCTCTTTGGTCCCTGGGGCATACGCTTCTGATGTCTTAATGGG 1694
OY      1066 TCTCTGACGTGACGATCTGCATATGA 1092
DB      1695 TCTTTCAGCTGATGATATGACATCTGA 1721

RESULT 15
AA072830
ID      AA072830 standard; cDNA; 1754 BP.
XX
AC      AA072830;
XX
DT      25-MAR-2003 (updated)
DT      23-JUN-1995 (first entry)
XX
DE      HA gene of A/SuIta/1/89 strain H1N1 subtype Influenza A virus DNA.
XX
KM      Conserved peptide: stem region: hemagglutinin; HA; H1N1; H2N2; PCR;
KM      subtype: human; Influenza A virus; immunogenic artificial peptide;
KM      antigen; vaccine; infection; polymerase chain reaction; primer;
KW      amplify; C179; region A; region B; ds.
XX
OS      Influenza A virus.
XX
XX      Key      Location/Qualifiers
FT      Misc_feature      1017..1031
FT      /tag= a
FT      /note= "Encodes A region of HA stem - TGLRN"
FT      Misc_feature      1191..1226
FT      /tag= b
FT      /note= "Encodes B region of HA stem - GITNKNVSVIEK"
XX
XX      EP621339-A2.
XX
XX      26-OCT-1994.
XX
XX      PD      20-APR-1994; 94EP-0302819.
XX
XX      PR      20-APR-1993; 93JP-0115216.
XX      PR      16-MAR-1993; 94JP-0070194.
XX
XX      PA      (TAKI ) TAKARA SHUZO CO LTD.
XX
XX      PI      Isegawa Y, Okuno Y, Sasao F, Ueda S;
XX      DR      WPI; 1994-325949/41.
XX
XX      PT      Human influenza-A virus haemagglutinin polypeptide(s) - useful in
XX      PT      influenza-A vaccine composition
XX
XX      Example A: Page 33-34; 68pp; English.
XX
XX      This sequence represents the hemagglutinin (HA) molecule of the H1N1
XX      CC      subtype of human influenza A virus, strain A/SuIta/1/89. This molecule
XX      CC      was amplified using the primers given in AA072808-17. The molecules
XX      CC      given in AA072830-36, represent the HA genes from various strains of
XX      CC      H1N1 subtype Influenza A virus. The proteins encoded by these cDNAs
XX      CC      contain two conserved regions, the A region, TGLRN and the B region,
XX      CC      GITNKNVSVIEK. These regions are close to each other in the stem of the
XX      CC      HA molecule and they represent epitopes which are recognised by the
XX      CC      antibody C179. C179 binds to the stem region of the HA molecule and
XX      CC      thus inhibits the membrane fusion action of the HA molecule and
XX      CC      neutralises the virus. Polypeptide molecules which contain the
XX      CC      conserved peptide regions, A and B, are antigenically equivalent to
XX      CC      the stem region of the HA molecule of Influenza A virus. These
XX      CC      artificial peptides may be used as vaccines for prophylaxis of
XX      CC      Influenza A virus infection.

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CC      (Updated on 25-MAR-2003 to correct PN field.)
XX      SO      Sequence 1754 BP; 615 A; 327 C; 394 G; 418 T; 0 other;
XX
XX      Query Match      39.5%; Score 447.8; DB 15; Length 1754;
XX      Best Local Similarity 69.8%; Pred. No. 26-108;
XX      Matches 605; Conservative 0; Mismatches 262; Indels 0; Gaps 0;
XX
OY      226 GGATCCGGGATCATGTAAGAACAGAGAACACTTGAGAACTGAGACCAATGCCAACT 285
DB      855 GGGTCAGGAATCATCTACCTCAACAGCATCAATGATGATGACCGCAAGTGTCAACCA 914
OY      286 CCTTTGGAGACATAAATACAACTTACCTTTTCACATGTCACCCACTGACATATAGT 345
DB      915 CCCACAGAGAGCTAIAAACAGTAGTCTCTTCCTTCAGAAATGTAACCCAGTCACATAGGA 974
OY      346 GAGTCCGCCCAATATGTAAATCGAGAACTTGGTCTTACCAACAGGACTAGCAATGTT 405
DB      975 GAGTGTCCAAAGATATCTCAGAGACTACAAATTAAGATGTTACAGCACTAAGCAACATC 1034
OY      406 CCCACATTTGAATCAAGAGATGTTTGGGGCAATAGCTGGTTTATGAGAGAGATGG 465
DB      1035 CCATCCATTCATCAACAGAGGTTTGTGAGCCATTGCCGTTTCATTGAAGGGGGTGG 1094
OY      466 CAAGGATGTTGACGGTTGTATGATACATCAACAGCAATGACCAAGGATCAGGATAT 525
DB      1095 ACTGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1154
OY      526 GCAGCAGACAAAGAAATCCACTCAAAAGCAATTTGATGGAATCCACAAAGTAATTC 585
DB      1155 GCTGGCGATCAAAAAGCACAAAGCAATTCATTAACGAATTAACAAAGTAATTC 1214
OY      586 GTGATTAAGAAAGTAATCAACCCATTTGAGCTGTGGGAAAGATTCGTAATCTAGAG 645
DB      1215 GTATATGACAAATATGAACCTAATTCACAGCTGTGGCCAAAGATTAACAAATTTGAA 1274
OY      646 AAAAGACTGAGAACTTGAACAAAGATGAAGAGGGTTTCTAGATGTGTGACATAC 705
DB      1275 AGAAGATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1334
OY      706 AATGCTGAGCTTTTACTGCTGATGGAATTAAGAGACACTTGCATGATTCATAT 765
DB      1335 AATGCAAAATTTGTTGCTTACTGGAATTAAGAGACTTTGATTTCAAGACTCAAT 1394
OY      766 GTCAAGAACTCTGTATAGTAAGTCAAGATGACAGAGACAAAGTCAAGAACTGGA 825
DB      1395 GTGAAGAACTCTGTATGAGAAATTAAGAAAGCCATTAAGAAATTAATGCCAAAGAAATGGA 1454
OY      826 AATGATGTTTGAATTTTATCACAATGTGATGATGATGATGATGATGATGATGATGAT 885
DB      1455 TACGGGTGTTTGAATTTTACCAAGGTGAATGAATGAATGAATGAATGAATGAATGAAT 1514
OY      886 GGGACATATGATTAATCCCAAGTATGAACAAGTCTTAACATAATTAAGAAATGAATAA 945
DB      1515 GGAACCTTAAGACTATCAAAATATTCGAGGAAATCAAAAGTTAAACAGGAAATTAATGAT 1574
OY      946 GGGGTAATATGACAGACAGAGGGGTTTAATCAATCTTGCATTTATGATGATGATGATGAT 1005
DB      1575 GGAGTGAATTCGAAATCAATGAGGACTCTATGAGATTTCTGGGATCTCTCACTAGTGGCC 1634
OY      1006 GGTTCATGTCACATGTCATCATGATGGGATGCTCTTCGGGTCGTCACACGGG 1065
DB      1635 AGTTCACGTGCTCTTTGGTCCCTGGGGCATACGCTTCTGATGTCTTAATGGG 1694
OY      1066 TCTCTGACGTGACGATCTGCATATGA 1092
DB      1695 TCTTTCAGCTGATGATATGACATCTGA 1721

```

Search completed: August 10, 2003, 02:11:17
 Job time : 220.814 secs

PenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 18:45:33 ; Search time 4490.7 Seconds

(without alignments)
16242.876 Million cell updates/sec

Title: US-09-918-568-46

Perfect score: 1783

Sequence: 1 CGCGTAGCAAAAGCAGGCGT.....ACCCCTGTTCCTGCTAGCCG 1783

Scoring table: IDENTITY_NUC

Gapop 10.0, Bapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match) 0%
Maximum Match) 100%
Listing first 45 summaries

Database :

1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
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41: em_vl:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	1783	100.0	1783	6 AR181961	AR181961 Sequence
2	1783	100.0	1783	6 132526	132526 Sequence 46
3	1783	100.0	1783	6 143471	143471 Sequence 46
4	1741	97.6	1773	14 FLAHAJ3055	L20407 Influenza A
5	1741	97.6	1773	14 FLAHAJ3055	J02127 Influenza A
6	1734.6	97.3	1773	14 FLAHAJ3055J	L20406 Influenza A
7	1734.6	97.0	1773	14 FLAHAJ3055J	L11134 Influenza A
8	1729.8	97.0	1773	14 FLAHAJ3055J	L20409 Influenza A
9	1728.2	96.9	1773	14 FLAHAJ3055J	L20410 Influenza A
10	1726.6	96.8	1773	14 FLAHAJ3055J	L20408 Influenza A
11	1726.6	96.8	1773	14 FLAHAJ3055J	L11142 Influenza A
12	1725	96.7	1773	6 AX399727	AX399727 Sequence
13	1720.2	96.5	1773	14 AB056699	AB056699 Influenza
14	1671.4	93.7	1773	14 FLAOR68HA	L11133 Influenza A
15	1659.4	93.1	1773	14 FLAOR68HA	L11126 Influenza A
16	1649.8	92.5	1773	14 FLAOR68HA	D13580 Influenza A
17	1648.2	92.4	1773	14 FLAOR68HA	D13580 Influenza A
18	1637	91.8	1773	14 FLAOR68HA	L11125 Influenza A
19	1606.4	90.1	1728	6 AR181943	AR181943 Sequence
20	1606.4	90.1	1728	6 E07248	E07248 Haemaggluti
21	1606.4	90.1	1728	6 I32508	I32508 Sequence 28
22	1606.4	90.1	1728	6 I32508	I32508 Sequence 28
23	1565	87.8	1773	14 FLAGDR72HA	L11129 Influenza A
24	1537.8	86.2	1773	14 FLAGDR72HA	L11136 Influenza A
25	1525	85.5	1773	14 FLAGDR72HA	L11139 Influenza A
26	1523.4	85.4	1773	14 FLAGDR72HA	L11140 Influenza A
27	1515.4	85.0	1773	14 FLAGDR72HA	L11141 Influenza A
28	1514.6	84.9	1772	14 FLAPRA76HA	L11141 Influenza A
29	1511.4	84.8	1772	14 FLAPRA76HA	L11141 Influenza A
30	1481.8	83.1	1773	14 FLADE88HA	L11132 Influenza A
31	1462.4	82.0	1773	14 FLADE88HA	AF290441 Influenza
32	1460.8	81.9	1773	14 FLADE88HA	AF290440 Influenza
33	1460.8	81.9	1773	14 FLADE88HA	AF290442 Influenza
34	1459.2	81.8	1773	14 FLADE88HA	AF290439 Influenza
35	1365	76.6	1773	14 FLAONT76HA	L11137 Influenza A
36	1348.2	75.6	1772	14 FLAONT76HA	L11138 Influenza A
37	1325	74.3	1773	14 FLAONT76HA	L11131 Influenza A
38	1322.6	74.2	1772	14 FLAONT76HA	L11130 Influenza A
39	1321	74.1	1772	14 FLAONT76HA	L11135 Influenza A
40	1262.4	70.8	1723	14 AF116201	AF116201 Influenza
41	1066.4	59.8	1077	14 AF231354	AF231354 Influenza
42	1063.2	59.6	1077	14 AF231355	AF231355 Influenza
43	999.4	56.1	1017	14 AF270717	AF270717 Influenza
44	997.8	56.0	1017	14 AF270716	AF270716 Influenza
45	997.8	56.0	1017	14 AF270728	AF270728 Influenza

ALIGNMENTS

RESULT 1
LOCUS AR181961 1783 bp DNA
DEFINITION Sequence 46 from patent US 6337070.
ACCESSION AR181961
VERSION AR181961.1 GI:20224877
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1783)
AUTHORS Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.
TITLE Polypeptides for use in generating anti-human influenza virus
antibodies
JOURNAL Patent: US 6337070-A 46 08-JAN-2002;

FEATURES		Location/Qualifiers	
source	1..1783	/organism="unknown"	
BASE COUNT	610 a 323 c 424 g 426 t		
ORIGIN			
Query Match	100.0%:	Score 1783;	DB 6; Length 1783;
Best Local Similarity	100.0%:	Pred. No. 0;	
Matches 1783;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
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QY	1	CGGCTGACAAAACGAGGGGTTATACCATAGAAAACCAAAAGCAAAACATGGCCATATT	60
Db	1	CGGCTGACAAAACGAGGGGTTATACCATAGAAAACCAAAAGCAAAACATGGCCATATT	60
QY	61	TATCTCATCTCTCTGTTCCACAGCAGTGAAGGGGACCAGATATGATTTGATACCATGCC	120
Db	61	TATCTCATCTCTCTGTTCCACAGCAGTGAAGGGGACCAGATATGATTTGATACCATGCC	120
QY	121	AATTAATTCACAGAGAGGTGACACATTCATAGAGGGGAAAGTCACTGTGACTCATGCC	180
Db	121	AATTAATTCACAGAGAGGTGACACATTCATAGAGGGGAAAGTCACTGTGACTCATGCC	180
QY	181	AAGGACATCTCTTGAGAGAGCCATTAACGGAAAGTTATGCAAACTAAACGGAAATCCCTCCA	240
Db	181	AAGGACATCTCTTGAGAGAGCCATTAACGGAAAGTTATGCAAACTAAACGGAAATCCCTCCA	240
QY	241	CTTGAACAGGGGAGCTGTAGCATTTGCCGATGGCTCTTGGAATCCAAATGTGATAGG	300
Db	241	CTTGAACAGGGGAGCTGTAGCATTTGCCGATGGCTCTTGGAATCCAAATGTGATAGG	300
QY	301	CTTCTAAGTGTCCAGAACGCTCTATATTTGAGAGAAAGAAACCCGAGAGCGGTTTG	360
Db	301	CTTCTAAGTGTCCAGAACGCTCTATATTTGAGAGAAAGAAACCCGAGAGCGGTTTG	360
QY	361	TGTTATCCAGGACGCTTCAATGATTATGAAAGATTGAACATCTCCTCAGCAGCGTGA	420
Db	361	TGTTATCCAGGACGCTTCAATGATTATGAAAGATTGAACATCTCCTCAGCAGCGTGA	420
QY	421	CATTTCGAGAAAGTAAAGATTCTGCCCAAGATAGATGACACAGCATACAACTGGA	480
Db	421	CATTTCGAGAAAGTAAAGATTCTGCCCAAGATAGATGACACAGCATACAACTGGA	480
QY	481	GGTTCACGGGCGCTGCGCGGTGTCTGTATCCATCATTTTTCAGAAACATGGTGGCTG	540
Db	481	GGTTCACGGGCGCTGCGCGGTGTCTGTATCCATCATCTTTTTCAGAAACATGGTGGCTG	540
QY	541	ACAAAGGAAGGATCAGATTATCCGGTGGCAAGAGATCGTACAACTAACACGAGAGA	600
Db	541	ACAAAGGAAGGATCAGATTATCCGGTGGCAAGAGATCGTACAACTAACACGAGAGA	600
QY	601	CAAAATGCTAATTAATTTGGGGGGTGACCAATCCCATTTGATGAGACAGAAACAACTTG	660
Db	601	CAAAATGCTAATTAATTTGGGGGGTGACCAATCCCATTTGATGAGACAGAAACAACTTG	660
QY	661	TACCAAGATGTGGGAACCTATGTTCCGTAGGCACATCAACATTGAAACAAAGGTCAAC	720
Db	661	TACCAAGATGTGGGAACCTATGTTCCGTAGGCACATCAACATTGAAACAAAGGTCAAC	720
QY	721	CCAGAAATAGCAACAAGGCTTAAGTGAATGACAAAGAGTGAATTTCTTTGG	780
Db	721	CCAGAAATAGCAACAAGGCTTAAGTGAATGACAAAGAGTGAATTTCTTTGG	780
QY	781	ACCCCTTGAGATATGTGGGACACCAATTAATTTTGAGAGTACGTATATTTGACACA	840
Db	781	ACCCCTTGAGATATGTGGGACACCAATTAATTTTGAGAGTACGTATATTTGACACA	840
QY	841	GAGTATGATTCACAAATATCGAAAAGAGTAGTTAGGAGATCATGAAACAGAGAACCA	900
Db	841	GAGTATGATTCACAAATATCGAAAAGAGTAGTTAGGAGATCATGAAACAGAGAACCA	900
QY	901	CTTGAGAACTGTGAGACCAAACTCCTTTGGAGCAATTAATCAACATTTACT	960
Db	901	CTTGAGAACTGTGAGACCAAACTCCTTTGGAGCAATTAATCAACATTTACT	960
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QY	961	TTTCACATGTCCACCCACTGACAAATAGTGAATGCCCAATATGTAAATCGAGAG	1020
Db	961	TTTCACATGTCCACCCACTGACAAATAGTGAATGCCCAATATGTAAATCGAGAG	1020
QY	1021	TTGGCTTTAGCAACAGAGCTTAAGGATGTTCCCAATTTGAATCAAGAGATTTGTTGG	1080
Db	1021	TTGGCTTTAGCAACAGAGCTTAAGGATGTTCCCAATTTGAATCAAGAGATTTGTTGG	1080
QY	1081	GCAATACCTGGTTTTATAGAGAGATGGCAAGAAATGTTGACGTTGATGATAC	1140
Db	1081	GCAATACCTGGTTTTATAGAGAGATGGCAAGAAATGTTGACGTTGATGATAC	1140
QY	1141	CATCACAGCAATGACAGGAGTACAGGTTATGACAGACAAAGAAATCCACTCAAAAGCA	1200
Db	1141	CATCACAGCAATGACAGGAGTACAGGTTATGACAGACAAAGAAATCCACTCAAAAGCA	1200
QY	1201	TTTGATGGAATTCACCAAGGTAATTTCTGTGATTGAAGAATTAACCCCAATTTGAA	1260
Db	1201	TTTGATGGAATTCACCAAGGTAATTTCTGTGATTGAAGAATTAACCCCAATTTGAA	1260
QY	1261	GCTGTTGGGAAAGAAATTCGGTAACTTAGAGAAAGACTGAGAACTTGAACAAAAGATG	1320
Db	1261	GCTGTTGGGAAAGAAATTCGGTAACTTAGAGAAAGACTGAGAACTTGAACAAAAGATG	1320
QY	1321	GAAGACGGGTTTCTAGATGTGTGACATACATGCTGACCTTTTATGTTGATGAGAAAT	1380
Db	1321	GAAGACGGGTTTCTAGATGTGTGACATACATGCTGACCTTTTATGTTGATGAGAAAT	1380
QY	1381	GAGAGGACATCTGATCTTCAATGATTTCTAATGTCACAACTGTATAGTAAATCGAATG	1440
Db	1381	GAGAGGACATCTGATCTTCAATGATTTCTAATGTCACAACTGTATAGTAAATCGAATG	1440
QY	1441	CAGCTGAGAGACACGCTCAAGAGACTAGGAAATGATGTTTGAATTTATCAAAATGT	1500
Db	1441	CAGCTGAGAGACACGCTCAAGAGACTAGGAAATGATGTTTGAATTTATCAAAATGT	1500
QY	1501	GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1560
Db	1501	GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1560
QY	1561	GAGTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1620
Db	1561	GAGTCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1620
QY	1621	CAAAATCTTGCATTTATGCTACAGTAGAGGTTTATGTCACCTGCAATCATGATGCT	1680
Db	1621	CAAAATCTTGCATTTATGCTACAGTAGAGGTTTATGTCACCTGCAATCATGATGCT	1680
QY	1681	GGGATCTCTTTCTGGGTGTCTCCAAAGGGTCTGCAAGTGCAGATGATGATGATTA	1740
Db	1681	GGGATCTCTTTCTGGGTGTCTCCAAAGGGTCTGCAAGTGCAGATGATGATGATTA	1740
QY	1741	TAAATGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1783
Db	1741	TAAATGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1783
<hr/>			
RESULT 2			
LOCUS	132526	1783 bp	DNA
DEFINITION	Sequence 46 from patent US 5589174.		
ACCESSION	132526		
VERSION	132526.1	GI:1823317	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1783)		
AUTHORS	Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.		
TITLE	Anti-human influenza virus antibody		
JOURNAL	Patent: US 5589174-A 46 31-DEC-1996;		
FEATURES	Location/Qualifiers		

Source		1. 1783	/organism="unknown"	
BASE COUNT	610 a	323 c	424 g	426 t
ORIGIN				
Query Match	100.0%;	Score 1783;	DB 6;	Length 1783;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1783;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0;
QY	1	CGGCTACCAAGCA	BSGGTTATACCATAGAAAAACCAAAACCAATGGCATAT	60
DB	1	CGGCTACCAAGCA	BSGGTTATACCATAGAAAAACCAAAACCAATGGCATAT	60
QY	61	TATCTCATCTCTCT	CTTCCAGAGTAGAGGGGACAGATATGTCATTTGATACCATGCC	120
DB	61	TATCTCATCTCTCT	CTTCCAGAGTAGAGGGGACAGATATGTCATTTGATACCATGCC	120
QY	121	AATTAATTCACAGAG	AGGTCGACACAATTTCTAGAGGGGAAAGTCACCTGTGACTCATGCC	180
DB	121	AATTAATTCACAGAG	AGGTCGACACAATTTCTAGAGGGGAAAGTCACCTGTGACTCATGCC	180
QY	181	AAGACATCTCTTGAG	AAGACCCATAGCGAAAGTTATGCAAACTAAACCGAATCCCTCCA	240
DB	181	AAGACATCTCTTGAG	AAGACCCATAGCGAAAGTTATGCAAACTAAACCGAATCCCTCCA	240
QY	241	CTTGAATAGGGGAC	CTAGCATTCGCGATGGCTCCTTGGAAATCCAAATGTGATAGG	300
DB	241	CTTGAATAGGGGAC	CTAGCATTCGCGATGGCTCCTTGGAAATCCAAATGTGATAGG	300
QY	301	CTTCTAAGTGTGCCA	BAAGGTCCTATATATTTGAGAAAGAAACCCGAGAGCGTTTG	360
DB	301	CTTCTAAGTGTGCCA	BAAGGTCCTATATATTTGAGAAAGAAACCCGAGAGCGTTTG	360
QY	361	TGTTATCCAGGACCT	TCATGATATAGAAATTTGAACATCTCCACAGAGGTAA	420
DB	361	TGTTATCCAGGACCT	TCATGATATAGAAATTTGAACATCTCCACAGAGGTAA	420
QY	421	CATTTCGAGAAAGT	PAAGATTCTGCCCAAGATAGATGACACAGCATACCAACTGGA	480
DB	421	CATTTCGAGAAAGT	PAAGATTCTGCCCAAGATAGATGACACAGCATACCAACTGGA	480
QY	481	GGTTACAGGGGCTGC	BCGGTGTCTGTAATCCATATTTTCAGAAACATGTGTGCTG	540
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QY	541	ACAAAGGAGGATCA	BAATTTCCGGTGGCAAGGATCTGACAAACATTAAGCGGAGAA	600
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QY	601	CAATGCTAATTAAT	TTGGGGGTGCACATCCATTTGATGAGACAGAAACAAAGCAAT	660
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DB	661	TACCAGATGTGGAG	ACCTATGTTTCCGTAGGCACATCAACATTTGAACAAAGGTCAAC	720
QY	721	CCGAAATAGCAACA	GGGCTTAAAGTGAATGACCAAGAGGTGAATGGAATTTCTTGG	780
DB	721	CCGAAATAGCAACA	GGGCTTAAAGTGAATGACCAAGAGGTGAATGGAATTTCTTGG	780
QY	781	ACCTCTTGATATG	TGGGACACCATTAATTTTGAAGTACTGTATTTCTAATTTGCACA	840
DB	781	ACCTCTTGATATG	TGGGACACCATTAATTTTGAAGTACTGTATTTCTAATTTGCACA	840
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DB	841	GAGTATGATTCAA	ATATTCGAAAAGAGTAGTTCCAGGATCATGAAAACAGAAAGACA	900
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QY	1681	GGGATCTCTT	CTGGTGTGCTCCACAGGGTCTCTGACAGTGCAGATCTGCATATGATTA	1740
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QY	1741	TAACTCAATTT	TAATTAATAAACACCTGTTCTGTAGCCG	1783
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ACCESSION	143471			
VERSION	143471.1	GI:2468715		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 1783)			
AUTHORS	Okuno, Y., Isejawa, Y., Sasao, F. and Ueda, S.			
TITLE	Anti-human influenza virus antibody			
JOURNAL	Patent: US 5631350-A 46 20-MAY-1997;			
FEATURES	location/Qualifiers			
source	1. 1783			

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RESULT 4
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 DEFINITION Influenza A/Japan/305-/57 (H2N2) haemagglutinin (seg 4) gene,
 complete cds.
 ACCESSION L20407.1 GI:305154
 VERSION L20407.1
 KEYWORDS haemagglutinin.
 SOURCE Influenza A virus
 ORGANISM Influenza A virus
 Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza
 A viruses; Influenzavirus A.
 1 (bases 1 to 1773)
 Connor,R.J., Kawoka,Y., Webster,R.G. and Paulson,J.C.
 Receptor specificity in human, avian, and equine H2 and H3
 influenza virus isolates
 Virology 205 (1), 17-23 (1994)

MEDLINE	95065649	
PUBMED	7975212	
COMMENT	Original source text: Influenza virus type A (individual isolate A/Japan/305-/57) RNA.	
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ORIGIN		
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 REFERENCE 1 (bases 1 to 177)
 AUTHORS McCauley, J., Bye, J., Elder, K., Gething, M.J., Skehel, J.J., Smith, A. and Waterfield, M.D.
 JOURNAL Influenza virus haemagglutinin signal sequence
 PUBLISHED FEB5 Lett. 108 (2), 422-426 (1979)
 MEDLINE 80092143
 PUBMED 520584
 TITLE 2 (bases 1 to 1773)
 AUTHORS Gething, M.J., Bye, J., Skehel, J. and Waterfield, M.
 JOURNAL Cloning and DNA sequence of double-stranded copies of
 PUBLISHED haemagglutinin genes from H2 and H3 strains elucidates antigenic
 MEDLINE shift and drift in human influenza virus
 PUBMED Nature 287 (5780), 301-306 (1980)
 COMMENT 81030852
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RESULT 6
FLAHA3055J
LOCUS
DEFINITION
complete cds.
ACCESSION
L20406.1 GI:305114
VERSION
L20406.1
KEYWORDS
haemagglutinin.
SOURCE
Influenza A virus
ORGANISM
viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A.
REFERENCE
1 (bases 1 to 1773)
AUTHORS
Connor,R.J., Kawabuka,Y., Webster,R.G. and Paulson,J.C.
TITLE
Receptor specificity in human, avian, and equine H2 and H3
JOURNAL
virology 205 (1), 17-23 (1994)
MEDLINE
95065649
PUBMED
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COMMENT
Original source text: Influenza virus type A (individual isolate
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DEFINITION
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VERSION
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Best Local Similarity 98.6%; Score 1734.6; DB 14; Length 1773;
Matches 1749; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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RESULT 8
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LOCUS
DEFINITION
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ACCESSION
L20409.1 GI:305116
VERSION
L20409.1 GI:305116
KEYWORDS
haemagglutinin.
SOURCE
Influenza A virus
ORGANISM
viruses: ssRNA negative-strand viruses: Orthomyxoviridae; Influenza A viruses; Influenzavirus A.

REFERENCE
AUTHORS
Connor, R.J., Kawacka, Y., Webster, R.G. and Paulson, J.C.
TITLE
Receptor specificity in human, avian, and equine H2 and H3 influenza virus isolates
JOURNAL
Virology 205 (1), 17-23 (1994)
MEDLINE
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PUBMED
7975212

COMMENT
Original source text: Influenza virus type A (individual isolate A/R1/5-/57) RNA.

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DB 1681 CTTGTTGAGTGTGCTCAACGGGCTCTGACAGTGCAGATGATGATGATGATGAT 1740
QY 1746 CATTTTATATTAATAAAGACCCCTGTTCTCT 1778
DB 1741 CATTTTATATTAATAAAGACCCCTGTTCTCT 1773

RESULT 9
FLAHAS157A 1773 bp RNA linear VRL 27-MAR-1995
LOCUS FLAHAS157A
DEFINITION Influenza A/Singapore/1/57 (H2N2) haemagglutinin (seg 4) gene,
complete cds.
ACCESSION L20410
VERSION L20410.1 GI:305170
KEYWORDS haemagglutinin.
SOURCE Influenza A virus
ORGANISM Influenza A virus
REFERENCE 1 (bases 1 to 1773)
A viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza
A viruses; Influenzavirus A.
AUTHORS Connor, R.J., Kawachi, Y., Webster, R.G. and Paulson, J.C.
TITLE Receptor specificity in human, avian, and equine H2 and H3
Influenza virus isolates

JOURNAL Virology 205 (1) 17-23 (1994)
MEDLINE 95065649
PUBMED 7975212
COMMENT Original source: Influenza virus type A (individual isolate A/Singapore/1/57) RNA.
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BASE COUNT 612 a 319 c 417 g 425 t
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Query Match 96.8%; Score 1728.2; DB 14; Length 1773;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 1745; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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DB 601 GCTAATAATTTTGGGGGGTGCACCAATCCCATTTGATGACAGACAGAACAAAGACATTTGTACA 660
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QY 726 AATGACAACAAGGCGCTAAAGTGAATGACAAAGAGAGTGAATGGAATTCCTTGACCCCT 785
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QY 1746 CATTATTAATTAACACCCCTGTTCTGCT 1778

Db 1741 CATTATTAATTAACACCCCTGTTCTGCT 1773

RESULT 10
FLAHARIS57
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT
FEATURES
source

FLAHARIS57 1773 bp RNA linear VRL 27-MAR-1995
Influenza A/R1/5+/57 (H2N2) haemagglutinin (seg 4) gene, complete
cds.
L20408
L20408.1 GI:305162
haemagglutinin.
Influenza A virus
Influenza A virus
Viruses: ssRNA negative-strand viruses; Orthomyxoviridae; Influenza
A viruses; Influenzavirus A.
1 (bases 1 to 1773)
Conor, R.J., Kawoka, Y., Webster, R.G. and Paulson, J.C.
Receptor specificity in human, avian, and equine H2 and H3
Influenza virus isolates
Virology 205 (1), 17-23 (1994)
95065649
7975212
Original source text: Influenza virus type A (individual isolate
A/R1/5+/57) RNA.
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BASE COUNT 610 a 321 c 418 g 424 t

ORIGIN

Query Match 96.8%; Score 1726.6; DB 14; Length 1773;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1744; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

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QY 66 CATTCTCTGTTACAGCAGTAGAGGAGCAGATATGATTCATGATACATGCAATA 125

Db 61 CATTCTCTGTTACAGCAGTAGAGGAGCAGATATGATTCATGATACATGCAATA 120

QY 126 TTCACAGAGAAGGTGACACATTTCTAGAGGGAAGCTCACTGTGACTATGCCAAGA 185

Db 121 TTCACAGAGAAGGTGACACATTTCTAGAGCGGAACCTGACTGACTATGCCAAGA 180

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Db 181 CATCTTGAAGAGACCCATTAACGAAAGTTATGCAATTAACGAATCCCTCCACTGA 240

QY 246 ACTAGGGAGCTGTAGCAATGGCGGATGCTCTGGAATTCGAATGTGATAGGCTTC 305

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QY 306 AAGTGGCCACAGCGTCTTATATTTGGAGAAAACCCGAGAGCGTTTGTGTTA 365

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QY	1326	CGGGTTTCTAATGATGCTGTGACATCAATGCTGAGACTTTTAACTTCTGATGGAATGAGAG	1385
Db	1321	CGGGTTTCTAATGATGCTGTGACATCAATGCTGAGACTTCTAATCTTCTGATGGAATGAGAG	1380
QY	1386	GACACTTGACCTTTCATGATTTCTAATGTGCAAAATCTGTATGTAAAGTCAGATGCACT	1445
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Db	1681	CTCTTTCTGGGTGTGTCTTCAACGGGGTCTCTGACAGTGCAGATCTGCATATGATTATAGT	1740
QY	1746	CATTTTATATTAATAACACCCCTGTTTCTCT	1778
Db	1741	CATTTTATATTAATAAACACCCCTGTTTCTACT	1773
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LOCUS	FLASIN57HA	Influenza A virus (A/Singapore/1/57 (H2N2))	hemagglutinin (HA)
DEFINITION	gene, complete cds.		
ACCESSION	L11142		
VERSION	L11142.1	GI:408676	
KEYWORDS	haemagglutinin.		
SOURCE	Influenza A virus (A/Singapore/1/57 (H2N2))		
ORGANISM	Influenza A virus (A/Singapore/1/57 (H2N2))		
REFERENCE	1 (bases 1 to 1773)		
AUTHORS	Schafer,U.R., Kawaboka,Y., Bean,W.J., Suss,J., Senne,D. and Webster,R.G.		
TITLE	Origin of the pandemic 1957 H2 influenza A virus and the persistence of its possible progenitors in the avian reservoir		
JOURNAL MEDLINE	Virology 194 (2), 781-788 (1993)		
PUBMED	93376567		
FEATURES	7684877		
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Matches 1744;	Conservative	0;	Mismatches	28;	Indels	0;	Gaps	0;	
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QY	246	ACTAGGGAGCTGACATTGGCGGATGGCTCCTTGGAAATCCAAATGATGATAGGCTCT	305						
DB	241	ACTAGGGAGCTGACATTGGCGGATGGCTCCTTGGAAATCCAGATGTGATAGGCTCT	300						
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DB	301	AAGTGTGCCAAGATGGTCTTATATATGAGAAAAGAAAACCCGAGAGAGGTTTGTTTA	360						
QY	366	TCCAGGCAAGCTTCAATGATTTATGAAGAATTGAACATCTCTCGACAGCGTGAACATTT	425						
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QY	606	GCTAATAATTTGGGGGGTGCACCAATCCCATTTGATGAGACAGACAAAGAAACATTTGTACA	665						
DB	601	GCTAATAATTTGGGGGGTGCACCAATCCCATTTGATGAGACAGACAAAGAAACATTTGTACA	660						
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RESULT 12
AX399727 1773 bp DNA linear PAT 06-JUN-2002
DEFINITION Sequence 4 from Patent WO0224876.
ACCESSION AX399727
VERSION AX399727.1 GI:21335485
KEYWORDS
SOURCE Influenza A virus (STRAIN A/SINGAPORE/1/57)

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ORGANISM Influenza A virus (STRAIN A/SINGAPORE/1/57)
VIRUSES; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza
A viruses; Influenzavirus A; Influenza A virus; unidentified
subtype.
REFERENCE 1
AUTHORS Perko,B., Borov,A., Romanova,I., Kalinger,D. and Kalinger,H.
TITLE Live vaccine and method of manufacture
JOURNAL Patent: WO 0224876-A 4 28-MAR-2002;
POLYMER SCIENT IMMUNO BIO FORSCH (AT)
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source location/Qualifiers
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BASE COUNT 611 a 321 c 417 g 424 t
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Best Local Similarity 98.3%; Pred. No. 0;
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RESULT 13
AB056699 1773 bp RNA linear VRL 10-DEC-2002
LOCUS AB056699
DEFINITION Influenza A virus A/Kayano/57(H2N2) HA gene for hemagglutinin,

complete cds.
AB056699
AB056699.1 GI:26453382
INFLUENZA A VIRUS (A/KAYANO/57(H2N2))
VIRUSES: ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A; Influenza A virus; H2N2 subtype.
REFERENCE
1 Tsuchiya, E., Sugawara, K., Hongo, S., Matsuzaki, Y., Muraki, Y. and Nakamura, K.
TITLE
The antigenic structure of the haemagglutinin of human influenza A/H2N2 virus.
JOURNAL
Unpublished
AUTHORS
2 (bases 1 to 1773)
Tsuchiya, E.
TITLE
Direct Submision
SUBMITTED (07-MAR-2001) EMI Tsuchiya, Yamagata University School of Medicine, Department of Bacteriology, Iida-Nishi 2-2, Yamagata, Yamagata 990-9585, Japan (E-mail: etakashi@med.id.yamagata-u.ac.jp, Tel:81-23-628-5249(ex.5249), Fax:81-23-628-5250)
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RESULT 14
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ORIGIN

Query Match	93.7%	Score 1671.4	DB 14	Length 1773
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Matches 1708	Conservative	0	Mismatches 61	Indels 0
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QY	306	AAGTGTCCAGAAAG	CTCTATATTTGAGAAAGAAACCCGAGAGACGGTTGTGTTA	365
DB	301	AAGTGTCCAGAAAG	CTCTATATTTGAGAAAGAAACCCGAGATACGTTGTGTTA	360
QY	366	TCCAGGAGGCTTCA	AGATTATGAAGATTGAACATCTCTCAGCAGCGTGAACAATTT	425
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DB	481	ATGGGCGCTGGCGG	CTCTGATATCCATCTTTTGAAGAACATGGTCTGGGCTGACACG	540
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 ACCESSION
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 Influenza A virus (A/Berlin/3/64 (H2N2))
 Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A; Influenza A virus; H2N2 subtype.
 REFERENCE
 Schaefer J.R., Kawoka, Y., Bean, W.J., Suss, J., Senne, D. and Webster, R.G.
 TITLE
 Origin of the pandemic 1957 H2 influenza A virus and the persistence of its possible progenitors in the avian reservoir
 JOURNAL
 Virology 194 (2), 781-788 (1993)
 MEDLINE
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PUBMED 7684877
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 Matches 1702; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

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Job time : 4495.7 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 19:11:43 ; Search time 2736.47 seconds
(without alignments)
15836.045 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	63.2	3.5	1201	13	BX376097 BX376097
C 2	62.2	3.5	1101	29	CNS0039G AL063921 Drosophila
C 3	35	3.1	639	29	CNS0170D AL108367 Drosophila
C 4	54.2	3.0	994	13	BX414650 BX414650

5	52.8	3.0	1101	29	CNS0006J	AL062049 Drosophila
C 6	52.4	2.9	997	29 <td>CNS005FE</td> <th>AL060767 Drosophila</th>	CNS005FE	AL060767 Drosophila
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C 10	49.6	2.8	468	29 <td>CNS06XGD</td> <th>AL419699 17 end of</th>	CNS06XGD	AL419699 17 end of
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C 13	48.6	2.7	938	29 <td>CNS006RT</td> <th>AL065906 Drosophila</th>	CNS006RT	AL065906 Drosophila
C 14	48.4	2.7	1201	13 <td>BX461128</td> <th>BX461128 BX461128</th>	BX461128	BX461128 BX461128
C 15	47.8	2.7	500	9	A0087765	A0087765 A0087765
C 16	47.6	2.7	1200	29 <td>CNS016CO</td> <th>AL106578 Drosophila</th>	CNS016CO	AL106578 Drosophila
C 17	47.4	2.7	1101	29 <td>CNS0106X</td> <th>AL098595 Drosophila</th>	CNS0106X	AL098595 Drosophila
C 18	47	2.6	1101	29 <td>CNS000D1</td> <th>AL065414 Drosophila</th>	CNS000D1	AL065414 Drosophila
C 19	46.8	2.6	1200	13 <td>BX414560</td> <th>BX414560 BX414560</th>	BX414560	BX414560 BX414560
C 20	46.2	2.6	1106	13 <td>BX438107</td> <th>BX438107 BX438107</th>	BX438107	BX438107 BX438107
C 21	46	2.6	1001	13 <td>BX329654</td> <th>BX329654 BX329654</th>	BX329654	BX329654 BX329654
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C 23	46	2.6	1201	9	AL536104	AL536104 AL536104
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C 25	45.8	2.6	1101	29 <td>CNS016HF</td> <th>AL106749 Drosophila</th>	CNS016HF	AL106749 Drosophila
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C 29	45.2	2.5	932	9	AL514901	AL514901 AL514901
C 30	45.2	2.5	941	28	A2682404	A2682404 ENT1016TF
C 31	45.2	2.5	1044	13 <td>BX415231</td> <th>BX415231 BX415231</th>	BX415231	BX415231 BX415231
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ALIGNMENTS

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DEFINITION CDNA Clone CS0DC022YH12 5-PRIME, mRNA sequence.

ACCESSION BX376097
VERSION BX376097.1 GI:30434756
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE
1 (bases 1 to 1201)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization

JOURNAL

COMMENT

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 2866.f

Contact: Feng Liang Email: fliang@life.techn.com URL :

http://fulllength.invitrogen.com/Invitrogen Corporation 1600

Fairday Avenue Genoscope sequence ID : CS0DC022B6060P1.

Location/Qualifiers

FEATURES

source

1..1201


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ORIGIN

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893 AAGGACACTTGAGAACTGTGAGACCAAAATGCCAACTCCTTTGGAGCAATTAACAA 952
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
872 MGTGKTKTGMKMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMM 813
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
953 CATTAACCTTTTACATGTCCACCCACATAGATAGTGGTCCCAATATATTAAT 1012
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
812 MTKMMHNVCAAAAADAGGAAAAAAGAAAAAAGAKAKAKMMHMMHMMHMMHMMHMMHMM 753
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
1013 CGGAGAGTGTGCTTACAGACAGCAAGTAAGATGTTCCCAATGTAATCAAGAGAT 1072
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
752 GKMKGKMTMHTMTKMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMM 693
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
1073 TGTTTGGGGCAATACCTGTTTATAGAAGAGAGATGCAAGATGTTGACGGTTGGT 1132
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
692 TTTMMGKTKTMTMTMBNMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMM 633
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
1133 ATGATACCATCACAGCAATGACAGGATCAGGATGATGACAGACAGCAAAATCCACTG 1192
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
632 KNNKKNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 575
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
1193 AAAAGGCACTTGTGAGAACTACCAACAAGTAATTTGTGATGAAAAATTAACACCC 1252
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
574 KNNKKNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 515
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
1253 AATTGAAGTGTGTGGAAAGATTCGTAATGAGAAAAAGACTGGGAACTTGAACA 1312
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
514 NMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMM 455
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
1313 AAAAGATGAGACAGCGTTTCTAGATGTGTGACATACATGCTGAGCTTTAGTCTGA 1372
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
454 KNNAAAAMAAAAGKCKKNNNAKAAAANAANAANAANAANAANAANAANAANAANAANA 395
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1373 TGAAGATGAGAGACACTTGACTTTCATGATTTCTAATGTCAGAATCTGTAGTAAG 1432
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394 KKKKAKNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 335
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
1433 TCAGAAATGCACTGAGACAAAGCTCAAGAACTGTGAAGATGTTTGAATTTTATC 1492
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
334 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 275
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
1493 ACAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1552
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274 KANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 215
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
1553 ATGAGAAGAGTCTAACTAATAGAAATGAATCAAGGGGTAATAA 1599
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
214 CCACAAAAACAATAAGTAATGACACCAAAAAAATAACAGCAAGA 168
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RESULT 2
CNS00396/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
BASE COUNT
ORIGIN
Query Match      3.5%; Score 62.2; DB 29; Length 1101;
Best Local Similarity 15.5%; Pred. No. 0.003;
Matches 87; Conservative 262; Mismatches 209; Indels 3; Gaps 1;

1065 AAGAGATGTTGGGCAATAGCTGTTTATAGAGAGATGCGAAGAGATGTTGA 1124
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
1099 AARWGDYDTRDTRKDDMDWTMTWTKMDRADRRMAGDADRMADGAGTMTATMMW 1040
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
1125 CGTTGTATGATACCATCACAGCAATGACAGGATCAGGATGATGACAGCAAGA 1184
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1039 HMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMMHMM 980
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1185 ATCCACTCAAAAGGACTTTGATGATATCAACAAGTAATTTCTGATTTGAAAAGAT 1244
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979 RRDGKRKRKDDKDDGDDKGGKRRKRAAAKAAKATKMDMDMDKMDKMDKADKRRAD 920
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1245 AAACCCCAATTTGAAGCTGTTGGAAAGATTCGGTACTTAAGAGAAAGACTGGGAA 1304
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919 DDDGAGDDKDDGKDDADDDTDGTRKDDDKKDDMDKAKGTWDDATWMAATDMMWGW 860
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
1305 CTGGAACAAAAGATGAGAGAGCGGTTCTGATGTGTGACATACATGATGAGCTTT 1364
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
859 ADADMMTDDAADDMMADDDRDNAAMKMDMAMGARTADRRDMDGAKRGAR--KR 803
      ::::::::::::::|::::::::::::|::::::::::::|::::::::::::|
1365 AGTCTGATGAGAAATGAGAGACACTTTCATGATTTCTAATGTCAGAATCTGTA 1424
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```

Db	802	NRKRAADKROA	AD	RDDAAATWTTT	TTTTTTT	NDTDDWKKKJDTWFWMA	DRHWDRDDDD	743
QY	1425	TAGTAAAGTCAG	ATGTCAGCTGAGACACACGTC	CAAGAACTAGCAAA	TGGATGTTTGA	1484		
Db	742	DRAGTAKRRR	RTWTRWRKRR	RDTRRDDADDDTA	ADDDRRRGGDDGADG	KKTKTKRRR	683	
QY	1485	ATTTATGACA	AAATGTCATGATGAA	TGCATGAATGCTGTG	AAAAACGGACATATG	ATTA 1544		
Db	682	RDRAATWDT	DMAWMD	MAWTTTDDT	DDWDRDRRRKARRRRRTT	ATAAWDWTWKXMD	623	
QY	1545	TCCCAAGTATG	AAAGACGCTAAACTAAATCA	AAATGAATCAAA	CGCGTAAATGAG	1604		
Db	622	MAKMDWKTR	ADRWMD	MAADTWT	DDAKRDWAKA	RAWARRDRRAA	ADRRWTKGTT	563
QY	1605	CAGCATGGG	GGGTTTATCAAT	1625				
Db	562	TATWTTMA	ARAAMWMA	WMAWAT	542			
RESULT 3								
CNS0170D								
LOCUS								
DEFINITION								
Drosophila melanogaster genome survey sequence SP6 end of BAC								
BACN37M13 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.								
AL108367								
AL108367.1 GI:5628671								
GSS.								
Drosophila melanogaster (fruit fly)								
Drosophila melanogaster								
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.								
1 (bases 1 to 639)								
Genoscope.								
Direct Submission								
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRI cedex - FRANCE (E-mail : sege@genoscope.cns.fr - Web : www.genoscope.cns.fr)								
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk/. This Drosophila melanogaster BAC library (DrosBAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelOBAC11.								
FEATURES								
source								
1. 639								
/organism="Drosophila melanogaster"								
/mol_type="genomic DNA"								
/db_xref="taxon:7227"								
/clone="BACN37M13"								
/clone_11b="DrosBAC"								
/plasmid="pBelOBAC11"								
/note="End : SP6"								
BASE COUNT								
389 a 53 c 46 g 52 t 99 others								
ORIGIN								
Query Match. 3.1% Score 55; DB 29; Length 639; Best Local Similarity 37.9%; Pred. NO. 0.11; Matches 136; Conservative 53; Mismatches 169; Indels 1; Gaps 1;								
QY	1238	AAAGATPAAC	CAACCC	AAATTGAC	CTGTTGGG	AAAGAAATTCGTA	CTTAGAGAAACAG	1297
Db	106	AAAAAATAT	ATATCYCC	GGGATATA	AKGTTTAA	AAAAAATATGCA	RAARAACAAMAY	165
QY	1298	TGGAACACT	GACA	AAAAGAT	GGAAGACGGG	TTCTAGATG	TGTGACATACAT	1357
Db	166	WRAWMWAT	WMAAAG	AAAAAATA	AAAAAARA	AAAGTAGT	AGAGCTATTAA	225
QY	1358	AGCTTTAGT	CTGAT	GGAAAAAT	GAGAGAC	ACTTGAC	TTCATGATTTCTA	1417

[illegible]

Db 813 AARAWMARWMAAAAMWAAADDDMMWMMWMDAADAAMW--AAMDTRDKRANRAADPAR 756

OY 1494 CAATGTGATGATGATCATGAATAGTGTGTAAGGAGCATATGTTTCCCACTA 1553

Db 755 AAAAAAMWGWGGGADAGADKRAAAWMDAGGDKRDWRAARDDDAARRAAAAA 696

OY 1554 TGAAGAGAGTCTAACTAAGTAAGTAATCAAAAGGGGTAAATTTGACACAGCATCGG 1613

Db 695 ATAWATWMMKKDKMAAAAMADPAKGRDDARDMMWAMTTTTTTTTTAAAADRAW 636

OY 1614 GGTATTCAATCCCTGCCATTTTATGCAACATGACAGGTCPTATGTCTACTGGCAATCAT 1673

Db 635 KKKKATTTTTTTTTTTTTTTTTTTTAKKTITAKMTDMADMTTTTTTTTTTTTTTAAAT 576

OY 1674 GATGGCTGGGATCTCTCTGGGAG 1698

Db 575 KKTKTCTKTCTKKTCTTTTDDTMD 551

RESULT 5	
CNS0006J	
LOCUS	1101 bp DNA linear GSS 03-JUN-1999
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC #
	BACR01M22 of RPCI-98 library from Drosophila melanogaster (fruit
	fly), genomic survey sequence.
ACCESSION	AL062049
VERSION	AL062049.1 GI:4938511
KEYWORDS	GSS.
SOURCE	Drosophila melanogaster (fruit fly) .

REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
1 (bases 1 to 1101)
Genoscope.
Direct Submission

COMMENT

Submitted 22-JUN-1999) Genoscope - Centre National de Séquençage
BP 191 91006 Evry cedex - FRANCE (E-mail : seque@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org/TheBDGP/Drosophila>
melanogaster BAC library was prepared by Kazutoyo Oseegawa and
Aaron Mamosser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPci-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y¹; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

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/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR01M22"
/clone.lib="RPCI-98"
/note="end : TET3"

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Best Local Similarity	25.7%	Pred. No. 0.39		
Matches 151	Conservative 165	Mismatches 268	Indels 4	Gaps 2

QY 1098 AGAAGGAGCATGGCCAGAAGATGGTGTGACGGTTGGTATGCATTACCATCACAGCATGACCA 1157
 Db 496 RRAATGAAATRRNARAGRTTAAWTTGAAGAAAAAAATTTAAAGAAAAAAAWATA 555

OY	1158	GGGATCAGGGATGCGAGCGCAAGAGCATCCACCTCAAAAGCATTTGTGGAATCACCA	121
Dd	556	TKAAATTTTTTTRRRRNGATATTTTDTAKAAAAAAAAAAATATTAGAAAAAGAAAAAA	615
OY	1218	CAAGTAAATTCGTGATTGAAAACATAAACACCCCAATTTGAAGCTGTGGGAAAGATT	1277
Dd	616	AARAAAGCTTTGGAAGAAAAAATAAARAKMAAAAAAGGAAAAAATAATMAA	675
OY	1278	CGGTAACTAGAGAAAAGCTGGAGACTTGAACAAAAGATGTGAAGCGGCTTTGAGA	1337
Dd	676	AAKAAATGKTATATAAAAAAAAAAAGAGGAKGGKRGCAARRGGGGRAMRAAAA	735
OY	1338	TGTGTGACATACATGCTGAGCTTTTAGTTCTGATGGAAAAATGAGAGACACTTGACTT	1397
Dd	736	KTKRKKKTKTKRRRAAGRRARRAAAGAAAAAARAADAATTKGTAKMAAMRTAAWKKD	795
OY	1398	TCGATGTTCTATGATCAAGATCGTATGATGATGATGATGATGACGCTGAGACAAAGCT	1457
Dd	796	WKATDAAAKAAARTRDWTAKADKTKWGAATAAGAAAGAAARRRRGKGGKOTRRR	855
OY	1458	CAAGAACATAGAAATGAGATCTTTGAATTTTATCACAATGTGATGATCATGAA	1517
Dd	856	ARGAGDGDAAKAAWMAAAMAATATATATADDRRAKAWDKRAAARAAAADRKD - KGRRA	914
OY	1518	TAGTGTGAAAAACCGGCACATATGATATCCCAAGATCAAGAACAGCTTAACCTAATAG	1577
Dd	915	GWGTGWRRAARTRTKAKARRGAGAGAKAKARRAKGDWKKGMKKMDKDAAMAARAKKGT	974
OY	1578	AAATGAATCAAGAGGGTAAATTTGAGCAGCATGGGGTGTATCAAACTCTTGCATTTA	1637
Dd	975	GDWKKRARK -- AKTGMKARADKBWRMAADDTWRFTKAMWMTDWRNATATKDKDFTDKA	1031
OY	1638	TGCTACATACAGAGCTTCTATGTACATCGGCAATCATATATGCTGGGAT	1685
Dd	1032	KKGAAMKTTTTRRAAKAKADDTATATATATAMDDADKAAARAKAK	1079

CNS005TE/c	CNS005TE	997 bp	DNA	linear	GSS 03-JUN-1999
LOCUS					
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC # BAC1K22 of Rpci-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
ACCESSION	AL060767				
VERSION	AL060767.1	GI:4943573			
KEYWORDS	GSS.				
SOURCE	Drosophila melanogaster (fruit fly)				
ORGANISM	Drosophila melanogaster				

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 997)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

COMMENT

determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see http://www.fruitfly.org/TheBDGP/Drosophila_melanogaster_BAC_library was prepared by Kazutoyo Osoegawa and Aaron Messemser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Kossell Park Cancer Institute in Buffalo, NY. The library is named RPc1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPac Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES	Location /Qualifiers
source	1..997 /organism="Drosophila melanogaster" /mol_type="genomic DNA" /db_xref="taxon:7227" /clone="BACR12K22" /clone_lib="RPCI-98" /note="end : TET3"
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ORIGIN	
Query Match.	2.9% ; Score 52.4; DB 29; Length 997;
Best Local Similarity	17.1% ; Pred. No.0.46;
Matches 68; Conservative	139; Mismatches 190; Indels 0; Gaps 0;
OY	1032 AACAGCAATGAAAGAATTGTCCCGCATTTGAATCAAAGAGATTCTTGGGCCAATAGCTGC 1091
Dd	827 RARARRRRGAARRARRRGRRAARAARRRRARGRRRRARGRRRGRRRGRRR 768
OY	1092 TTTTATAGAACGAGCATTGTCGCAAGCAATGTTTGACCGCTGTA TGATGCATCACAGCA 1151
Dd	767 GRRRAARAARAARAARGAARAARRRRARAATAAARRRRRRRRRRBGARARARRRA 708
OY	1152 TGACCAGGCATCAGGATATGCAACAACAAGAATCCACTCAAAAAGCATTTGATGAAT 1211
Dd	707 RRARAGAGAAARRRRRRRGAGAGARRRGRRGAGARRRRRRRMRTRRARRRRAR 648
OY	1212 CACCACAGGTAATTTCTGTGATTGAAGATAACACCCAATTTGAAGCTGTTGGGA 1271
Dd	647 RGAGARRRARGARRRRRRGRGRRRRRGARRRRRARGRRRARGARRRRRR 588
OY	1272 AGAATTCGCTAATTAGAAAAAGACTGAGACTTGAAAAAAGATGGAAGACGGGTT 1331
Dd	587 RRRARAGAGARRRRRRRGARRARRARARRRRRRRAAARBAGABAGARAGRA 528
OY	1332 TCTGATGCTGTGACATTCATCATGCTGCAGCTTTTGTTCTGATGGAATAATGAGACACT 1391
Dd	527 GRAARRARRRRRRRRRGARRRRGRRGRRRARRRRARAARAARRRRRRRAGAR 468
OY	1392 TGACCTTCATGATTCATATGTCAGAAATCTGTATAGT 1428
Dd	467 RRTNTNNNNNNNNNNNNNNNNNNNAGCNTNNTNTNTNT 431
RESULT 7	
LOCUS BX463903/c	1167 bp mRNA linear EST 22-MAY-2003
DEFINITION	CSDDP015VA21 5-PRIME, RNA sequence.
VERSION	BX463903
KEYWORDS	BX463903.1 GI:31629582
SOURCE	EST.
ORGANISM	Homo sapiens (human)
LOCUS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1167) Full-length CDNA libraries and normalization Unpublished Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seqre@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to technology cluster 6974.f For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CSIAF004ZELIOP1&cluster=6974.f . Contact : Feng Liang Email : fliang@life.techn.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSIAF004ZELIOP1.
TITLE	
AUTHORS	
JOURNAL	
COMMENT	Location /Qualifiers
FEATURES	

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   /clone="CS0DF015YA21"
   /tissue_type="FETAL BRAIN"
   /dev_stage="fetal"
   /clone_1lb="Homo sapiens FETAL BRAIN"
   /note="Organ: Brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

BASE COUNT      190 a      163 c      114 g      356 t      344 others

ORIGIN

Query Match          2.9%; Score 52.2; DB 13; Length 1167;
Best Local Similarity 26.5%; Pred. No. 0.53; Mismatches 237; Indels 0; Gaps 0;
Matches 127; Conservative 115;

QY    1112 AAGCAATGGTTGACGGTTGGTATGATGCATCCACAGCAATGACCAGGATCAGCGTATG 1171
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Db     1097 AAAAAARCKHKVHKBKKTFTHMAMGMMAAAMAAGAARGAAARKKTDAGAAAAMCG 1038

QY    1172 CAGCAGACAAGAATCCACTCAAAGCATTTGATGGAATCACCAACAGSTAATTCTG 1231
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Db     1037 TAMMMHGSCCGMNMNGAMCGMKWVGSGKKTTTTTTTTTTTAMKTMCGAMKAATGK 978

QY    1232 TGATTGAAAGATTAACACCCCAATTTTGAAAGTCGTGGGAAAGATTCGGTACTTAGA 1291
       | | :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db     977 TAAKKAADKDKTKTKMTWTNTTKKGKGGTMMGKNTKKMGKAAAMMTKMTTGTGGAAA 918

QY    1292 AAAGACTGGAGACCTTGACAAAGAAGATGAGAGAGCGGTTTCTGATGTGTGACATACA 1351
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Db     917 AAAAMAKKGAARAGAGCGKKAATAAAMPTKKKMGTGMMKMMKAAAKKMDKAAAKATAT 858

QY    1352 ATGCTGACCTTTTACTTCTGATGGAANAATGAGAGACACTTGACTTTCATGATTCATG 1411
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QY    1412 TCAGAATCTGTATAGTAAGTGAAGTGCAGCTGAGACAGCAACGTCOAAGACTAGAA 1471
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QY    1472 ATGATGATTTTGAATTTTATCACAATGATGATGATGCATGATGAATGATGTAAGAACG 1531
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QY    1532 GGACATATGATTAATCCCAAGTATGACAAGAGAGTCTAAACTPAATAGAAATGAATCAA 1590
       :|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|
Db     677 KAAAAAANKKAKAGKRTAMKRRKATTAAMAMWMTKKAHTTKTAAAAAAMAAKAAAMWRAA 619


RESULT 8
CONS02JEX/c
LOCUS      CNS02JEX               847 bp      DNA           linear      GSS 01-SEP-2000
DEFINITION Tetradodon nigroviridis genome survey sequence PUC-Ori end of clone
              14310 of library G from Tetradodon nigroviridis, genomic survey
              sequence.
ACCESSION   AL200130
VERSION     AL200130.1   GI:7858475
KEYWORDS    GSS: genome survey sequence.
SOURCE      Tetradodon nigroviridis
ORGANISM   Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
              Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
              Tetraodontidae; Tetradodon.
REFERENCE   1
AUTHORS    Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
              Bernot,A., Pizanes,C., Wincker,P., Brottier,P., Quetier,F.,
              Saurin,W. and Weissendach,J.
TITLE      Estimate of human gene number provided by genome-wide analysis

```

[illegible]

JOURNAL

Submitted (23-JUL-1999) Genoscope - Centre National de Séquençage
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)

COMMENT

Determination of this BAC-end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (EDGP) -
<http://www.edgp.ebi.ac.uk> . This Drosophila melanogaster BAC
 library (Dros BAC) was made by Alain Billaud at CEPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MRC
 project grant . The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector
 pBelobAC11.

FEATURES

source

Location/Qualifiers

1. 1101
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACN37D10"
 /clone_1lb="DrosBAC"
 /plasmid="pBelobAC11"
 /note="end : Sp6"

BASE COUNT 274 a 268 c 128 g 73 t 358 others

ORIGIN

Query Match 2.8%; Score 50.2; DB 29; Length 1101;
 Best Local Similarity 21.0%; Pred. No. 1.5;
 Matches 109; Conservative 198; Mismatches 208; Indels 4; Gaps 2;

QY 1208 GAATCACCACACAGCAAGTAATTCGTGATTTGAAAAGATTAACCCCAATTTGAAGCTGTGG 1267
 Db 584 KDRWDARGAARAAARAAAADAARAAKATWMAAAAAAAAAAAAAAAAAAATTTTAA 643
 QY 1268 GGAAGAAATTCGGTTAATTGAGAAAAGACGTGCAACTGGAACAAAAGATGAAGACG 1327
 Db 644 AAAAAGCGMGKTGKGGKAAADGGAAGAAAMRGGRGRRRAARAAADAKFAAAAAA 703
 QY 1328 GGTTCAGATGTGTGACATCAATGCTGAGCTTTAGTTGATGAGGAAAATGAGAGAGA 1387
 Db 704 AAAAAAAAAAADAGK-RRKKKDGKDGSKATKTATMAAGKRDWGTATMAWTWDATWA 760
 QY 1388 CACTGACTTTCATGATTTCTAATGTCAAGAAATCTGTATAGTAAAGTCAGATGACGTGA 1447
 Db 761 DTWKATATPDADRAAAGRRKRDARTTAADGRRARTRRRAAAGKRRARGARBARAARR 820
 QY 1448 GAGACAACGCAAGACAGTACAGAAATGATGATTTTGAATTTTATCACAATGTGATGATG 1507
 Db 821 AADRDMDMAAAAAAAAAA- AATWTTWRDWMWDMDWDRWDDTTAAWMDARARARR 879
 QY 1508 AATGATGAATAGTGTGTAACAAAACGGACATATGATTTCCAGATATGAAGAAGATCTA 1567
 Db 880 RRRRRRRRRARRARARAADDTDKRADAATDXTTKTWTYTTDDDDMKARDRWMAAK 939
 QY 1568 AACTAATATGAATGAATCAATCAAGGGCTAAATATGACACAGCATGGGGTTTATCAATCC 1627
 Db 940 AADAMWRRARRADMAATAKDDDKWKMGGRGKRGKDKKRWDKGKTGKKDDDDMDKTW 999
 QY 1628 TTGCCCTTATGCTCATAGCAGGTCTATGTACAGCGGAATCATGATGCGTGGGATCT 1687
 Db 1000 TTRMMWMTWTRTWMDWMDGGRGRGKRWTRKRGKAMRADAMARDDTCKDTRADKDRRT 1059
 QY 1688 CTTTCTGGGTGTGCTCAACGGGCTCTGCAGTGCAGA 1726
 Db 1060 DTTKRDGDWRRKDRKDKRRDKKGDXTTKKDATTWDDDA 1098

RESULT 10

CNS06XGD/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

CNS06XGD 468 bp DNA linear GSS 06-JUL-2001
 T7 end of clone XAX0A00207 of library XAX0A from strain CBS 7064
 of *Pichia farinosa*, genomic survey sequence.
 AL419699
 AL419699.1 GI:12202877
 GSS.
Pichia farinosa


```

RESULT 12
BX406178/c 1201 bp mRNA linear EST 13-MAY-2003
LOCUS BX406178 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION CS0DM010YN11 3-PRIME, mRNA sequence.
ACCESSION BX406178
VERSION BX406178.1 GI:30639385
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0AM010CG06NP1.
FEATURES
Source
1.1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM010YN11"
/tissue_type="FETAL LIVER"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL LIVER"
/notes="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT 239 a 246 c 241 g 220 t 255 others
ORIGIN
Query Match 2.7%; Score 48.8; DB 13; Length 1201;
Best Local Similarity 25.0%; Pred. No. 3.1; Mismatches 0; Gaps 0;
Matches 70; Conservative 100;
1282 AACCTAGAGAAAAGCTGAGAACTGAACAAAAGAGAGCGGTTCTAGATGTG 1341
DB 1193 AAAAAAAAAAATATWTATATATTTTWTATATADATADWATATATATTTT 1134
QY 1342 TGCAATACATGCTGAGCTTTTGTGATGGAAGAGAGAGAGAGAGAGAGAGAG 1401
DB 1133 TTTTDRDDRRRTDRDTDTTADWADAARADAARAARAARATWDRTTTAMWRTTDT 1074
QY 1402 GATTCTAATGTCAGAAATCTGTATAGTAAGTCAGATGACGCTGAGAGCAACGTC 1461
DB 1073 MDTWAKADTTTAAADADATRTTDDTAAATADWAKATWADWAKATADATTTWRA 1014
QY 1462 GAATGAGAAATGATGTTTGTATATCAAAATGATGATGATGATGATGATGATG 1521
DB 1013 TWWAAMARRATTRKADTTADRRTTCTTTTDDDRDTADBRADTARDCRRRTG 954
QY 1522 GTGAAAAACGGACATATGATATCCCAAGTATGAGAAG 1561
DB 953 AVDRTWDMWMAATTTDTWBRKTDADADADADADADAD 914

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ACCESSION AL065906
VERSION AL065906.1 GI:4944874
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 938)
AUTHORS Direct Submission
TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
COMMENT - Web: www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org/The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPc1-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp. The same strain used for the BDGP's
PI and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
Source
1.938
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR14J11"
/clone_lib="RPc1-98"
/notes="end: T7"
BASE COUNT 86 a 98 c 85 g 334 t 335 others
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Best Local Similarity 22.6%; Pred. No. 3.3; Mismatches 211; Indels 5; Gaps 1;
Matches 106; Conservative 148;
1007 TAAATCGAGAGATTGCTTACCAACAGAGTAAGATGTCCTCCAGATTGATCA 1066
DB 925 DAKADAKADAKADAKADAKADAKADAKADAKADAKADAKADAKADAKADAK 866
QY 1067 GAGAGATTGTTGGCAATAGCTGTTTATATGAAG----GAGGATGCAAGAGTGT 1121
DB 865 KKKKKADKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 806
QY 1122 TGACGGTGTGATGATCATTACATCAGCAAGTACCAAGGATGAGGTATGACG 1181
DB 805 AKDKADADADADADADADADADADADADADADADADADADADADADADAD 746
QY 1182 AGAATCCACTCAAAAGCATTTGATGATGATGATGATGATGATGATGATGAT 1241
DB 745 ADAKADAKAKAAAKKAAKADKADKADKADKADKADKADKADKADKADKAD 686
QY 1242 GATTAACACCCATTTGAAGCTGTTGGGAAGAATTCGTTAAGTATGAGAAAG 1301
DB 685 KAKRAAAAAMWMAADADADADADADADADADADADADADADADADADAD 626
QY 1302 GAACCTGAACAAAAGATGAGAGAGGAGGTTCTACATGTTGGATGATGATG 1361
DB 625 RKDAGTAATKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAK 566
QY 1362 TTATGCTGATGAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1421
DB 565 GKATGKTWTTTATATATATATATATATATATATATATATATATATATATAT 506
QY 1422 GTATAGTAAAGTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1471

```


[illegible]

FEATURES

cg1-bin/cluster.cgi?seq=CS0DF023AC050p1&cluster=3830.f. Contact :
Feng Liang Email : liang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DF023AC050p1.
Location/Qualifiers

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/clone="CSDDP023YD09"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_id="Homo sapiens FETAL BRAIN"
/notes="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

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Query Match	2.7%	Score 48.4	DB 13	Length 1201
Best Local Similarity	28.5%	Pred. NO. 3.8		
Matches 94	Conservative 87	Mismatches 149	Indels 0	Gaps 0

QY	1256	TTGAACTGTTGGGA	AAGAATTCGTACCT	TAGAGAAAGCTGGAGACCTTGAAACAA	1315
Db	872	TTAAATAATATKGA	AAAAKADWAKMAAA	ADKKADADDKKAAAAAKKARAAAAAA	931
QY	1316	AGATGAGACGCGGT	TTCTAGATGTGTGCA	CAATTCGTACCTTTTACTTGTGATGG	1375
Db	932	KKAAADKADWADAA	AAKKKKDKKKKKRA	MAAADKKKKDKKKDAADAAADAAWKKK	991
QY	1376	AAATGAGAGACAC	TTGACTTTCATCATCT	TAATGTCAGAAATCTGTATATGTAAGCA	1435
Db	992	AAAAAAAKBTPAAKA	AATKKKKKKKKKKK	AAAAAADAAGAAKARDAAAAKAAVATPKA	1051
QY	1436	GAATGACGCTGAGAG	CAACGCTCAAGAACT	AGAAATGATGTTTGAATTTATACAA	1495
Db	1052	AAAAAAAKKAAWKA	AAAAKKKKAAADKA	AAAAADKGAARAKKKAKAAAGAAAAAA	1111
QY	1496	AATCTGATGATGAT	TCATCAATATGTTG	AAAAACGGACATATGATTTATCCCAAGATG	1555
Db	1112	ATTKAAAAAATAAAA	KADRAAAAAKPAAD	AAAKRRAAAABAAADAAKAAKKA	1171

```

QY      1556 AAGAGAGCTCTAAACTTAATGAGAAATGAAA 1585
          | : | | : | | | | | | |
Db      1172 AKKAAAAAAKKKKAAAAAAAAAAAAAAAA 1201

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RESULT 15	
LOCUS	AU087765
DEFINITION	AU087765 Sugano Malaria cDNA library Plasmidium falciparum 3D7 cDNA clone XPFn5652, mRNA sequence.
ACCESSION	AU087765
	500 bp mRNA linear EST 27-JAN-2001

VERSION	AU087765.1	GI:12389906
KEYWORDS	EST.	
SOURCE	Plasmodium falciparum 3	

ORGANISM	Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium	
1 (bases 1 to 500)	
REFERENCE	
1. Kachikwa, T., Garske, M., Garske, M., and Garske, M.	

TITLE Full-malaria: a database for a full-length enriched cDNA library from human malaria parasite, *Plasmodium falciparum*
JOURNAL Nucleic Acids Res. 29 (1), 70-71 (2001)
DOI 10.1093/nar/29.1.70

COMMENT

COMMENT

Contact: Junichi Watanabe
Institute of Medical Science
The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Tel.: 81-3-5449-5378
Fax: 81-3-5449-5410
Email: jwatanabe@medicine.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).

FEATURES	SOURCE	Location/Qualifiers
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		/mol_type="mRNA"
		/isolate="3D7"
		/db_xref="taxon:36329"
		/clone="Xpfn5652"
		/dev_stage="erythrocytic stage"
BASE COUNT	252 a	/clone_lib="Sugano Malaria cDNA library"
ORIGIN	41 c	88 g 113 t 6 others

Query Match	2.7%	Score 47.8;	DB 9;	Length 500;
Best Local Similarity	48.9%	Pred. No. 4.2;		
Matches 157; Conservative	0;	Mismatches 162;	Indels 2;	Gaps 1;

OY	1270	AAAAGATTCGGTACTTAGACAAAAAGCTGAGAACTTGGAACAAAAAATGTGAAGACGGG	1329
Dd	76	AACAACAAAAAGAAAAAATAAAGTTAATGATTAATAAAAAAATATATCAAAAAAATAATTAATACCTG	135
OY	1330	TTTTCTAGATGTTGSGACATACAAATCGTGAAGCTTTTAACTTGATGAAATAAGAGGACA	1389
Dd	136	CAAAACATGATACAAATTCCGATTAATCTCGAAGTACTGATCAGATGGGAAAAAACAAATA	195
OY	1390	CTTGACATTCCTCATGATTCATATGTCAGAATGCTGATGTAAAGTCAGAGATGCACCTGA -	1447
Dd	196	GTTATATATTCAGCTTTGTATACGTATATATGAAGAGGAAAGGAAAGATGATGATATAG	255
OY	1448	GAGACAAACGTCAAAGAACTAGGAATGATGTTTGAATTTATCACAAATGTGATGATG	1507
Dd	256	ATGAAATATGGAAGATGAAGATCAAATTAAGATGAAGATGAAATGAAGATGAAATGAG	315
OY	1508	AATGCATGAAATAGTGTGAAAAACGGCATGTGATTTGCCAATATGAAGAAAGAGCTTA	1567
Dd	316	AAGATGTAGAAAAATGACACAAATAATAAATAATATATGATCTGGAATTAATAATCACAATTA	375
OY	1568	AACATAATAGCAATGAATCA	1588
Dd	376	ACATAAAAAGAAAAAATAATTA	396

Tue Aug 12 10:28:18 2003

Search completed: August 10, 2003, 10:57:43
Job time : 2740.47 secs

us-09-918-568-46.rst

penCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 18:45:33 ; Search time 2858.63 Seconds

(without alignments)
16242.876 Million cell updates/sec

Title: US-09-918-568-49

Perfect score: 1135

Sequence: 1 CTGCAAAAGCGGGTAT.....AACACCTGTGTTCTGCTAG 1135

Scoring table: IDENTITY_NNC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_hiv:*
32: em_htg_other:*
33: em_htg_mms:*
34: em_htg_pn:*
35: em_htg_rpd:*
36: em_htg_mim:*
37: em_htg_vtl:*
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39: em_htg_hum:*
40: em_htg_mms:*
41: em_htg_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1135	100.0	1135	6 AR181964	AR181964 Sequence
2	1135	100.0	1135	6 E08993	E08993 DNA encodin
3	1135	100.0	1135	6 I32529	I32529 Sequence 49
4	1135	100.0	1135	6 I43474	I43474 Sequence 49
5	908.8	80.1	1783	6 AR181961	AR181961 Sequence
6	908.8	80.1	1783	6 I32526	I32526 Sequence 46
7	908.8	80.1	1783	6 I43471	I43471 Sequence 46
8	887.6	78.2	1773	14 FLAHAJ3055	L20407 Influenza A
9	887.6	78.2	1773	14 FLAHA5157A	L20410 Influenza A
10	887.6	78.2	1773	14 FLAKRA59HA	L11134 Influenza A
11	886	78.1	1773	14 FLAHA3055J	L20406 Influenza A
12	884.4	77.9	1773	6 AX399727	AX399727 Sequence
13	884.4	77.9	1773	14 FLAHA1K	J02127 Influenza A
14	884.4	77.9	1773	14 FLAHA1557	L20408 Influenza A
15	884.4	77.9	1773	14 FLASIN57HA	L11142 Influenza A
16	882.8	77.8	1773	14 FLAHA575RI	L20409 Influenza A
17	879.6	77.5	1773	14 AB056699	AB056699 Influenza A
18	869.2	76.6	1773	14 FLAKOR68HA	L11133 Influenza A
19	866.8	76.4	1773	14 FLABING4HA	L11126 Influenza A
20	860.4	75.8	1773	14 FLAHA1ZU	D13579 Influenza A
21	858.8	75.7	1773	14 FLAHA1ZR	D13580 Influenza A
22	852.4	75.1	1773	14 FLABER68HA	L11125 Influenza A
23	838	73.8	1728	6 AR181943	AR181943 Sequence
24	838	73.8	1728	6 E07248	E07248 Haemaggluti
25	838	73.8	1728	6 I32508	I32508 Sequence 28
26	838	73.8	1728	6 I43453	I43453 Sequence 28
27	814	71.7	1773	14 FLAGDR72HA	L11129 Influenza A
28	808.4	71.2	1773	14 FLAMT61HA	L11136 Influenza A
29	799.6	70.4	1773	14 FLAPOR83HA	L11139 Influenza A
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31	798	70.3	1773	14 FLAPOR85HA	L11140 Influenza A
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33	793.2	69.9	1773	14 FLADE88HA	L11132 Influenza A
34	791.6	69.7	1772	14 FLAPRA76HA	L11141 Influenza A
35	761.8	67.1	1717	14 AF290440	AF290440 Influenza
36	760.2	67.0	1717	14 AF290441	AF290441 Influenza
37	760.2	67.0	1717	14 AF290442	AF290442 Influenza
38	758.6	66.8	1717	14 AF290439	AF290439 Influenza
39	698.8	61.6	1772	14 FLAONT76HA	L11138 Influenza A
40	698.8	61.6	1773	14 FLANY78HA	L11137 Influenza A
41	697.2	61.4	1773	14 FLANY91HA	L11131 Influenza A
42	689.2	60.7	1772	14 FLAAB88HA	L11135 Influenza A
43	687.6	60.6	1772	14 FLAMD77HA	L11130 Influenza A
44	651.4	57.4	1723	14 AF116201	AF116201 Influenza
45	551.8	48.6	1768	14 INFHA112	X07869 Influenza A

ALIGNMENTS

RESULT 1
LOCUS AR181964 1135 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 49 from patent US 6337070.
ACCESSION AR181964
VERSION AR181964.1 GI:20224880
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1135)
AUTHORS Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.
TITLE Polypeptides for use in generating anti-human influenza virus
antibodies
JOURNAL Patent: US 6337070-A 49 08-JAN-2002;

FEATURES
 source
 BASE COUNT 395 a 197 c 265 g 278 t
 ORIGIN

Query Match 100.0%; Score 1135; DB 6; Length 1135;
 Best Local Similarity 100.0%; Pred. No. 2.2e-260;
 Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 CTAGAAAAGCAGGGGTTATACCATAGAAACCAAAAGCAAAACATGGCCATCATTTAT 60
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121 AATTCCACAGAGAGAGTGCACACATTTAGAGCGGACGTCACCTGTCATGCGCAAG 180
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181 GACATCCTTGAGAGAACCCATTAACGGAAGTTATGCAAACTAAACGATCCGGGATCATG 240
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721 GTTCTGATGGAATGAGAGCACTTGATTCATGATTTCTTAAGTGAAGAAATCTGAT 780
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781 AGTAAGTCAAGATGACAGTGAAGACAACTCAAAAGAACTAGAAATGATGTTTAA 840
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841 TTTTATCAAAATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
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901 CCCAAGTGAAGAGAGTCTAAACTAAATGAATGAATGAATGAATGAATGAATGAAT 960
901 CCCAAGTGAAGAGAGTCTAAACTAAATGAATGAATGAATGAATGAATGAATGAAT 960
  
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Query 961 AGCATGGGGTTATACAAATCCTTGCCATTTATGCTACAGTAGACAGTTCTATGCTACTG 1020
 Db 961 AGCATGGGGTTATACAAATCCTTGCCATTTATGCTACAGTAGACAGTTCTATGCTACTG 1020

Query 1021 GCATCATGATGAGCTGGATCTCTTCTGGGTGCTCCACAGGCTCTCTGACAGCGAG 1080
 Db 1021 GCATCATGATGAGCTGGATCTCTTCTGGGTGCTCCACAGGCTCTCTGACAGCGAG 1080

Query 1081 ATTCGATATGATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1135
 Db 1081 ATTCGATATGATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1135

RESULT 2
 E08993 1135 bp DNA linear PAT 29-SEP-1997
 LOCUS E08993
 DEFINITION DNA encoding an immunogenic peptide derived from human Influenza A virus haemagglutinin that doesn't have globular region.
 ACCESSION E08993
 VERSION E08993.1 GI:22024631
 KEYWORDS JP 199508992-A/3.
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE
 1 (bases 1 to 1135)
 Okuno, Y., Isekawa, Y., Sasao, F. and Ueda, S.
 IMMUNOGENIC ARTIFICIAL POLYPEPTIDE
 Patent: JP 199508992-A 3 04-APR-1995;
 TAKARA SHUZO CO LTD
 OS None
 CC Artificial sequences.
 PN JP 199508992-A/3
 PD 04-APR-1995
 PE 16-MAR-1994 JP 1994070194
 PF 20-APR-1993 JP 93P 115216
 PI OKUNO YOSHINOBU, ISEKAWA YUUI, SASAO FUYOKO, UEDA SHIGEHARU PC
 C07K1/08, A61K39/145, C12N15/44, C12P21/02, C12N15/06, C12P21/08, PC
 (C12P21/02)
 PC C12R1:91), (C12P21/08, C12R1:91), C07K99:00;
 CC strandedness: Double;
 CC topology: linear;
 FH key
 FH key
 FT source 1. 1135 Location/Qualifiers
 FT 46. 1092 /product='immunogenic peptide' FT CDS

FEATURES
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 Location/Qualifiers
 1. 1135
 /organism='unidentified'
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BASE COUNT 395 a 197 c 265 g 278 t

Query Match 100.0%; Score 1135; DB 6; Length 1135;
 Best Local Similarity 100.0%; Pred. No. 2.2e-260;
 Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
LOCUS 132529 1135 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 49 from patent US 5589174.
ACCESSION 132529
VERSION 132529.1 GI:182320
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1135)
AUTHORS Okuno, Y., Isegawa, Y., Sasao, F. and Ueda, S.
TITLE Anti-human influenza virus antibody
JOURNAL Patent: US 5589174-A 49 31-DEC-1996;
FEATURES
source location/Qualifiers
1. 1135
BASE COUNT 395 a 197 c 265 g 278 t
ORIGIN
Query Match 100.0%; Score 1135; DB 6; Length 1135;
Best Local Similarity 100.0%; Pred. No. 2.2e-260;
Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Q _y	901	CCCAAGTATGAAGAAGACTCTAAACCTAAATGGAATGAAATCCAAAGGGGTAAATTGAGC	960
D _b	901	CCCAAGTATGAAGAAGACTCTAAACCTAAATGGAATGAAATCCAAAGGGGTAAATTGAGC	960
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Q _y	1021	GCATTCATGATGGGCGGATCTCTTTCGGGTGTCGCCAAGGGGTCTGCATGGCAGG	1080
D _b	1021	GCATTCATGATGGGCGGATCTCTTTCGGGTGTCGCCAAGGGGTCTGCATGGCAGG	1080
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D _b	1081	ATCTGCATATGATTAATAGTCATTTTATTAATTAATAAACCCCTTGTTCTGCTG	1135

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DEFINITION	I43474	1135 bp	DNA	linear	PAT 07-OCT-1997
ACCESSION	I43474	Sequence 49 from patent US 5631350.			
VERSION	I43474.1	GI:2468718			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1135)				
TITLE	Okuno,Y., Iseigawa,Y., Sasao,F. and Ueda,S.				
JOURNAL	Anti-human Influenza virus antibody				
FEATURES	Patent: US 5631350-A 49 20-MAY-1997;				
source	Location/Qualifiers				
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	/organism="unknown"				
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ORIGIN					

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Best Local Similarity	100.0%;	Pred. No. 2.2e-260;		
Matches 1135; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

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QY	121	AATTCACAGAGAAAGGTGCACAAATTCATAGAGCGGAACGTCACTGATCTATGCGCAAG	180
Db	121	AATTCACAGAGAAAGGTGCACAAATTCATAGAGCGGAACGTCACTGATCTATGCGCAAG	180
QY	181	GACATCCTTGAGAAAGCACCATTAAAGGAAAGTTATGCAACTAAACGATCCGGATCATG	240
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QY	241	AAAACAGAGAACACTTGAGAACTGTGAGACCACCAATGCCAACTCTTTGGAGGCAATA	300
Db	241	AAAACAGAGAACACTTGAGAACTGTGAGACCACCAATGCCAACTCTTTGGAGGCAATA	300
QY	301	AATACCAACATTACCTTTTACAAATGTCCACCACCTGACAAATAGTGAGTGGCCCAATAT	360
Db	301	AATACCAACATTACCTTTTACAAATGTCCACCACCTGACAAATAGTGAGTGGCCCAATAT	360
QY	361	GTAATAATCGAGAAAGTTGGTCTTTAGCAACAGGACTAAGGAATGTTCCCGAGATTGAATCA	420
Db	361	GTAATAATCGAGAAAGTTGGTCTTTAGCAACAGGACTAAGGAATGTTCCCGAGATTGAATCA	420
QY	421	AGAGGATGTTGTTGGGGCAATAGACTGTTTATAGAAAGAGATGGCAGGAATGTTGGAC	480

Db	421	AGAGGATTGTTGGGCAATACCTGGTTTATACAGAGAGGATGCGAAGCAATGGTTGAC	480
Oy	481	GTTGGTATGATATCCATCACAGCAATACCAGGGATCAGGGTATGACGACGACAAAGAA	540
Db	481	GGTTGGATGATACCATCACAGCAATGCCAGGATACAGGATATGACGACGACAAAGAA	540
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Db	541	TCCACTCAAAAGGCATTTGATGAAATTCACCAAGTAATTTCTGATTTGAAAAGATA	600
Oy	601	AACACCAATTTGAAGCTGTGGGAAACAATTCGTAACTTACGAAAGAGCTGGGAGAC	660
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Oy	781	AGTAAAGTCAGATGACCTGAGACCAACCTCAAAAGTAAGTAAAGATGGATTTTGA	840
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Oy	841	TTTTATACAAATGTGATGATCAATGCATGATAGTGTGAAAAACGGGACATATGATTAT	900
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Db	901	CCCAAGTATGAAGAGAGTCTAACTAAATGAATAAATCAAAGGGTAAATTTGAGC	960
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Db	961	AGCATGGGGTTTATCAAACTCTTCCATTATCTCAAGTACAGAGTTCTATGTCACG	1020
Oy	1021	GCAATCATGATGGCTGGGATCTTTCGGGCTGTCGCAAGCGGCTCTGCACTGCACAG	1080
Db	1021	GCAATCATGATGGCTGGGATCTTTCGGGCTGTCGCAAGCGGCTCTGCACTGCACAG	1080
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Db	1081	ATCTGATATGATTAATAGTCAATTTATATATTAATAAACACCCCTTGTCTCTAG	1135

RESULT 5					
AR181961					
LOCUS	AR181961	1783 bp	DNA	linear	PAT 20-APR-2002
DEFINITION	Sequence 46 from patent US 6357070.				
ACCESSION	AR181961				
VERSION	AR181961.1	GI:20224877			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1783)				
TITLE	Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S. Oligopeptides for use in generating anti-human influenza virus antibodies				
JOURNAL	Patent: US 6357070-A 46 -08-JAN-2002;				
FEATURES	Location/Qualifiers				
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BASE COUNT	610 a	323 c	424 g	426 t	
ORIGIN					

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Best Local Similarity	98.7%	Pred. No. 2.2e-206;		
Matches 916; Conservative	0;	Mismatches 12;	Indels 0;	Gaps 0;

OY 208 AAGTTATGCAACTTAAACGATCCGGATCATGAAAACAGAGAACACTTGAGAACTGT 267
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Db 853 AAAATATGCAAAAGAGTAGTTCAGGATCATGAAAACAGAGAACACTTGAGAACTGT 912
OY 268 GAGACCAATGCGCAATCTTGGGAGCAATTAATACAAATTAACCTTTTACAAATGTC 327
| | | | |
Db 913 GAGACCAATGCGCAATCTTGGGAGCAATTAATACAAATTAACCTTTTACAAATGTC 972
OY 328 CACCCACTGACAAATGCTGAGTGGCCCCCAATATGTAATGTAATGGAAGTGGTCTTACCA 387
| | | | |
Db 973 CACCCACTGACAAATGCTGAGTGGCCCCCAATATGTAATGTAATGGAAGTGGTCTTACCA 1032
OY 388 ACAGAGCTAAGGAATGTTCCCAATGTAATCAAGAGGATTTGGGGCAATAGCTGT 447
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Db 1033 ACAGAGCTAAGGAATGTTCCCAATGTAATCAAGAGGATTTGGGGCAATAGCTGT 1092
OY 448 TTTATAGAGAGAGGTTGGCAAGGAATGTTGACGGTGTATGATACCATCACAGCAAT 507
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Db 1093 TTTATAGAGAGAGGTTGGCAAGGAATGTTGACGGTGTATGATACCATCACAGCAAT 1152
OY 508 GACCAAGGATCAGGTTATGACAGACAAAGATTCACCTCAAAAGGCAATTTGATGATATC 567
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Db 1153 GACCAAGGATCAGGTTATGACAGACAAAGATTCACCTCAAAAGGCAATTTGATGATATC 1212
OY 568 ACCAACAAGGTAAATCTGTGATTTGAAAAGATTAACACCCCAATTTGAAGCTTTGGGAAA 627
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Db 1273 GAATTCGGTACTT/GAGAAAAGCTGAGAACTTGAACAAAAGATGGAAGACGGGTTT 1332
OY 688 CTAGATGTGTGACATACAAATGCTGAGCTTTAGTTCTGATGAAATGAGAGGCACTT 747
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Db 1333 CTAGATGTGTGACATACAAATGCTGAGCTTTAGTTCTGATGAAATGAGAGGCACTT 1392
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OY 928 AATAGAAATGAATTAAGAGGGGTAAATTTGAGCAGCATGGGGGTTTATCAAAATCCTTGC 987
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Db 1573 AATAGAAATGAATTAAGAGGGGTAAATTTGAGCAGCATGGGGGTTTATCAAAATCCTTGC 1632
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Db 1753 TAATTAATAACACCTTTGTTTCTGCTAG 1780

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1783)
AUTHORS Okuno, Y., Isegawa, Y., Sasao, F. and Ueda, S.
TITLE Anti-human influenza virus antibody
JOURNAL Patent: US 5589174-A 46 31-DEC-1996;
FEATURES
source Location/Qualifiers
BASE COUNT 610 a 323 c 424 g 426 t
ORIGIN
Query Match 80.1%; Score 908.8; DB 6; Length 1783;
Best Local Similarity 98.7%; Pred. No. 2.2e-206;
Matches 916; Conservative 0; Mismatches 12; Indels 0; Gaps 0.
OY 208 AAGTTATGCAACTTAAACGATCCGGATCATGAAAACAGAGAACACTTGAGAACTGT 267
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Db 853 AAAATATGCAAAAGAGTAGTTCAGGATCATGAAAACAGAGAACACTTGAGAACTGT 912
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OY 448 TTTATAGAGAGAGTGTGCAAGGAATGTTGACGGTGTATGATACCATCACAGCAAT 507
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Db 1093 TTTATAGAGAGAGTGTGCAAGGAATGTTGACGGTGTATGATACCATCACAGCAAT 1152
OY 508 GACCAAGGATCAGGTTATGACAGACAAAGATTCACCTCAAAAGGCAATTTGATGATATC 567
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Db 1333 CTAGATGTGTGACATACAAATGCTGAGCTTTAGTTCTGATGAAATGAGAGGCACTT 1392
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Db 1573 AATAGAAATGAATTAAGAGGGGTAAATTTGAGCAGCATGGGGGTTTATCAAAATCCTTGC 1632
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Db 1633 ATTATAGTACAGTGTCTATGCACTGGCAATCATGATGGCTGGGATCTCTTTC 1692
OY 1048 TGGGTGTGCTCCAAAGGGTCTCTGACAGTGCAGATCTGCATATGATTAAGTCAATTTTA 1107

RESULT 6
LOCUS 132526 1783 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 46 from patent US 5589174.
ACCESSION 132526
VERSION 132526.1 GI:182317
KEYWORDS Unknown.


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Db      1693 TGGGTGCTCTCAACGGGCTCTCTGCGATGCGAGATCTGCATATGATTAATGATTTTA 1752
Qy      1108 TAATTAACACACCTTTCTTCTGCTAG 1135
Db      1753 TAATTAACACACCTTTCTTCTGCTAG 1780

RESULT 7
LOCUS   143471 1783 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 46 from patent US 5631350.
ACCESSION 143471
VERSION 143471.1 GI:2468715
KEYWORDS
SOURCE  Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 1783)
AUTHORS Okuno,Y., Iseigawa,Y., Sasao,F. and Ueda,S.
TITLE Anti-human influenza virus antibody
JOURNAL Patent: US 5631350-A 46 20-MAY-1997;
FEATURES
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BASE COUNT 610 a 323 c 424 g 426 t
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Query Match 80.1%; Score 908.8; DB 6; Length 1783;
Best Local Similarly 98.7%; Pred. No. 2.2e-206;
Matches 916; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy      268 GAGACCAAAATGCCAAACTCTTTGGAGCAATAATACACATTACCTTTGACAAATGTC 327
Db      913 GAGACCAAAATGCCAAACTCTTTGGAGCAATAATACACATTACCTTTGACAAATGTC 972
Qy      328 CACCCACTGACATAGGTGAGTGCCCAATATGTAATAATCGAGAGAGTGGCTTAGCA 387
Db      973 CACCCACTGACATAGGTGAGTGCCCAATATGTAATAATCGAGAGAGTGGCTTAGCA 1032
Qy      388 ACAGACTAAGAGATGTTCCCGATGATGATCAAGAGAGATGTTGGGCAATAGCTGCT 447
Db      1033 ACAGACTAAGAGATGTTCCCGATGATGATCAAGAGAGATGTTGGGCAATAGCTGCT 1092
Qy      448 TTTATAGAGAGAGATGCGAAGAGATGTTGACGGTGTATGATACATACAGCAAT 507
Db      1093 TTTATAGAGAGAGATGCGAAGAGATGTTGACGGTGTATGATACATACAGCAAT 1152
Qy      508 GACACAGGATCAGGGATGACGACGACAAAGATCCATCAAAAGCATTTGATGATC 567
Db      1153 GACACAGGATCAGGGATGACGACGACAAAGATCCATCAAAAGCATTTGATGATC 1212
Qy      568 ACCAACAAGGTAAATCTGTGATTGAAAGATATAACACCAATTTGAGCTGTTGGAAA 627
Db      1213 ACCAACAAGGTAAATCTGTGATTGAAAGATATAACACCAATTTGAGCTGTTGGAAA 1272
Qy      628 GAATTCGGTAACTTAGAGAAAAGACTGGAACTTGAACAAAAGATGGAAGACGGTTT 687
Db      1273 GAATTCGGTAACTTAGAGAAAAGACTGGAACTTGAACAAAAGATGGAAGACGGTTT 1332
Qy      688 CAGATGCTGACATACATGCTGCTGCTTTTACTTCTGATGGAATAATGAGAGACACTT 747
Db      1333 CAGATGCTGACATACATGCTGCTGCTTTTACTTCTGATGGAATAATGAGAGACACTT 1392
Qy      748 GACTTTCATGATTCTAATGCAAGATCTGTATAGTAAGTGAATGCAAGCTGGAAGAC 807
Db      1393 GACTTTCATGATTCTAATGCAAGATCTGTATAGTAAGTGAATGCAAGCTGGAAGAC 1452
Qy      808 AACGTCAAGAAGACTAGAAATGATGCTTTTGAATTTATACCAAAATGTATGATGAATGC 867
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Db      1453 AACGTCAAGAAGACTAGAAATGATGCTTTTGAATTTATACCAAAATGTATGATGAATGC 1512
Qy      868 ATGAATAGTGTGAAGAGGGGACATATATATCCCAAGTGTGAAGAGATCTAAACTA 927
Db      1513 ATGAATAGTGTGAAGAGGGGACATATATATCCCAAGTGTGAAGAGATCTAAACTA 1572
Qy      928 AATGAAATGAAATCAAGGGGTAAATTTGAGCAATGAGGGGTTTATCAATCTTGGC 987
Db      1573 AATGAAATGAAATCAAGGGGTAAATTTGAGCAATGAGGGGTTTATCAATCTTGGC 1632
Qy      988 ATTATGCTACAGTAGAGAGGTTTATGTCACATGCAATCATGATGCTGGGATCTCTTC 1047
Db      1633 ATTATGCTACAGTAGAGAGGTTTATGTCACATGCAATCATGATGCTGGGATCTCTTC 1692
Qy      1048 TGGGTGCTCTCAACGGGCTCTCTGAGTGCAGATGTCATATCATATATAAGCATTTTA 1107
Db      1693 TGGGTGCTCTCAACGGGCTCTCTGAGTGCAGATGTCATATCATATATAAGCATTTTA 1752
Qy      1108 TAATTAACACACCTTTGTTCTGCTAG 1135
Db      1753 TAATTAACACACCTTTGTTCTGCTAG 1780

RESULT 8
LOCUS   FLAHUJ3055 1773 bp RNA linear VRL 27-MAR-1995
DEFINITION Influenza A/Japan/305-/57 (H2N2) haemagglutinin (seg 4) gene,
ACCESSION L20407
VERSION L20407.1 GI:305154
KEYWORDS haemagglutinin.
SOURCE Influenza A virus
ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza
REFERENCE 1 (bases 1 to 1773)
AUTHORS Connor,R.J., Kawaoaka,Y., Webster,R.G. and Paulson,J.C.
TITLE Receptor specificity in human, avian, and equine H2 and H3
JOURNAL Virology 205 (1), 17-23 (1994)
MEDLINE 95065649
PUBMED 7975212
COMMENT Original source text: Influenza virus type A (individual)_isolate
A/Japan/305-/57) RNA.
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            MWLTKRSGDYPAVANGSYNNISGEOMLIIWGVHNHNDTEORTLIYONGVTVSGTS
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BASE COUNT 608 a 320 c 421 g 424 t
ORIGIN

Query Match 78.2%; Score 887.6; DB 14; Length 1773;
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Best Local Similarity 97.4%; Pred. No. 2.6e-201; Matches 902; Conservative 0; Mismatches 24; Indels 0; Gaps 0;			
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Db	848	AAATATTCGAAAGACGCTAGTTCAGGATCTGTGAAAACGAGAGAACCTTGACAACTGT	907
Oy	268	GAGACCAATGCCAATCTCTTTGGGAGCAATAAATACACATTCCTTTTACAAATGTC	327
Db	908	GAGACCAATGCCAATCTCTTTGGGAGCAATAAATACACATTCCTTTTACAAATGTC	967
Oy	328	CACCACTGACAAATAGTGAAGTCCCAATATGTAAATTCGGAAGTTGGCTTACGA	387
Db	968	CACCACTGACAAATAGTGAAGTCCCAATATGTAAATTCGGAAGTTGGCTTACGA	1027
Oy	388	ACAGACTAAGGAATTTTCCCAATGTAATCAAGAGATTTGTTGGGGCAATAGCTGCT	447
Db	1028	ACAGACTAAGGAATTTTCCCAATGTAATCAAGAGATTTGTTGGGGCAATAGCTGCT	1087
Oy	448	TTTATAGAGGAGATTCGCAAGGAATGTTGACGTTGTATGATACCATACAGCAAT	507
Db	1088	TTTATAGAGGAGATTCGCAAGGAATGTTGATGTTGATGATGATACCATACAGCAAT	1147
Oy	508	GACCAAGGATCAGGGTATGACAGCAGACAAAGATCCACTCAAAAGCATTTGATGAAATC	567
Db	1148	GACCAAGGATCAGGGTATGACAGCAGACAAAGATCCACTCAAAAGCATTTGATGAAATC	1207
Oy	568	ACCAACAAGGTAATTTCTGTGATGTAAGAAAGTAACACCAATTTGAAAGCTTTGGGAAA	627
Db	1208	ACCAACAAGGTAATTTCTGTGATGTAAGAAAGTAACACCAATTTGAAAGCTTTGGGAAA	1267
Oy	628	GAATTCGTAACCTTAAGAAAGAGCTGAGAACCTTGAACAAAAGATGGAAGAGCGGTTT	687
Db	1268	GAATTCGTAACCTTAAGAAAGAGCTGAGAACCTTGAACAAAAGATGGAAGAGCGGTTT	1327
Oy	688	CTAGATCTGTGACATACAAATGCTGAGCTTTTACTTGTATGGAAGATGAGAGACACTT	747
Db	1328	CTAGATCTGTGACATACAAATGCTGAGCTTTTACTTGTATGGAAGATGAGAGACACTT	1387
Oy	748	GACCTTATGATGTTCTAATGCAAGAATCTGTATGTAAGTCAGATGCAAGCTGAGAGAC	807
Db	1388	GACCTTATGATGTTCTAATGCAAGAATCTGTATGTAAGTCAGATGCAAGCTGAGAGAC	1447
Oy	808	AACGTCAAGAACTAATCAAAATGATGTTTGAATTTTATCAACAATGTGATGATGAAATGC	867
Db	1448	AACGTCAAGAACTAATCAAAATGATGTTTGAATTTTATCAACAATGTGATGATGAAATGC	1507
Oy	868	ATGATATGTTGAAAACGAGCATATGATTTATCCCAAGTATGGAAGAGAGCTTAAACTA	927
Db	1508	ATGATATGTTGAAAACGAGCATATGATTTATCCCAAGTATGGAAGAGAGCTTAAACTA	1567
Oy	928	AATGAATGTAATCAAAAGGGTAAATTTGAGCAGCATGGGGGTTTCAAAATCCTTGCC	987
Db	1568	AATGAATGTAATCAAAAGGGTAAATTTGAGCAGCATGGGGGTTTCAAAATCCTTGCC	1627
Oy	988	ATTATGCTCAAGTAACAGGTTCTATGCTCACTGGCAATCATGATGGCTGGATCTTTTC	1047
Db	1628	ATTATGCTCAAGTAACAGGTTCTCTGCTCACTGGCAATCATGATGGCTGGATCTTTTC	1687
Oy	1048	TGGGTGTGCTCAACGGTCTCTGAGTGCAGATCTGCATATGATTAAGTATTTTA	1107
Db	1688	TGGGTGTGCTCAACGGTCTCTGAGTGCAGATCTGCATATGATTAAGTATTTTA	1747
Oy	1108	TAATTAACACACCTTTGTTTCTGCT	1133
Db	1748	TAATTAACACACCTTTGTTTCTACT	1773

RESULT 9
FLAHAS157A
LOCUS
DEFINITION
complete cds.

ACCESSION L20410 VERSION L20410.1 GI:305170 KEYWORDS haemagglutinin. SOURCE ORIGIN Influenza A virus REFERENCE AUTHORS Connor, R.J., Kawakita, Y., Webster, R.G. and Paulson, J.C. TITLE Receptor specificity in human, avian, and equine H2 and H3 JOURNAL Virology 205 (1), 17-23 (1994) MEDLINE 95065649 PUBMED 7975212 COMMENT Original source text: Influenza virus type A (individual isolate A/Singapore/1/57) RNA. FEATURES Source 1. .1773. /organism="Influenza A virus" /mol_type="genomic RNA" /isolate="A/Singapore/1/57" /db_xref="taxon:11320" 44. .1732 /gene="HA" 44. .1732 /gene="HA" /codon_start=1 /product="haemagglutinin" /protein_id="JAA64366.1" /db_xref="GI:305171" /translation="MAITVYLLETTAVRGDQICIGYHANNSTKEDVLTLENNVTHA KDIIEKHNKIKLKLNCIPIPLELDCSIAAGLLNPPCDRLSYSPMSYIENKPNPD GLCPYGFSENYDEELKHLSSVYKHEKXILKPKDHTOHTTHGSRACVAGSNPFEN MVLTKTESNPVPAKGSYNNSTSGROMILIMVHPNDPETHRTLYOVAVGVSYGCTG LNKSTPDIDATRPVNLGSRMESSWLLDMWDIINESTGNLTAPEYKRSRGS GIMKEGTLENCETKQTPUGALNTTLPFHVHPLTIGECPRVKSRLVATLRLV POIESRGLFPAIGAFIEGQWGVGYHNSDQSGYAADKESQKAFDGTITNV NSVLEKNKTOFEAVGEFSLERLELNKMKEDGFIDWYNAELVLVLENNETLDF HDSNVKMLDYKRMQLDNVYKELNGCFEFYHKCDKDDCMNSVKNGTYDYPYEESEKL NRNRIKVKVLSMVGVOYLAIYATVAGSLSLAIMMAGISFMCSNGSLQCRICI"			
BASE COUNT 612 a 319 c 417 g 425 t			
ORIGIN			
Query Match 78.2%; Score 887.6; DB 14; Length 1773; Best Local Similarity 97.4%; Pred. No. 2.6e-201; Matches 902; Conservative 0; Mismatches 24; Indels 0; Gaps 0;			
Oy	208	AAATTATGCAACCTAAACGATCCGGATCATGTAAGAAACAGAGAACACTTGACAACTGT	267
Db	848	AAATATTCGAAAGACGCTAGTTCAGGATCTGAAAACAGAGAACACTTGACAACTGT	907
Oy	268	GAGACCAATGCCAATCTCTTTGGGAGCAATAAATCAACATTAACCTTTTACAAATGTC	327
Db	908	GAGACCAATGCCAATCTCTTTGGGAGCAATAAATCAACATTAACCTTTTACAAATGTC	967
Oy	328	CACCACTGACAAATAGTGAAGTCCCAATATGTAAATTCGGAAGTTGGCTTACGA	387
Db	968	CACCACTGACAAATAGTGAAGTCCCAATATGTAAATTCGGAAGTTGGCTTACGA	1027
Oy	388	ACAGACTAAGGAATTTTCCCAATGTAATCAAGAGATTTGTTGGGGCAATAGCTGCT	447
Db	1028	ACAGACTAAGGAATTTTCCCAATGTAATCAAGAGATTTGTTGGGGCAATAGCTGCT	1087
Oy	448	TTTATAGAGGAGATTCGCAAGGAATGTTGACGTTGTATGATACCATACAGCAAT	507
Db	1088	TTTATAGAGGAGATTCGCAAGGAATGTTGATGTTGATGATACCATACAGCAAT	1147
Oy	508	GACCAAGGATCAGGGTATGACAGACAAAGATCCACTCAAAAGCATTTGATGAAATC	567
Db	1148	GACCAAGGATCAGGGTATGACAGACAAAGATCCACTCAAAAGCATTTGATGAAATC	1207
Oy	568	ACCAACAAGGTAATTTCTGTGATGTAAGAAAGTAACACCAATTTGAAAGCTTTGGGAAA	627

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Db      1208 ACCAACAGGTAATTCTGTGATTGAAGAAGTACACCCCAATTTGAGCTGTGGGAAA 1267
OY      628 GAATTCGTAAGTCTAGAGAAAAGACGTGAGAACTTGAAACAAAAGATGAAAGCGGGTTT 687
Db      1268 GAATTCAGTACTTACAGAGAAAGACTGAGAACTTGAAACAAAAGATGAAAGCGGGTTT 1327
OY      688 CTAGATGTGTGACATACATAGCTGAGCTTTTGTGATCTGTGATGAAAATGAGAGACACTT 747
Db      1328 CTAGATGTGTGACATACATAGCTGAGCTTTTGTGATCTGTGATGAAAATGAGAGACACTT 1387
OY      748 GACTTCATGATTTCTAATGTCAAGATCTGTATAGTAAGTCAAGATGCAAGCTGAGAGAC 807
Db      1388 GACTTCATGATTTCTAATGTCAAGATCTGTATAGTAAGTCAAGATGCAAGCTGAGAGAC 1447
OY      808 AACGTCGAAGCACTAGGAATGATGATTTGTAATTTTATACAAATGTGATGTAATGC 867
Db      1448 AACGTCGAAGCACTAGGAATGATGATTTGTAATTTTATACAAATGTGATGTAATGC 1507
OY      868 ATGATAGTGTGAAAAACGGGACATATGATATCCAACTATGAAAGAGAGTCTAAACTA 927
Db      1508 ATGATAGTGTGAAAAACGGGACATATGATATCCAACTATGAAAGAGAGTCTAAACTA 1567
OY      928 AATAGAAATGAATCAAAAGGGGTAATTAATGAGCAGATGGGGGTTTATCAATCCCTTCC 987
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OY      988 ATTATGCTACAGTACAGTACAGTCTATGTCAGTGCATGATGATGATGATGATGATGATG 1047
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Db      1748 TAATTAATAAACACCCCTGTGTTCTGCT 1773

RESULT 10
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LOCUS      FLAKRA59HA      1773 bp ss-RNA      linear      VRL_13-OCT-2000
DEFINITION      Influenza A virus (A/Krasnodar/101/59 (H2N2)) hemagglutinin (HA)
ACCESSION      L11134
VERSION      L11134.1 GI:408524
KEYWORDS      haemagglutinin.
SOURCE      Influenza A virus (A/Krasnodar/101/59 (H2N2))
ORGANISM      Influenza A virus (A/Krasnodar/101/59 (H2N2))
VIRUSES: ssRNA negative-strand viruses: Orthomyxoviridae; Influenza
A viruses; Influenzavirus A; Influenza A virus; H2N2 subtype.
Schäfer, J. R., Kawakoka, Y., Bean, W. J., Suss, J., Senne, D. and
Webster, R. G.
TITLE      Origin of the pandemic 1957 H2 influenza A virus and the
JOURNAL      persistence of its possible progenitors in the avian reservoir
MEDLINE      Virology 194 (2), 781-788 (1993)
PUBMED      93276567
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BASE COUNT      608 a 321 c 420 g 424 t
ORIGIN
Query Match      78.2% Score 887.6; DB 14; Length 1773;
Best Local Similarity 97.4%; Pred. No. 2.6e-201;
Matches 902; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
OY      208 AACTATGCAAACTAAGCGATCCGGATCATGAAGAGAAAGAACTTGAAGACTGT 267
Db      848 AAAATATCGAAAAGAGGTAGTTCAGGATCATGAAGAGAAAGAACTTGAAGACTGT 907
OY      268 GAAACCAATGCGAACTCCTTTGGAGCAATTAATACAACTTACCTTTTACCAATGTC 327
Db      908 GAACCAAAATGCGAACTCCTTTGGAGCAATTAATACAACTTACCTTTTACCAATGTC 967
OY      328 CACCACATGACATAGTGTAGTCCCAATATGTAATCGGAGAAATGCTGCTTACGA 387
Db      968 CACCACATGACATAGTGTAGTCCCAATATGTAATCGGAGAAATGCTGCTTACGA 1027
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Db      1028 ACAGCACTAAGGAATGTTCCCAATGATGATCAAGAGATGTTGGGGCAATAGCTGT 1087
OY      448 TTTATGAAGGAGATGAGCAAGGAATGTTGAGCGTGTGATGATGATGATGATGATGATG 507
Db      1088 TTTATGAAGGAGATGAGCAAGGAATGTTGAGCGTGTGATGATGATGATGATGATGATG 1147
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Db      1148 GACACAGGATCAAGGATGATCAGCAGACAGCAAGAAATCCAGCAAAAGCAATTTGATGAATC 1207
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Db      1208 ACCAACAGGTAAATTTCTGTGATGAAAGATTAACACCCAAATTTGAGCTGTGGGAAA 1267
OY      628 GAATTCGTAAGTGTGAGAAAGACTGGAGACTGGAGCACTTGAACAAAAGATGGAAGCGGTTT 687
Db      1268 GAATTCGTAAGTGTGAGAAAGACTGGAGACTGGAGCACTTGAACAAAAGATGGAAGCGGTTT 1327
OY      688 CTAGATGTGTGACATACATAGCTGAGCTTTTGTGATGATGAAATGAGAGACACTT 747
Db      1328 CTAGATGTGTGACATACATAGCTGAGCTTTTGTGATGATGAAATGAGAGACACTT 1387
OY      748 GACTTCATGATTTCTAATGTCAAGATCTGTATAGTAAGTCAAGATGCAAGCTGAGAGAC 807
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OY      808 AACGTCGAAGCACTAGGAATGATGATTTGTAATTTTATACAAATGTGATGTAATGC 867
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Db      1568 AATAGAAATGAATCAAAAGGGGTAATTAATGAGCAGATGGGGGTTTATCAATCCCTTCC 1627
OY      988 ATTATGCTACAGTACAGTCTATGTCAGTGCATGATGATGATGATGATGATGATGATG 1047
Db      1628 ATTATGCTACAGTACAGTCTATGTCAGTGCATGATGATGATGATGATGATGATGATG 1687

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Oy	1048	TGGGTGTCGCCAAC	BCGTCTCTCAGTGCAGGAGATCGCAATGATATATAGCATTTTA	1107	
Db	1688	TGGATGTGCTTCAAC	BSGTCTCTCAGTGCAGGAGATCGCAATGATATATAGCATTTTA	1747	
Oy	1108	TAATTAACAACACCC	TGTTTCTCTCT	1133	
Db	1748	TAATTAACAACACCC	TGTTTCTCTACT	1773	
RESULT 11	FLAHA3055J	FLAHA3055J	1773 bp	RNA linear	VRL 27-MAR-1995
LOCUS	FLAHA3055J	Influenza A/Japan/305+/57 (H2N2)	haemagglutinin (seg 4)	gene,	
DEFINITION	Complete cds.				
ACCESSION	L20406				
VERSION	L20406.1	GI:3051114			
KEYWORDS	haemagglutinin.				
SOURCE	Influenza A virus				
ORGANISM	Vitruvius; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A.				
REFERENCE	1 (bases 1 to 1773)				
AUTHORS	Comor,R.J., Kawapacka,Y., Webster,R.G. and Paulson,J.C.				
TITLE	Receptor specificity in human, avian, and equine H2 and H3				
JOURNAL	Influenza virus isolates				
MEDLINE	Virolology 205 (1), 17-23 (1994)				
PUBMED	7975212				
COMMENT	Original source text: Influenza virus type A (individual isolate A/Japan/305+/57) RNA.				
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	NRNRIK				
BASE COUNT	607 a	319 c	421 g	426 t	
ORIGIN					
Query Match	78.1%	Score 886:	DB 14:	Length 1773:	
Best Local Similarity	97.13%:	Pred. No. 6.2e-201:			
Matches 901:	Conservativity	0:	Mismatches 25:	Indels 0:	Gaps 0:
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Db	848	AAATATTCGAAAAG	GGTAGTTCCAGGGATCTGTGAAGAACAGAGACACTTGAGAACTGT	907	
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Dd		1088	TTTTTATAGAGGAGGATGGCAAGGAATGGTTGATGGTTGGTATGGATATCCATCACAGCAAT	1147
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ACCESSION	AX399727			
VERSION	AX399727.1	GI:21335485		
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	subtype.			
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AUTHORS	Ferko,B., Egorov,A., Romanova,J., Kalinge,r.D. and Kalinge,r.H.			
JOURNAL	Live vaccine and method of manufacture			
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VERSION						
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AUTHORS						
TITLE						

Journal	Medline	Pubmed	Comment	Features
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Best Local Similarity	97.2%	Pred. No. 1.5e-200:		
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 VERSION L11142.1 GI:408676
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 REFERENCE Schaefer, J.R., Kawakoka, Y., Bean, W.J., Suss, J., Senne, D. and Webster, R.G.
 AUTHORS Origin of the pandemic 1957 H2 influenza A virus and the persistence of its possible progenitors in the avian reservoir. Virology 194 (2), 781-788 (1993)
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Tue Aug 12 10:28:19 2003

us-09-918-568-49.rge

Page 13

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GenCore version 5.1.6
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Post-processing: Minimum Match 0%

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4	695.6	39.0	1754	US-09-918-568-27	Sequence 27, Appl
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6	397	22.3	409	US-09-918-568-34	Sequence 34, Appl
7	382.4	21.4	410	US-09-918-568-35	Sequence 35, Appl
8	379.6	21.3	394	US-09-918-568-36	Sequence 36, Appl
9	318.6	17.9	1777	US-09-918-568-54	Sequence 54, Appl
10	291	16.3	1711	US-10-099-619-1	Sequence 1, Appl
11	252.4	14.2	1110	US-09-918-568-57	Sequence 57, Appl
12	251.6	13.6	442	US-09-918-568-29	Sequence 29, Appl
13	241.8	13.1	424	US-09-918-568-32	Sequence 32, Appl
14	233.6	13.1	424	US-09-918-568-30	Sequence 30, Appl
15	233.6	13.1	424	US-09-918-568-31	Sequence 31, Appl
16	125.2	7.0	334	US-09-918-568-38	Sequence 38, Appl

17	123.6	6.9	329	9	US-09-918-568-39	Sequence 39, Appl
18	123.6	6.9	334	9	US-09-918-568-40	Sequence 40, Appl
19	121	6.8	329	9	US-09-918-568-37	Sequence 37, Appl
20	118.8	6.7	329	9	US-09-918-568-41	Sequence 41, Appl
21	44.4	2.5	1115	14	US-10-184-634-440	Sequence 440, App
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26	41.8	2.3	3441	9	US-09-880-192-41	Sequence 41, Appl
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31	40.8	2.3	4239	10	US-09-070-927A-450	Sequence 450, App
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33	40	2.2	1777	13	US-10-042-817-51	Sequence 51, Appl
34	40	2.2	2843	11	US-09-822-846-421	Sequence 421, App
35	40	2.2	3058	14	US-10-106-698-468	Sequence 468, App
36	39.8	2.2	1257	9	US-09-877-065-2	Sequence 2, Appl
37	39.6	2.2	653	14	US-10-123-155-438	Sequence 438, App
38	39.6	2.2	653	15	US-10-146-731-438	Sequence 438, App
39	39.2	2.2	1955	8	US-08-781-968A-598	Sequence 598, App
40	39.2	2.2	2232	10	US-09-925-637-71	Sequence 71, Appl
41	39.2	2.2	2232	14	US-10-084-205-71	Sequence 71, Appl
42	39.2	2.2	2235	9	US-09-815-242-8697	Sequence 8697, Ap
43	38.8	2.2	678	13	US-10-027-632-212662	Sequence 212662, A
44	38.6	2.2	2000	10	US-09-938-842A-3817	Sequence 3817, Ap
45	38	2.1	1214	13	US-10-027-632-30819	Sequence 30819, A

ALIGNMENTS

RESULT 1
US-09-918-568-46
Sequence 46, Application US/09918568
Patent No. US20020054882A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESS: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <unknown>
ANTI-SENSE: <unknown>
FRAGMENT TYPE: <unknown>
ORIGINAL SOURCE:
ORGANISM: A/Okuda/57
STRAIN: <unknown>
INDIVIDUAL ISOLATE: <unknown>
DEVELOPMENTAL STAGE: <unknown>
HAPLOTYPE: <unknown>
TISSUE TYPE: <unknown>
CELL TYPE: <unknown>
ORGANELLE: <unknown>
IMMEDIATE SOURCE:
LIBRARY: <unknown>
CLONE: <unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <unknown>
MAP POSITION: <unknown>
UNITS: <unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-918-568-46

Query Match 100.0%; Score 1783; DB 9; Length 1783;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	1381	GAGGGGACACTGGAC	TTTCATGATTTCTTAAGTCAAGAACTGTTAGTAAAGTCAGATG	1440
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QY	1441	CAGCTGAGAGACAAC	ATCAAGAAGCTAGGAATGATGTTTGAAATTTATACAAATGT	1500
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QY	1501	GATGATCAATGCATG	AATAGTGTGAAAAAGGGACATATGATTATCCCAAGTATGANGAA	1560
Db	1501	GATGATCAATGCATG	AATAGTGTGAAAAAGGGACATATGATTATCCCAAGTATGANGAA	1560
QY	1561	GAGCTCAAACTAAAT	AGAAATGAATCAAAAGGGGTAAATTTGACACAGATGGGGCTTAT	1620
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QY	1621	CAATCCCTTCCCAT	ATGCTACAGTAGCAGAGTTCTATGTACACAGGCAATCATATGCGT	1680
Db	1621	CAATCCCTTCCCAT	ATGCTACAGTAGCAGAGTTCTATGTACACAGGCAATCATATGCGT	1680
QY	1681	GCGATCTCTTCTCGG	ATGCTCTCCAAAGGGGTCTCTGCAAGTGCAGAGATCTGCATATGATTA	1740
Db	1681	GCGATCTCTTCTCGG	ATGCTCTCCAAAGGGGTCTCTGCAAGTGCAGAGATCTGCATATGATTA	1740
QY	1741	TAACTCATTTATATA	TTAAAAACACCTTGTTCTGTGTACCG	1783
Db	1741	TAACTCATTTATATA	TTAAAAACACCTTGTTCTGTGTGTACCG	1783

RESULT 2
US-09-918-568-28
; Sequence 28, Application US/09918568
; Patent No. US20020054882A1
; GENERAL INFORMATION:

APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING

```

: ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
:
: NUMBER OF SEQUENCES: 58
:
:

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
ADDRESS: 3033 W. North
CITY: Chicago, Ill. 60640

STREET: 2033 K
CITY: Washington
STATE: DC

STATE: D.C.
COUNTRY: U.S.A.
YTD: 2006

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
MEDIA: 5.25, 3.5 INCH, 1.44 MB

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SOFTWARE: wordperfect 5.1
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001

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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998

APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995

APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994

APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993

ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33 20

REGISTRATION NUMBER: 33,38/
REFERENCE/DOCKET NUMBER: <Unknown>

TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250

TELEX: <Unknown>
INFORMATION FOR SEO ID NO. 28:

SEQUENCE CHARACTERISTICS:

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1 LENGTH: 1728 base pairs
2 TYPE: nucleic acid
3 STRANDEDNESS: double
4 TOPOLOGY: linear
5 MOLECULE TYPE: cDNA to genomic RNA
6 HYPOTHETICAL: <Unknown>
7 ANTI-SENSE: <Unknown>
8 FRAGMENT TYPE: <Unknown>
9 ORIGINAL SOURCE:
10 ORGANISM: A/12um1/5/65
11 STRAIN: <Unknown>
12 INDIVIDUAL ISOLATE: <Unknown>
13 DEVELOPMENTAL STAGE: <Unknown>
14 HAPLOTYPE: <Unknown>
15 TISSUE TYPE: <Unknown>
16 CELL TYPE: <Unknown>
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18 ORGANELLE: <Unknown>
19 IMMEDIATE SOURCE:
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21 CLONE: <Unknown>
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23 CHROMOSOME/SEGMENT: <Unknown>
24 MAP POSITION: <Unknown>
25 UNITS: <Unknown>
26 FEATURE:
27 NAME/KEY:
28 LOCATION:
29 IDENTIFICATION METHOD:
30 OTHER INFORMATION:
31 PUBLICATION INFORMATION:
32 AUTHORS:
33 TITLE:
34 JOURNAL:
35 VOLUME:
36 ISSUE:
37 PAGES:
38 DATE:
39 DOCUMENT NUMBER:
40 FILING DATE:
41 PUBLICATION DATE:
42 RELEVANT RESIDUES IN SEQ ID NO:
43 SEQUENCE DESCRIPTION: SEQ ID NO: 28:
44 US-09-918-568-28

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Query Match	90.18;	Score 1606.4;	DB 9;	Length 1728;
Best Local Similarity	95.63;	Pred. No. 0;		
Matches 1652; Conservative	0;	Mismatches 76;	Indels 0;	Gaps 0;

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Db 61 GAGGGGGGACGATATGCATTGGATACCATGCCAAATATTCCACAGAAAAAGGTCGACAC 120

14/ AATTCTAGAGCGGAACGTCACCTGTGACTCATGCCAAGGACATCCTTGAGGAAGACCCATAA 206

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207 CGGAAGTTATGCCAACCTAAACGGAATCCCTCCACTTGAACTAGGGGACTGTACCAATTC 266
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Db 181 CGGAAGCTATGCCAACTAACGSAATCCCTCCACTTGAAC TAGGGGACTGTACATTGC 240

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Db 1441 AGGAAATGATGATTTTGAATTTATCACAAAATGTCAGATGATGATGATGATGATGAT 1500
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RESULT 3
US-09-918-568-49
Sequence 49, Application US/09918568
Patent No. US20020054882A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 1135 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:

Query Match	Best Local Similarity	Matches	916: Conservative	51.9%: Score	908.8: DB	9: Length	1135:
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913	GAGACCAATGCCAA	ACTCTTTGGGAGCAATAATACACATTACCTTTTACAAATGTC	972				
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328	CACCCACTGACAAATA	GTGAGTGTGCCCAAAATATGTAAATCGGAGAAATGGTGTCTTACCA	387				
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508	GACCAGGATCAGGG	TATGCAGCAGACAAAGAAATCCACTCAAAAGGCAATTTGATGAAATC	567				
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568	ACCAACAAGGTAAT	TCGTGATTTGAAAGATTAACACCCCAATTTGAAGCTGTGGGAAA	627				
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628	GAATTCGTAACCTTA	TAGAAAAGACTGAGAACTTGAACAAAGAGATGGAAGACGGGTTT	687				
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QY      1453      AACGTCAAAGCACTAGCAAAATGATGTTTGAATTTTATCACAAAATGATGATGAATGC      1512
Db      808      AACGTCAAAGCACTAGCAAAATGATGTTTGAATTTTATCACAAAATGATGATGAATGC      867
QY      1513      ATGAATAGTGTGAAGAAACGGGACATATGATTTATCCCAAGTATGAAGAAAGACTTAAACTA      1572
Db      868      ATGAATAGTGTGAAGAAACGGGACATATGATTTATCCCAAGTATGAAGAAAGACTTAAACTA      927
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Db      928      AATGAATAGTGAAGAAACGGGATTTAAATTTGAGCAGCATGGGGGTTTATCAAAATCCTTGCC      987
QY      1633      ATTATATGCTACAGTAGCAGAGCTTCTATGTCTACTGCGCAATCATGATGATGCTGGAGTCCTTTC      1692
Db      988      ATTATATGCTACAGTAGCAGAGCTTCTATGTCTACTGCGCAATCATGATGATGCTGGAGTCCTTTC      1047
QY      1693      TGGGTGTGCTCCACAGCGGTCTCTCCACAGCGCAATCCCATATGATATATAGTCATTTTA      1752
Db      1048      TGGGTGTGCTCCACAGCGGTCTCTCCACAGCGCAATCCCATATGATATATAGTCATTTTA      1107
QY      1753      TAATTAAAAACACCCCTTGTTCTGCTGTA      1780
Db      1108      TAATTAAAAACACCCCTTGTTCTGCTGTA      1135

RESULT 4
US-09-918-568 -27
Sequence 27, Application US/09918568
Patent No. US20020054882A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250

```


TELEX: <Unknown>
INFORMATION FOR SEQ. ID NO: 27 :
SEQUENCE CHARACTERISTICS:
LENGTH: 1754 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna to genomic RNA
HYPOHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/Suila/1/89
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ. ID NO:
SEQUENCE DESCRIPTION: SEQ. ID NO: 27:
us-09-918-568-27

Query Match 39.0%; Score 695.6; DB 9; Length 1754;
Best Local Similarity 64.0%; Pred. No. 5,9e-183;
Matches 1068; Conservative: 0; Mismatches 594; Indels 6; Gaps 1;

QY 76 TTCACAGCAGTAGAGGGGACCAAGATATGATGATACCAATTAATTCACAGAG 135
DB 54 TTACAGTACAGATGACACACATATGTATAGGCTACCAATCGAACAACCTCAACCGAC 113
QY 136 AAGTCGACACATTTCTAGAGCGGAAAGCTGACGTGACATGCCAAGACATCCTTGAG 195
DB 114 ACTGTGGACACAGTACTTGAGAAAGACGTGACAGTACACACTCTGTCAACTACTTGGAG 173
QY 196 AAGACCCATTAAGGAAAGTTATGCAAACTAAACGGAATCCCTTCACCTTGAAGTAGGGGAC 255
DB 174 GACAGTACAAAGGAAACTATGTGAGCTAAAGAAAGATGCCCACTACAAATTTGGSTAAT 233
QY 256 TGTAGCATTTGCCGATGGCTCTTGGAATCCAAAATGTGATAGGCTTAAAGTGTGCA 315
DB 234 TGCAGCATTTGCCGATGGATCTTAAAGAAACCCAGATGCGAATCACTGTTTCTAAGAA 293
QY 316 GAAGGCTCTATATTTGGAGAAAGAAACCCGAGAGCGTTTGTGTTATCCAGGAC 375
DB 294 TCATGTGCTCTACATTTGAGAAACACCAAACTCCGGAATGGAACATGTACACAGGATAT 353
QY 376 TTCAATGATATGAAGATTAACATCTCTCAGCAGCGTGAACATTTGAGAAAGTA 435

DB 354 TTGCGCCAGCTATGAGAGAACTGAGAGCAATTTGATTCAGTATCATTCATTCGAGATTC 413
QY 436 AAGATTCGCCCCAAGATAGAT-----GGACACAGCATACCAACTGAGATTACGG 489
DB 414 GAAATATTTCCCAAGAAAGCTCATGGCCCAACCAACCGTACCAAGAGGATACGGCA 473
QY 490 GCCTGCGGGGTGTCTGTATTCATCTTTTCAGAACATGTCTGTGACAAAGAA 549
DB 474 TCATGTCTCCCATTAATGGAAAGACAGTTTACGAAATTTGCTATGGCTGACGGGAAG 533
QY 550 GGATCAGATTTATCCGGTTGCCAAGAGTGTACACATATCAAGCGGAGACAAATGCTA 609
DB 534 AATGGCTTGAACCAAACTGAGCAAGTCTGATGTGAACCAAGAGAAAGATGCTT 593
QY 610 ATAATTTGGGGGTGCACCATCCATGATGAGACACAGAAAGAAACATTTACCGAAT 669
DB 594 GTACTATGGGTGTTCATTCACCCGCTCATCATATAGGGACCAAGGGCATCTATTCATPA 653
QY 670 GTGGAACTATGTTCCGTAAGCACATCAACATTTGAACAAAGGTCAACCCGAAATA 729
DB 654 GAAATGCTTATGTCTCTGTAGTGTCTTACATTTATAGCAGGATTCACCCGAAATA 713
QY 730 GCAACAGGCGCTAAGATGAGATGACAAAGAGATGAAATGTAATTTCTTGACCCCTTG 789
DB 714 GCAAAAAGCCCAAGATGAGAGTCAAGAGAAAGATTAACATCTACATGAGACTGCTG 773
QY 790 GATATGTGGACACACATTAATTTTGTAGTACTGTAATCTTAATTCACAGATGTA 849
DB 774 GAACCCGGGACACACAAATATTTTGAAGCAATATGAAATCTTAATAGCCCATGTATGCT 833
QY 850 TTCAAATATGCAAAAGAGTACTTACAGGATCATGAAACAGAAAGAACACTTGAAC 909
DB 834 TTGCACTGATGAGGCTTTGGGTGACAGATCATCCTCAAAACCATCAATGATGTA 893.
QY 910 TGTGAGACCAATATGCAAACTCTTTGGAGCAATATATCAACATTTACTTTTCAAT 969
DB 894 TGTGAGCGGAGAGTGAACACCCAGGAGCTATTAACAGTATGCTCTTCCACAT 953
QY 970 GTCCACCACCTGACATAGTGTGAGTCCCAATATGTAATTCGGAAGTTGGCTTA 1029
DB 954 GTACACCCAGTCAATATGAGAGTGTCCAAAGTATGTCAAGAGTCAAAATTAAGATG 1013
QY 1030 GCAACAGACTAAGAAATGTTCCCAAGTTGAATCAAGAGATTTGTTGGCAATAGCT 1089
DB 1014 GTTACAGGACTAAGAAATCCCATTCATCAATCCAGAGTTGTTGAGACCAATGCG 1073
QY 1090 GGTTTATGAAGAGAGATGCAAGAAATGTTGACGTTGTTGATGATACATCACAC 1149
DB 1074 GGTTCATTTGAGGGGGGTGAGTGAATGATGATGATGATGATGATGATGATGATGATG 1133
QY 1150 AATGACAGGATCAGGATATGACAGACAAAGAAATCACTCAAAAGCATTTATGTA 1209
DB 1134 AATGAACAGAGATCTGCTATGTGTGAGATCAAAAAAGCACAAATATCCCTTAACGGA 1193
QY 1210 ATACCAACAGGTAATTTCTGTGATGTAAGAAATTAACACCAATTTGAAGCTTTGG 1269
DB 1194 ATTAACAAAGGTGAATTTCTGTAATCGAAGAAATGAACACTCAATTCACACCTGTGGC 1253
QY 1270 AAGAAATTCGTACTTGAAGAAAGCTGGAACCTGGAACCAAAAGATGGAAGACGG 1329
DB 1254 AAGAAATTAACAAATTAAGAAAGAGATGGAATCTTAATAAAGAAAGTTGATGATGTA 1313
QY 1330 TTTTATGATGTGACATACATACCTGTTTATGTTCTGATGGAAGATGAGAGCA 1389
DB 1314 TTTCTGACATTTGGACATATATGACAGATTTGTTGTTCTTACTGGAAGAAAGAGCT 1373
QY 1390 CTTGACTTTCATGATTTCTAATGTCAAGATCTGTACTAAGAGTCAAGTCAAGTCA 1449
DB 1374 TTGGAATTTTCATGACTCAATATGTAAGATCTGTATGAAAGTAAAGCAATTAAG 1433
QY 1450 GACACGTCAAGACTAGGAATGATGTTTGAATTTTATCACAATTTGATGATGAA 1509

Db 1434 AATAATGCCAAGA/ATAGATACGGGTGTTTGAATCTACACACAGTGAACATGAA 1493
QY 1510 TGCATGATAGTGTAAAAACGGGACATATGATATCCAGTATGAGAGAGCTGAAA 1569
Db 1494 TGCATGAGAACTGTAAAAATGAGACTTATGACTATCCAAATATTCGAGGAATCAAG 1553
QY 1570 CTAATATGAAATGATATCAAGGGGTAAATTTAGACAGACATGGGGTTTATCAATCCCTT 1629
Db 1554 TTAACAGGGAATAATGATGAGATGAATTTGGAATCAATGGGAGCTCTATCAGATTCTG 1613
QY 1630 GCCATTATGCTACATGACAGCTTCTATGTCACCTGCCAATCAGATGGCTGGCATCTCT 1689
Db 1614 GCGATCTACTCAACCTGTCGCCAGTTCACCTGCTTGTCTCTCCCTGGGGCAATCCAGC 1673
QY 1690 TTCGCGGTGCTCTCAACGGGTCTCTGAGTGCAGGATCTGCATATGA 1737
Db 1674 TTCTGATGTCTTCTTAATGGGTCTTTGCACTGTGAAATATGATCTGA 1721

RESULT 5
US-09-918-568-33
Sequence 33, Application US/09918568
Patent No. US20020054882A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenceroth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993

ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/Okuda/57

STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-918-568-33

Query Match 22.4%; Score 400; DB 9; Length 400;
Best Local Similarity 100.0%; Pred. No. 5.2e-101;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 940 CCAATAATACACATTACCTTTTCACATGTCACCCACGACATGACATAGTGATGCCCC 999
Db 1 GCAATTAATACACATTACCTTTTCACATGTCACCCACGACATGACATAGTGATGCCCC 60

QY 1000 AATATGTAAATGGAGAACTGTGCTTACACAGGACGTAAGAAATGCCAGATT 1059
Db 61 AATATGTAAATGGAGAACTGTGCTTACACAGGACGTAAGAAATGCCAGATT 120

QY 1060 GAATCAAGAGATTGTTGGGGCAATAGCTGTTTATAGAAGAGATGCAAGAAATG 1119
Db 121 GAATCAAGAGATTGTTGGGGCAATAGCTGTTTATAGAAGAGATGCAAGAAATG 180

QY 1120 GTTACGGTGTGATGATACCATCAGCAATGACAGGATCAGGGTATGACAGCAG 1179
Db 181 GTTACGGTGTGATGATACCATCAGCAATGACAGGATCAGGGTATGACAGCAG 240

QY 1180 AAAGATTCATCAAAAGCATTTGATGGAATCACCACAGGTAATTTCTGTATGAA 1239
Db 241 AAAGATTCATCAAAAGCATTTGATGGAATCACCACAGGTAATTTCTGTATGAA 300

QY 1240 AAGATTAACACCCATTTGAAGCTGTGGGAAATTCGTTACTTGAAGAAAGACTG 1299
Db 301 AAGATTAACACCCATTTGAAGCTGTGGGAAATTCGTTACTTGAAGAAAGACTG 360

QY 1300 GAGAACTTGAACAAAGATGGAAGACGGCTTCTAGATG 1339
Db 361 GAGAACTTGAACAAAGATGGAAGACGGCTTCTAGATG 400

RESULT 6
US-09-918-568-34
Sequence 34, Application US/09918568
Patent No. US20020054882A1
GENERAL INFORMATION:

APPLICANT: Yoshinobu OKUNO et al.
 TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
 ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
 STREET: 2033 K Street, N.W., #800
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20006

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/918,568
 FILING DATE: 02-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/004,422
 FILING DATE: January 8, 1998
 APPLICATION NUMBER: 08/443,862
 FILING DATE: May 22, 1995
 APPLICATION NUMBER: 08/229,781
 FILING DATE: April 19, 1994
 APPLICATION NUMBER: 08/054,016
 FILING DATE: April 29, 1993

ATTORNEY/AGENT INFORMATION:
 NAME: Warren M. Cheek, Jr.
 REGISTRATION NUMBER: 33,367
 REFERENCE/DOCKET NUMBER: <Unknown>
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-721-8200
 TELEFAX: 202-721-8250

INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 409 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

MOLECULE TYPE: cDNA to genomic RNA
 HYPOTHEICAL: <Unknown>
 ANTI-SENSE: <Unknown>
 FRAGMENT TYPE: <Unknown>
 ORIGINAL SOURCE:
 ORGANISM: A/Adachi/2/57
 STRAIN: <Unknown>
 INDIVIDUAL ISOLATE: <Unknown>
 DEVELOPMENTAL STAGE: <Unknown>
 HAPLOTYPE: <Unknown>
 TISSUE TYPE: <Unknown>
 CELL TYPE: <Unknown>
 CELL LINE: <Unknown>
 ORGANELLE: <Unknown>
 IMMEDIATE SOURCE:
 LIBRARY: <Unknown>
 CLONE: <Unknown>
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: <Unknown>
 MAP POSITION: <Unknown>
 UNITS: <Unknown>

FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION:
 PUBLICATION INFORMATION:
 AUTHORS:
 TITLE:
 JOURNAL:

VOLUME:
 ISSUE:
 PAGES:
 DATE:
 DOCUMENT NUMBER:
 FILING DATE:
 PUBLICATION DATE:
 RELEVANT RESIDUES IN SEQ ID NO:
 SEQUENCE DESCRIPTION: SEQ ID NO: 34:
 US-09-918-568-34

Query Match 22.3%; Score 397; DB 9; Length 409;
 Best Local Similarity 98.8%; Pred. No. 3,6e-100;
 Matches 400; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 935 TGGGAGCAATTAATACACATTACCTTTCCAAATGTCACCCACGACGACAAATAGTGAGT 994
 Db 5 TTGGAGCAATTAATACACATTGCTTTCCAAATGTCACCCACGACGACAAATAGTGAGT 64

QY 995 GCCCAATATGTAAATCGAGAAAGTTGCTTACCAACAGAGACTAAGAAATGTTCCCC 1054
 Db 65 GCCCAATATGTAAATCGAGAAAGTTGCTTACCAACAGAGACTAAGAAATGTTCCCC 124

QY 1055 AGATTGAATCAGAGAGATTGTTGGGCAATAGCTGTTTATAGAGAGAGATGGCAAG 1114
 Db 125 AGATTGAATCAGAGAGATTGTTGGGCAATAGCTGTTTATAGAGAGAGATGGCAAG 184

QY 1115 GAATGTTGACGGTGTGATGATACCATCAGCAAGTACGAGGATCAGGTTATGCGAG 1174
 Db 185 GAATGTTGATGTTGATGATGATACCATCAGCAAGTACGAGGATCAGGTTATGCGAG 244

QY 1175 CAGACAAGAAATCCACTCAAAAGGCAATTTGATGATGATCACCACAGGTAATTTCTGTA 1234
 Db 245 CAGACAAGAAATCCACTCAAAAGGCAATTTGATGATGATCACCACAGGTAATTTCTGTA 304

QY 1235 TTGAAAAGATTAACACCCCAATTTGAAGCTGTTGGGAAGAATTCGGTACTTAGAGAAA 1294
 Db 305 TTGAAAAGATTAACACCCCAATTTGAAGCTGTTGGGAAGAATTCGGTACTTAGAGAAA 364

QY 1295 GACTGGAGAACTTGAACAAAAGATGGAAGACGGGTTTCTAGATG 1339
 Db 365 GACTGGAGAACTTGAACAAAAGATGGAAGACGGGTTTCTAGATG 409

RESULT 7
 US-09-918-568-35
 Sequence 35, Application US/09918568
 Patent No. US20020054882A1

GENERAL INFORMATION:
 APPLICANT: Yoshinobu OKUNO et al.
 TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
 ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
 STREET: 2033 K Street, N.W., #800
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20006

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/918,568
 FILING DATE: 02-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/004,422
 FILING DATE: January 8, 1998
 APPLICATION NUMBER: 08/443,862

```

? FILING DATE: May 22, 1995
? APPLICATION NUMBER: 08/229,781
? FILING DATE: April 19, 1994
? APPLICATION NUMBER: 08/054,016
? FILING DATE: April 29, 1993
? ATTORNEY/AGENT INFORMATION:
?   NAME: Warren M. Cheek, Jr.
?   REGISTRATION NUMBER: 33,367
? REFERENCE/DOCKET NUMBER: <Unknown>
? TELECOMMUNICATION INFORMATION:
?   TELEPHONE: 202-721-8200
?   TELEFAX: 202-741-8250
?   TELEX: <Unknown>
? INFORMATION FOR SEQ ID NO: 35:
? SEQUENCE CHARACTERISTICS:
?   LENGTH: 410 base pairs
?   TYPE: nucleic acid
?   STRANDEDNESS: double
?   TOPOLOGY: linear
? MOLECULE TYPE: cDNA to genomic RNA
? HYPOTHETICAL: <Unknown>
? ANTI-SENSE: <Unknown>
? FRAGMENT TYPE: <Unknown>
? ORIGINAL SOURCE:
?   ORGANISM: A/Kuhamoto/1/65
? STRAIN: <Unknown>
? INDIVIDUAL ISOLATE: <Unknown>
? DEVELOPMENTAL STAGE: <Unknown>
? HAPLOTYPE: <Unknown>
? TISSUE TYPE: <Unknown>
? CELL TYPE: <Unknown>
? CELL LINE: <Unknown>
? ORGANELLE: <Unknown>
? IMMEDIATE SOURCE:
?   LIBRARY: <Unknown>
? CLONE: <Unknown>
? POSITION IN GENOME:
? CHROMOSOME/SEGMENT: <Unknown>
? MAP POSITION: <Unknown>
? UNITS: <Unknown>
? FEATURE:
?   NAME/KEY:
?   LOCATION:
? IDENTIFICATION METHOD:
? OTHER INFORMATION:
? PUBLICATION INFORMATION:
? AUTHORS:
? TITLE:
? JOURNAL:
? VOLUME:
? ISSUE:
? PAGES:
? DATE:
? DOCUMENT NUMBER:
? FILING DATE:
? PUBLICATION DATE:
? RELEVANT RESIDUES IN SEQ ID NO:
? SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-918-568-35

Query Match      21.4% Score 382.4 DB 9 Length 410
Best Local Similarity 96.1% Pred. No. 4.2e-96
Matches 392: Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 932 CTTGGAGCATATATAACACATTACTCTTTCACAATGTCCACCACCAATGAATAGTG 991
Db 3 CTTGGAGCATATATAACACATTACTCTTTCACAATGTCCACCACCAATGAATAGTG 62
QY 992 AGTCCCCCAAATATATAAATCGAGAGATTGCTTTAGCAACAGAGACTAAGAATGTC 1051
Db 63 AATGCCCAATATATAAATCGAGAACTGTCTTAGCAACAGAGACTAAGAATGTC 122
QY 1052 CCCAGATTGAATCAGAGATTGTTGGGGCAATAGCTGTTTATAGAACAGAGATGCC 1111

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Dd 123 |CCCCGATTGCATCAAGAGATTGTTTGGGGCAATAGCTGGCTTGTAGAAAGAGATGCG| 182

QY 1112 |AAGGAATGTTGACGGTTGGTATGATAACATCATCAGACAATACCAGGATCAGGGTATG| 117U

Dd 183 |AAGGAATGATGTATGATGGTTGGTATGATRCATCATCAGACAATGATCAGGATCAGGGTTTG| 242

QY 1172 |CAGCAGACAAAAGAATCCACTCACTAAAAAGCATTTGATGATATCCAACACAGTAATTCTG| 1231

Dd 243 |CAGCAGACAAAAGAATCCACTCACTAAAAAGCATTTGATGATATCCAACACAGTAATTCTG| 302

QY 1232 |TGATTGAAAAGATATAACCCCATTGTAGAGCTGTGGAAAGAAFTGCGTAACTTAGGA| 1291

Dd 303 |TGATTGAAAAGATATAACCCCATTGTAGAGCTGTGGAAAGAAFTGCGTAACTTAGGA| 362

QY 1292 |AAAGACTGCGAACACTGACAAAAGAATGGAAGACGGGTTTCATGATG| 1339

Dd 363 |AAAGACTGCGAACACTGACAAAAGAATGGAAGACGGGTTTCATGATG| 410

RESULT 8
US-09-918-568-36
Sequence 36, Application US/09918568
Patent No. US20020054882A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
City: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHEetical: <unknown>
ANTI-SENSE: <unknown>
FRAGMENT TYPE: <unknown>
ORIGINAL SOURCE:

ORGANISM: A/Kaizuka/2/95
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 36;
US-09-918-568-36

Query Match 21.3%; Score 379.6; DB 9; Length 394;
Best Local Similarity 97.7%; Pred. No. 2.5e-95;
Matches 385; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

946 AATACACATTCCTTTTCACATGTCACCCCTGACATAGTAGTCCCAATAT 1005
|||||
1 AATACACATTCCTTTTCACATGTCACCCCTGACATAGTAGTCCCAATAT 60
1006 GTAATATCGAGAGTGGCTTTCAGCAGACAGACTAAGATGTTCCCGATGATCA 1065
|||||
61 GTAATATCGAGAGTGGCTTTCAGCAGACAGACTAAGATGTTCCCGATGATCA 120
1066 AGAGATTTGTTGGGCAATAGCTGTTTATGAAGAGAGATGCCAAGATGTTGAC 1125
|||||
121 AGAGATTTGTTGGGCAATAGCTGTTTATGAAGAGAGATGCCAAGATGTTGAT 180
1126 GGTGGTATGATACCATCAGACAGCATGACAGGGATCAGGGATCAGACAGCAAGAA 1185
|||||
181 GGTGGTATGATACCATCAGACAGCATGACAGGGATCAGGGATCAGACAGCAAGAA 240
1186 TCCACTCAAAAGCAATTTGATGGAATCACCACAAAGTAAATCTGATGTTGAAGATA 1245
|||||
241 TCCACTCAAAAGCAATTTGATGGAATCACCACAAAGTAAATCTGATGTTGAAGATG 300
1246 AACACCCCAATTTGAAGCTGTTGGGAAAGATTCGAATTTAGAGAAAGACTGGAGAAC 1305
|||||
301 AACACCCCAATTTGAAGCTGTTGGGAAAGATTCGAATTTAGAGAAAGACTGGAGAAC 360
1306 TTGAACAAAAGATGGAAGACGGGTTTCTAGATG 1339
|||||
361 TTGAACAAAAGATGGAAGACGGGTTTCTAGATG 394

GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
City: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/034,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A2/Alchi/2/68
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:

QY 216 ATGCAACTAAACGGAATCCCTCACTTAAGAGGGAAGTGTAGCAATGGCCGATGGCT 275
 Db 187 CTGC---TCMAAGGGAAGGAAGCAAGTGTACCTCGGTCAATGTGACCTCTGTGGAAACAT 243
 QY 276 CTTGGAATCCAAATGTGATAGCTTACTAGTGTGCCAAGAGCTCTATATATTTGA 335
 Db 244 CACTGGGACCCCAATGTGACCAAGTCTCTAGAAATTTTCAAGCCGATCTAATATATAGAG 303
 QY 336 GAAAGAAAACCCGAGAGAGGTTTGTGTATCCAGCAGCTTCAATGATATAGAAAT 395
 Db 304 GCGAG-----GGAAGTGTGTCTGTATCTGTGGAAATTCGTGAATGAAGAGCTCT 357
 QY 396 GAAACATCTCTCAAGCAGCTGTGAACATTTGAGAAAAGTAAAGATTTGGCCCAAGAT 455
 Db 358 GAGCAAAATTCCTCAGAGAGTCAAGGGAATTTGACAGAGGCAATGGATTCACATACAG 417
 QY 456 ATGACACAGCATCAACACTGAGGTTCAAGGAGCTCGCGGCTGTGGTAATTCATC 515
 Db 418 CGGAATTAAGACTAATGAAACACCAAGTACATGTAGAGATCAGATCTTCAATCTATGC 477
 QY 516 ATTTTTCAGAACATGCTGTGCTGACAAAGGAAGATCAGATTAATCCGGTTCGCAAGG 575
 Db 478 AGAG---ATGAAATGGCTCTGTGTCAACACAGACATGCTCTCCCGCATGACTAA 534
 QY 576 ATGTCACACATCAACAGCGGAGCAACAAATCTAATATTTGGGGGTGCACCATCCAT 635
 Db 535 GTCTACAAAAACCAAGGAAGACCAAGCTCTGTATATATGGGGATTCACATATCCGG 594
 QY 636 TGTAGACACAGAACAAAGACATGTGTACCAAGATGTGGAGCATGTTCCGTAGACAC 695
 Db 595 ATCAACTACAGAACACCAAGCTATATGTGAGTGAACCAACTGATTAACAGATGGAG 654
 QY 696 ATCAACTTAACAAAAGGTCAACCCAGAAATAGCAACAGGCTTAAGTAATGAGCA 755
 Db 655 TTCTAATTAACACAGCTCTTGTGACCGAGTCCAGAGAGAGACACCAAGTATGGCA 714
 QY 756 AGGAGTAAGTAAGTAATCTCTGTGACCTCTGTGATATGTGGACACCATTAATTTGA 815
 Db 715 ATCTGGAAGATGTGACTTCTTCAATGCTGATGTAAACCCCAATGACAGCTCTTACG 774
 QY 816 GAGTACTGTAACTAATTTGACACAGTATGTGTTCAAAATATGCAAAAGAGTACTTC 875
 Db 775 TTTCATTTGGGCTTATAGCTTCACAGCTGCA---AGTTTCTGTAGAGGAGTCTAT 831
 QY 876 AGGATCATGAAGAAACGAAGAACTGTGAACTGTGAGACCAATGCCAACTCTTT 935
 Db 832 GGGGATTCAGAGTGTGACAGTGTGATGCAATTAATAGCAGGAGTGTAGGAAATG 951
 QY 936 GGGCAATTAATTAACAACTTACCTTTTCACAATGTCCACCTGACCAATAGGTGATG 995
 Db 892 AGGGAATTAATTAATTTGCCCTTTGAGAACTAATTAATAGCAGGAGTGTAGGAAATG 951
 QY 996 CCCCATAATTAATTAATTCGTAAGTGTGTAAGACAGGACTAAGGATTTCCCA 1055
 Db 952 TCCGAGATATGTTAAGCAAGAGTGTGCTGTGCAACAGGATTAAGATTTCCCA 1011
 QY 1056 GATTAAATCA-----AGAGATTTGTTGGGCAATAGCTGTTTATAGA 1100
 Db 1012 AATTCCAAAAGAGTGTGTGAGAGAGGCTATTTGTTGCTATAGCGGTTTCAATTA 1071
 QY 1101 AGGAGATGTGCAAGATGTGTGAGGTTGTATGATACCATCACAGCAATGACAGG 1160
 Db 1072 AAATGTGATGGAGTGTGATGTGAGGTTGTATGCTTCAAGCATCAAAATGCAACAG 1131
 QY 1161 ATCAGGATGTGACAGCAAGAAATCACTCAAAAGCAATTTGATGATGATACCAACA 1220
 Db 1132 AGAGGGAATCTGTGATTAACAAAGACCAATTAATGATCAAGTAAACAGGAA 1191
 QY 1221 GGTAAATCTGTGATTAAGAAATTAACCAATTTGAAGCTGTGGAAAGAAATTCGG 1280
 Db 1192 ATTGAACCGGCTTATAGAAAAAATCAACCAATTTGATTAATAGCAATGAATTCAC 1251
 QY 1281 TAACTTAGAGAAAAGACTGTGGAACCTTAACAAAAAGATGGAAGAGCGGTTTCTAGATG 1340

Db 1252 TGAGTTGAAAACCAATTTGGCAATGTGTAATTTGACACAGAGTTCATGACAGAGT 1311
 QY 1341 GTGACATCAATAGCTGAGCTTTTACTGTGTATGTAAGAAATGAGAGACACTTCA 1400
 Db 1312 GTGTCTCTTAAGCTGAACTCTTGTAGCAATGGAACCAAGCATTAATTTGATCTGAC 1371
 QY 1401 TGAATTAATGTCAGAAATCTGTATAGTAAGTCAAGAAATGCAAGTGAAGACACGTCOA 1460
 Db 1372 CGACTCAGAAATGAACAACTATAGCAAGCAAGTGAAGAGACTACTGAGAGAAATGCTGA 1431
 QY 1461 AGAATAGAAATGATGTTTGAATTTTATACAAATGTATGATGATGATGATGATGATG 1520
 Db 1432 AGAATAGCACTGTTGCTTCAAAATTTTCAAGGATGATGATGATGATGATGATGATG 1491
 QY 1521 TGTGAAAACGAGACATATGATTTATCCCAAGTATCAAGAGTCAAACTAATTAACAA 1580
 Db 1492 TATTTGAAAACCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1551
 QY 1581 TGAATTAAGGCTTAAATTTGACAGCAGTATGAGGAGTATGATGATGATGATGATGATG 1640
 Db 1552 ACAGATTAACCAAGTCAAACTAAGCAGGCTTACAAAGATGATGATGATGATGATGATG 1611
 QY 1641 TACAGTACAGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1700
 Db 1612 CGGGCATCATGTTTCACTTCTGCGCATGCAATGAGGCTTGTCTTCAATGATGATGATG 1671
 QY 1701 CTCACAGGCTCTGCTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1741
 Db 1672 --AATGGAACCAATGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1709

RESULT 11
 US-09-918-568-57
 ; Sequence 57, Application us/09918568
 ; Patent No. US20020054882A1
 GENERAL INFORMATION:
 APPLICANT: Yoshinobu OKUNO et al.
 TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
 ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Mendelsohn, Lind & Ponack, L.L.P.
 STREET: 2033 K Street, N.W., #800
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20006
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: us/09/918, 568
 FILING DATE: 02-Aug-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/004,422
 FILING DATE: January 8, 1998
 APPLICATION NUMBER: 08/443,862
 FILING DATE: May 22, 1995
 APPLICATION NUMBER: 08/229,781
 FILING DATE: April 19, 1994
 APPLICATION NUMBER: 08/054,016
 FILING DATE: April 29, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren M. Cheek, Jr.
 REGISTRATION NUMBER: 33,367
 REFERENCE/DOCKET NUMBER: <Unknown>
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-721-8200
 TELEFAX: 202-721-8250

TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 1110 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <unknown>
ANTI-SENSE: <unknown>
FRAGMENT TYPE: <unknown>
ORIGINAL SOURCE:
ORGANISM: A2/A13h1/2/68
STRAIN: <unknown>
INDIVIDUAL ISOLATE: <unknown>
DEVELOPMENTAL STAGE: <unknown>
HAPLOTYPE: <unknown>
TISSUE TYPE: <unknown>
CELL TYPE: <unknown>
ORGANELLE: <unknown>
IMMEDIATE SOURCE:
LIBRARY: <unknown>
CLONE: <unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <unknown>
MAP POSITION: <unknown>
UNITS: <unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-918-568-57

Query Match 14.4%; Score 252.4; DB 9; Length 1110;
Best Local Similarity 56.4%; Pred. No. 1.2e-59;
Matches 507; Conservative 0; Mismatches 376; Indels 9; Gaps 2;

QY 885 GAAACGAGAGAGAC/CTTGAGAACTGTGAGACCAATGCCAATCTTTGGAGCAAT 944
DB 228 GAAATATGCAACAA/ATTGATACCTGCTATTCTGGAATGCATCCTCAATGGAGCAAT 287
QY 945 AAATACAACTTACC/TTTCACAATGTCCACCCACGACATGAGATGAGGCCCAATA 1004
DB 288 TCCCAATGACAAAGCC/TTTCAAAAACGTAACAGATACATATGACATGCCCCAAGTA 347
QY 1005 TGTAAATCGGAGAA/TTGGTCTTAGCAGACAGACTAAGGAATGTTCCCAAGATTGAATC 1064
DB 348 TGTAAAGCAAAACAC/CTGAAGTTGGCAGACAGGATCGGAATGTACAGAGAAACAAC 407
QY 1065 AAGAGATTTTGGG/CCCATAGCTGTGTTTATGAAGAGAGATGCGAAGATGTTGA 1124
DB 408 TAGAGGCTTATTGG/CCCAATAGCAGGTTTCATAGAAAATGTTGGAGGGAATGATAGA 467
QY 1125 CGGTGTGTATGATAT/CATCAGACAGATGACAGGATGAGGATGATGACAGACAAAGA 1184
DB 468 CGGTGTGTATGATAT/CATCAGACAGATGACAGGATGAGGATGATGACAGACAAAGA 1184
QY 1185 ATCCACTCAAAAGGC/TTTGATGGAATCACCACAAAGTAATTCGTGATGAAAAAGAT 1244

DB 528 AAGCACTCAAGCACCATCGCACCAATCAATGGAATAATTGAAACAGGGTAATCGAGAGAC 587
QY 1245 AAACACCAATTTTAAGCTGTGTGGAAAGATTTGGTACTTAAGAAAGACGTGGAGA 1304
DB 588 GAACGAGAAATTCATCAATCGAAATCGAAATGGAATGTAAGGAAATTCAGCA 647
QY 1305 CTTCAGCAAAATGAGAGACGCGGTTCTCATGTGTGTGACATCAATGCTGAGCTTT 1364
DB 648 CTTGAGAAATACGTTGAGACACTAAATATGATCTGTGCTTACATAGGAGCTTCT 707
QY 1365 AGTTCTGATGAAATGAGAGACACTGACTTTCATGATTTCTAATGTCAGAAATCTGTA 1424
DB 708 TGTGCTGTGAGAAATCAATCAATGAAATGAAATGAAATGAAATGAAATGAAATG 767
QY 1425 TAGTAAGTCAAGATGACGTGAGAGACACGTAAGAAAGAACTAGAAATGATGTTTGA 1484
DB 768 TGAATAAAACAAAGGAGCACTGAGGAAATGCTGAAGAGATGGGCAATGCTTCA 827
QY 1485 ATTTATCACAAATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1544
DB 828 AATATACCAATATGTGACACAGCTTGCATGATGATGATGATGATGATGATGATGAT 887
QY 1545 TCCCAATGATGAGAGAGAGCTTAACATAATGAAATGAAATGAAATGAAATGAAATGAG 1604
DB 888 TGATGTATACAGAGACAGAGATTAACAACCGCTTCAATGATGATGATGATGATGAT 947
QY 1605 CAGCATGGGGTTTATCAATCTTCCATTTATGCTACAGTACAGTACAGTACAGTACT 1664
DB 948 GTCTGATACAAAGACGATCCTGTGATGATGATGATGATGATGATGATGATGATGAT 1004
QY 1665 GGCATCATGATGCTGGATCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1724
DB 1005 TTGTGTTGTTTGTGCTGGCTTCAATGATGATGATGATGATGATGATGATGATGAT 1064
QY 1725 GATCTGATATGATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1776
DB 1065 CATTTGATTTGAGTGA-----TTAGTATTAATAAACCCTTTGTTCTG 1110

RESULT 12
US-09-918-568-29
Sequence 29, Application US/09918568
Patent No. US20020054882A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918, 568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016

FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8250
TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/PR/8/34
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-918-568-29

Query Match 14.1%; Score 251.6; DB 9; Length 442;
Best Local Similarity 73.1%; Pred. No. 1.2e-59;
Matches 323; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 958 CCTTTCACATGTCACCCACCTGACATAGAGTGTGCTCCCAATGATCAAGAGATTGTT 1017
DB 1 CCTTTCACAAATATACACCCACCTGACATAGAGTGTGCTCCCAATGATCAAGAGATTGTT 1017
QY 1018 AAGTGTGCTTGTAGCAAGAGATGATGTTCCCAATGATCAAGAGATTGTT 1077
DB 61 AATGTGAGATGTGTACAGAGATGATGTTCCCAATGATCAAGAGATTGTT 120
QY 1078 GGGGCAATAGCTGTTTATAGAGAGAGATGCAAGAAATGTTGACGTTGTATGGA 1137
DB 121 GGAGCAATGCGCGTTTATAGAGAGAGATGCAAGAAATGATGATGATGATGAT 180
QY 1138 TACCATCAGACATGACAGGATCAGGATGATGACAGACAAAGATCCACTCAAG 1197

DB 181 TATCATCATCAGATGACAGAGATGACGCTATGACGCGATCAAAAAAGCACACAAAT 240
QY 1198 GCATTTGATGATATCAACCAAGATTAATTCGTGATTTGAAAAGATTAACCAATTT 1257
DB 241 GCCATTACAGGATTAACCAAGATTAATTCGTGATTTGAAAAGATTAACCAATTT 300
QY 1258 GAAGCTGTGGGAAAGATTCGTTACTAGAGAAAGACGTGAGAACTTGAACAAAG 1317
DB 301 ACAGCTGTGGGATTAACCAAGATTAATTCGTGATTTGAAAAGATTAACCAATTT 360
QY 1318 ATGGAAGACGGTTTCTAGATGTGTGACATCAATGCTGAGCTTTTACTGTGATGAA 1377
DB 361 GTTGATGATGATTTCTGACATTTGACATATTAATGACAAATGTTAGTTCTACTGAA 420
QY 1378 AATGAGAGCACTTACTTTC 1399
DB 421 AATGAAAGACCTGTGATTTCC 442

RESULT 13
US-09-918-568-32
Sequence 32, Application US/09918568
Patent No. US2002005482A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:

ORGANISM: A/Osaka/930/88
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION SEQ ID NO: 32:
US-09-918-568-32

Query Match 13.4%; Score 241.8; DB 9; Length 429;
Best Local Similarity 72.1%; Pred. No. 6.3e-57;
Matches 312; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

958 CCTTTTCACATCTCACCACCTAGCAATAGTGTAGTCCCAATATGTAAATCGGAG 1017
1 CCTTTCAGATGTATACCCAGTCAATAGAGAGTCCCAAGATATGTCAGAGTACA 60
1018 AAGTGTCTTAGCAACAGACTAAGATGTTCCAGATTGAATCAAGAGATTGTT 1077
61 AATTAAAGATGTATAGGACTAAGAACTCCATCCATTCAATCCAGGTTGTTT 120
1078 GGGGCAATAGCTGTTTATAGAGAGAGATGSCAAGAAATGTTGACGTTGATGA 1137
121 GGACCAATTTGGCGGTTCATATGAAGGGGGGTGACTGGAATGATGATGATGTT 180
1138 TACCATCAGCAATGACCAAGGATCAGGATGACAGACAAGAAATCCACTCAAG 1197
181 TATCATCATCAGATGAACAAGGATCTGGCTATGCTCGGATCAAAAAGACCAAAAT 240
1198 GCATTGATGAATC/CCAACAAGTAAATCTGTGATTGAAAGATAAACACCAATTT 1257
241 GCCATTAAAGCAATTTCAACAAAGTCAATTTCTTAATCGAATAATGACACTCAATTC 300
1258 GAAGCTGTGGGAAAGAAATTCGGTAACTAGAGAAAAGACTGGAACCTTGAACAAAAG 1317
301 ACAGCTGTGGGCAAGAAATTCACAAATTTAGAAAGAAAGATGGAATAAATAAAAAA 360
1318 ATGAAGAAGCGGTTTATAGATGTGTGACATACATGCTGAGCTTTAGTTCTATGAA 1377
361 GTTGATATGATGATTGTGACATTTTGACATATATATGACAAATGTTGTTCTACTGAA 420
1378 AATGAGAG 1386
421 AATGAAGG 429

RESULT 14
US-09-918-568-30
Sequence 30, Application US/09918568
Patent No. US20020054882A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCE ADDRESSES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918, 568
CLASSIFICATION: <Unknown>
FILING DATE: 02-Aug-2001
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/Bangkok/10/83
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:

OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-918-568-30

Query Match 13.1%; Score 233.6; DB 9; Length 424;
Best Local Similarity 71.9%; Pred. No. 1.2e-54;
Matches 305; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

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QY 1018 AATTGGTCTTACACACAGAGACTAAGAAATGTTCCCGAGTTGATCAAGAGATTGTTT 1077
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QY 1198 GCATTTGATGATGATCCACCAAGAGATGATGCTGCTGATGATGATGATGATGATGAT 1257
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QY 1258 GAAGCTGTTGGGAAAGATTCGTTAGTGAAGAAAGAGTGAAGAAAGTGAAGAAAG 1317
301 ACAGCTGGGTGAAGATTCACCAATTCAGAAAGAAAGATGGAAGAAAGTGAAGAAAG 360
QY 1318 ATGGAAGAGCGGTTTCTAGATGTTGACATACATGCTGAGCTTTAGTTGATGAGAA 1377
361 GTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 1378 AATG 1381
421 AATG 424

RESULT 15
US-09-918-568-31
Sequence 31, Application US/09918568
Patent No. US2002005482A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/Yamagata/120/86
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-918-568-31

Query Match 13.1%; Score 233.6; DB 9; Length 424;
Best Local Similarity 71.9%; Pred. No. 1.2e-54;
Matches 305; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

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OY 1018 AAGTTGGCTTAGCAACAGGACTAAGAAATGTTCCCAATGATCAAGAGATGTTT 1077
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Db 61 AAATTAGGATGGTTACAGGACTAAGGAACATCCCATCAATCCATCCAGAGTGTGTTT 120
OY 1078 GGGGCATACCTGGTTTATAGAGGAGATGSCAAGAAATGTTGACGGTTGATGGA 1137
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Db 121 GGAGCCATGCGCGGTTTCATTTGAAGGGGGGTGACTGGAATGATGATGGATGGTATGGT 180
OY 1138 TACCATCACAAGCAATCACCAAGGATCAGGGTATGACAGACAAGAAATCCACTCAAAAG 1197
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Db 241 GCCATTACGGGATTAACAACAAAGTGAATCTGTATCGAANAATGAACACTCAATTTC 300
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OY 1318 ATGGAAGACGGGTTTATAGATGTGTGACATACAAATGCTGAGCTTTAGTTCTGATGAA 1377
    || || || ||||| || || ||||| ||||| || || || |||||
Db 361 GTTGATGATGATTTTGTGACATTTGACATATATATGACAGATTTGTTGGTCTACTGGA 420
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Db 421 AATG 424
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Job time : 289.395 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
8672.640 Million cell updates/sec

Title: US-09-918-568-49

Perfect score: 1135

Sequence: 1 CTAGCAAGCGGGGTAT.....AACACCTGTCTCTAG 1135

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 20691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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SUMMARIES

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1	1135	100.0	1135	US-08-229-781-49	Sequence 49, Appl
2	1135	100.0	1135	US-08-630-918-49	Sequence 49, Appl
3	1135	100.0	1135	US-09-004-422-49	Sequence 49, Appl
4	908.8	80.1	1783	US-08-229-781-46	Sequence 46, Appl
5	908.8	80.1	1783	US-08-630-918-46	Sequence 46, Appl
6	908.8	80.1	1783	US-09-004-422-46	Sequence 46, Appl
7	838	73.8	1728	US-08-229-781-28	Sequence 28, Appl
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10	461.2	40.6	1721	US-08-686-968C-226	Sequence 226, App
11	451	39.7	1766	US-08-453-848-8	Sequence 8, Appl
12	451	39.7	1766	US-09-169-027-8	Sequence 8, Appl
13	448.6	39.5	1724	US-09-197-679A-1	Sequence 1, Appl
14	447.8	39.5	1754	US-08-229-781-27	Sequence 27, Appl
15	447.8	39.5	1754	US-08-630-918-27	Sequence 27, Appl
16	447.8	39.5	1754	US-09-004-422-27	Sequence 27, Appl
17	443	39.0	1701	US-09-232-468A-13	Sequence 13, Appl
18	443	39.0	1701	US-09-784-984B-11	Sequence 11, Appl
19	400	35.2	400	US-08-229-781-33	Sequence 33, Appl
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21	400	35.2	400	US-09-004-422-33	Sequence 33, Appl
22	397	35.0	409	US-08-229-781-34	Sequence 34, Appl
23	397	35.0	409	US-08-630-918-34	Sequence 34, Appl
24	397	35.0	409	US-09-004-422-34	Sequence 34, Appl
25	382.4	33.7	410	US-08-229-781-35	Sequence 35, Appl
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27	382.4	33.7	410	US-09-004-422-35	Sequence 35, Appl

28	379.6	33.4	394	1	US-08-229-781-36	Sequence 36, Appl
29	379.6	33.4	394	1	US-08-630-918-36	Sequence 36, Appl
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31	373	32.9	924	5	PCT-US94-01149-15	Sequence 15, Appl
32	372.6	32.8	810	5	PCT-US94-01149-19	Sequence 19, Appl
33	368.2	32.4	670	5	PCT-US94-01149-5	Sequence 5, Appl
34	361.4	31.8	912	5	PCT-US94-01149-31	Sequence 31, Appl
35	263.8	23.2	729	5	PCT-US94-01149-17	Sequence 17, Appl
36	263	23.2	1777	1	US-08-229-781-54	Sequence 54, Appl
37	263	23.2	1777	1	US-08-630-918-54	Sequence 54, Appl
38	263	23.2	1777	4	US-09-004-422-54	Sequence 54, Appl
39	259.2	22.8	630	5	PCT-US94-01149-21	Sequence 21, Appl
40	256.4	22.6	474	5	PCT-US94-01149-33	Sequence 33, Appl
41	254.6	22.4	1762	1	US-08-105-483-284	Sequence 284, App
42	254.6	22.4	1762	1	US-08-709-209-284	Sequence 284, App
43	254.6	22.4	1762	1	US-08-458-101-284	Sequence 284, App
44	253.6	22.3	1793	2	US-08-453-848-6	Sequence 6, Appl
45	253.6	22.3	1793	3	US-09-169-027-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-229-781-49
; Sequence 49, Application US/08229781
; Patent No. 5589174
; GENERAL INFORMATION:
; APPLICANT: Yoshinobu OKUNO et al.
; TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,781
; FILING DATE: April 19, 1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/054,016
; FILING DATE: April 29, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELETYPE:
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1135 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: A/Okuda/57
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:

HAFLTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELL:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-229-781-49

Query Match 100.0%; Score 1135; DB 1; Length 1135;
Best Local Similarity 100.0%; Pred. No. 6-4e-315;
Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1081 ATCTGATATGATATTAATGATATTAATTAATTAATTAATTAATTAATTAATTAAT 1135
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RESULT 2

US-08-630-918-49
Sequence 49, Application US/08630918
Patent No. 5631350
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,918
FILING DATE: April 5, 1996
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-8830
 TELEFAX:
 TELEX:
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1135 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to genomic RNA
 ORIGINAL SOURCE:
 ORGANISM: A/Okuda/57
 US-08-630-918-49

Query Match 100.0%; Score 1135; DB 1; Length 1135;
 Best Local Similarity 100.0%; Pred. No. 6, 4e-315;
 Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGCAAAAGCAGGCGTTATACCATAGAAAACCAAAAGCAAAACAATGGCCATCATTTAT 60
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RESULT 3
 US-09-004-422-49
 ; Sequence 49, Application us/09004422
 ; Patent No. 6337070
 ; GENERAL INFORMATION:
 ; APPLICANT: Yoshinobu OKUNO et al.
 ; TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
 ; NUMBER OF SEQUENCES: 58
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Wenderoth, Lind & Ponack, L.L.P.
 ; STREET: 2033 K Street, N.W., #800
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: Wordperfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/004,422
 ; FILING DATE: January 8, 1998
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/443,862
 ; FILING DATE: May 22, 1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/229,781
 ; FILING DATE: April 19, 1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/054,016
 ; FILING DATE: April 29, 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren M. Cheek, Jr.
 ; REGISTRATION NUMBER: 33,367
 ; REFERENCE/DOCKET NUMBER:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-721-8200
 ; TELEFAX: 202-721-8250
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 49:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1135 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to genomic RNA
 ; HYPOTHETICAL:

ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: A/Okuda/57
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-09-004-422-49

Query Match 100.0%; Score 1135; DB 4; Length 1135;
Best Local Similarity 100.0%; Prid. No. 6.4e-315;
Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGCAAAAGCGGGGTTATACCATAGAAAACCAAAAGCAAAACCAATGGCCATTTAT 60
DB 1 CTAGCAAAAGCGGGGTTATACCATAGAAAACCAAAAGCAAAACCAATGGCCATTTAT 60
QY 61 CTCATCTCTCTGTCACAGCAGTGAAGGGGACGATTCGATTCGATTCATTCAT 120
DB 61 CTCATCTCTCTGTCACAGCAGTGAAGGGGACGATTCGATTCGATTCATTCAT 120
QY 121 AATTCACAGAGAAAGTGCACACATTTAGAGCGGAACGTCAGTGCATGCGCAG 180
DB 121 AATTCACAGAGAAAGTGCACACATTTAGAGCGGAACGTCAGTGCATGCGCAG 180
QY 121 AATTCACAGAGAAAGTGCACACATTTAGAGCGGAACGTCAGTGCATGCGCAG 180
DB 121 AATTCACAGAGAAAGTGCACACATTTAGAGCGGAACGTCAGTGCATGCGCAG 180
QY 181 GACATCTTTGAGAGAACCCATAGCGAAAGTTATGCAAACTAAGCGATCCGGGATCATG 240
DB 181 GACATCTTTGAGAGAACCCATAGCGAAAGTTATGCAAACTAAGCGATCCGGGATCATG 240
QY 241 AAAACAGAGAGAACTGAGACAGTGTGAGACCAATGCGCAATCTTTGGGAGCAATA 300
DB 241 AAAACAGAGAGAACTGAGACAGTGTGAGACCAATGCGCAATCTTTGGGAGCAATA 300
QY 301 AATACACATTAACCTTTTACACATGTCCACCCACTGACATAGTGAGTGGCCCAATAT 360
DB 301 AATACACATTAACCTTTTACACATGTCCACCCACTGACATAGTGAGTGGCCCAATAT 360
QY 361 GTAAATGAGAGAAAGTGTCTTACACACAGCACTAAGCAATGTTCCCGAGTTGATCA 420
DB 361 GTAAATGAGAGAAAGTGTCTTACACACAGCACTAAGCAATGTTCCCGAGTTGATCA 420
QY 421 AGAGATTTGTTGGGCAATAGCTGTTTATAGAGAGAGATGCGCAAGGAATGTTGAC 480
DB 421 AGAGATTTGTTGGGCAATAGCTGTTTATAGAGAGAGATGCGCAAGGAATGTTGAC 480

QY 481 GGTGGTATGATACCATCAGACATGACGAGGATCGGGTATGACAGACAAAGAA 540
DB 481 GGTGGTATGATACCATCAGACATGACGAGGATCGGGTATGACAGACAAAGAA 540
QY 541 TCCACTCAAAAGCATTTGATGGAATCACAACAAGGTAATTTCTGATTTGAAAGTA 600
DB 541 TCCACTCAAAAGCATTTGATGGAATCACAACAAGGTAATTTCTGATTTGAAAGTA 600
QY 601 AACACCAATTTGAAAGCTTTGGGAAAGATTTGGTAACTTAGAGAAAAGCTGGAGAC 660
DB 601 AACACCAATTTGAAAGCTTTGGGAAAGATTTGGTAACTTAGAGAAAAGCTGGAGAC 660
QY 661 TTGAACAAAAGATGAGAGAGCGTTCTAGATGTGAGACATCAATGCGACTTTTA 720
DB 661 TTGAACAAAAGATGAGAGAGCGTTCTAGATGTGAGACATCAATGCGACTTTTA 720
QY 721 GTTCGTATGAAATGAGAGACACTTACATTTCAATGATTCATGCAAGATCTGAT 780
DB 721 GTTCGTATGAAATGAGAGACACTTACATTTCAATGATTCATGCAAGATCTGAT 780
QY 781 AGTAAAGTGAATGACGCTGAGAGACAAAGCTCAAGAACTAGCAATGATTTTGA 840
DB 781 AGTAAAGTGAATGACGCTGAGAGACAAAGCTCAAGAACTAGCAATGATTTTGA 840
QY 841 TTTTATCACAATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 841 TTTTATCACAATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 CCCAAGTATGAAGAGTCTAACTAAATAGAAATGAATCAAGGGGTAAATTTGAGC 960
DB 901 CCCAAGTATGAAGAGTCTAACTAAATAGAAATGAATCAAGGGGTAAATTTGAGC 960
QY 961 AGCATGGGGTTATCAAAATCTTCCCATTTATGCTAGAGAGAGTTATGTCATG 1020
DB 961 AGCATGGGGTTATCAAAATCTTCCCATTTATGCTAGAGAGAGTTATGTCATG 1020
QY 1021 GCAATCATGATGCTGGGATCTCTTCTGGGTCGTCACAGGCTCTGCAATGAGG 1080
DB 1021 GCAATCATGATGCTGGGATCTCTTCTGGGTCGTCACAGGCTCTGCAATGAGG 1080
QY 1081 ATCTGCATATGATTAATGATCTTTTATTAATTAATAAACACCCCTGTTCTGCTAG 1135
DB 1081 ATCTGCATATGATTAATGATCTTTTATTAATTAATAAACACCCCTGTTCTGCTAG 1135

RESULT 4
US-08-229-781-46
Sequence 46, Application US/08229781
Patent No. 5589174
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,781
FILING DATE: April 19, 1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993

ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 83,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8880
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna to genomic RNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: A/Okuda/57
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-229-781-46

Query Match 80.1%; Score 908.8; DB 1; Length 1783;
Best Local Similarity 98.7%; Pred. No. 3.7e-250;
Matches 916; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 208 AAGTTATGCAACTAAGCGATCCGGATCATGAAAAAGAGAGAACTTGAGAACTGT 267
DB 853 AAGATATCGAAAAAGCTAGTTCAGGATCATGAAAAAGAGAACTTGAGAACTGT 912
QY 268 GAGACCAAAATGCCAACTCTCTTTGGGAGCAATAAACAACATTACCTTTCCAAATGTC 327
DB 913 GAGACCAAAATGCCAACTCTCTTTGGGAGCAATAAACAACATTACCTTTCCAAATGTC 972
QY 328 CACCCACTGCAATAGTGTAGTCCCAAAATATGTAATAATCGAGAGATTGCTCTTAGCA 387
DB 973 CACCCACTGCAATAGTGTAGTCCCAAAATATGTAATAATCGAGAGATTGCTCTTAGCA 1032
QY 388 ACAGGACTAAGAAATGTTCCCGCATTTGAATCAAGAGATTGTTGGGGCAATAGCTGCT 447
DB 1033 ACAGGACTAAGAAATGTTCCCGCATTTGAATCAAGAGATTGTTGGGGCAATAGCTGCT 1092

QY 448 TTTATAGAGAGATGCGAAGAAATGTTGACGTTGTATGGATACCATCAGCAAT 507
DB 1093 TTTATAGAGAGATGCGAAGAAATGTTGACGTTGTATGGATACCATCAGCAAT 1152
QY 508 GACCAGGATCAGGGATGCGACGACAGACAAGAAATCCACTCAAAAGCATTTGATGAATC 567
DB 1153 GACCAGGATCAGGGATGCGACGACAGACAAGAAATCCACTCAAAAGCATTTGATGAATC 1212
QY 568 ACCAACAAGTAAATTTGTGATTGTAAGAAATTAACCCCAATTTGAAGCTGTGGGAAA 627
DB 1213 ACCAACAAGTAAATTTGTGATTGTAAGAAATTAACCCCAATTTGAAGCTGTGGGAAA 1272
QY 628 GAATTCGTAAGTATAGAGAAAAGACTGAGAACTTGAACAAAAGATGGAAGAGCGGTTT 687
DB 1273 GAATTCGTAAGTATAGAGAAAAGACTGAGAACTTGAACAAAAGATGGAAGAGCGGTTT 1332
QY 688 CTAGATGTGTGACATCAATGCTGACCTTTTAACTGTGATGAAATGAGAGACACTT 747
DB 1333 CTAGATGTGTGACATCAATGCTGACCTTTTAACTGTGATGAAATGAGAGACACTT 1392
QY 748 GACTTTGATGATCTAATGTCAGAAATCTGTATAGTAAGTCAGAAATGACGTCGAGAC 807
DB 1393 GACTTTGATGATCTAATGTCAGAAATCTGTATAGTAAGTCAGAAATGACGTCGAGAC 1452
QY 808 AACGTCAAGACATGAGAAATGATGTTTGAATTTATACAAATGATGATGATGATG 867
DB 1453 AACGTCAAGACATGAGAAATGATGTTTGAATTTATACAAATGATGATGATGATG 1512
QY 868 ATGAATAGTGTGAAAAAGGAGCATATGATATCCCAAGTATGAAGAAGATCTAAACTA 927
DB 1513 ATGAATAGTGTGAAAAAGGAGCATATGATATCCCAAGTATGAAGAAGATCTAAACTA 1572
QY 928 AATGAAATGAATCAAAAGGGGTAAATTTAGACAGCATGGGGTTTATCAATCTTGGC 987
DB 1573 AATGAAATGAATCAAAAGGGGTAAATTTAGACAGCATGGGGTTTATCAATCTTGGC 1632
QY 988 ATTATGCTACAGTACAGGATGCTATGTCACCTGCAATCATGATGCTGGGATCTTTTC 1047
DB 1633 ATTATGCTACAGTACAGGATGCTATGTCACCTGCAATCATGATGCTGGGATCTTTTC 1692
QY 1048 TGGGTGTGTCCAACGGGCTCTGCACTGCAAGATCGATATGATTAATGATCTTTTA 1107
DB 1693 TGGGTGTGTCCAACGGGCTCTGCACTGCAAGATCGATATGATTAATGATCTTTTA 1152
QY 1108 TAATTAATAACACCTTGTCTGCTAG 1135
DB 1753 TAATTAATAACACCTTGTCTGCTAG 1780

RESULT 5
US-08-630-918-46
Sequence 46, Application US/08630918
Patent No. 5631350
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
City: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,918
FILING DATE: April 5, 1996

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
PRIOR APPLICATION DATA: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Mairen M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ. ID NO.: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
ORIGINAL SOURCE:
ORGANISM: A/Oxuda/57
US-08-630-918-46

Query Match 80.1%; Score 908.8; DB 1; Length 1783;
Best Local Similarity 98.7%; Pred. No. 3.7e-250;
Matches 916; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 208 AAGTATGCAACTAAGCGATCCGGATCAGTGAAGAGAGAACTTGAGAACTGT 267
DB 853 AAAATATCCAAAAGAGAGTTCAGGAGCATGAAACAGAGAACACTTGAGAACTGT 912
QY 268 GAGACCAATGCAACTCCTTTGGAGCAATTAATACCAATTTACTTTTCAATGTC 327
DB 913 GAGACCAATGCAACTCCTTTGGAGCAATTAATACCAATTTACTTTTCAATGTC 972
QY 328 CACCACATGACATAGTGTGTCGCCAATATGTAATCGAGAGAGTTGGCTTAGCA 387
DB 973 CACCACATGACATAGTGTGTCGCCAATATGTAATCGAGAGAGTTGGCTTAGCA 1032
QY 388 ACAGGACTAAGAGATGTTCCAGATTTGAATCAAGAGATTTGTTGGGCAATAGCTGT 447
DB 1033 ACAGGACTAAGAGATGTTCCAGATTTGAATCAAGAGATTTGTTGGGCAATAGCTGT 1092
QY 448 TTTATAGAGAGAGATGGAAGATGTTGATGATGATGATGATGATGATGATGATGAT 507
DB 1093 TTTATAGAGAGAGATGGAAGATGTTGATGATGATGATGATGATGATGATGATGAT 1152
QY 508 GACGAGGATCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 567
DB 1153 GACGAGGATCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1212
QY 568 ACCAACAAGTAAATTTCTGTATGTAAGATTAACACCCCAATTTGAAGCTGTTGGGAAA 627
DB 1213 ACCAACAAGTAAATTTCTGTATGTAAGATTAACACCCCAATTTGAAGCTGTTGGGAAA 1272
QY 628 GAATTCGGTAATTTGAGAAAAGACTGGAAGCTTGAACAAAAGATGGAAGCGGTTT 687
DB 1273 GAATTCGGTAATTTGAGAAAAGACTGGAAGCTTGAACAAAAGATGGAAGCGGTTT 1332
QY 688 CTAGATGTTGACATACAAATCTGAGCTTTTATGTTCTGATGGAAGATGAGAGACATT 747
DB 1333 CTAGATGTTGACATACAAATCTGAGCTTTTATGTTCTGATGGAAGATGAGAGACATT 1392
QY 748 GACTTTCATGATTTTAATGTCAGAAATCTGTATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAG 807
DB 1393 GACTTTCATGATTTTAATGTCAGAAATCTGTATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1452
QY 808 AACGTCAAAGAACTGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 867
DB 1453 AACGTCAAAGAACTGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1512

QY 868 ATGATAGTGTGTAAGAAAGCGGACATATGATTTATCCAAATATGAGAGAGTCTAAACTA 927
DB 1513 ATGATAGTGTGTAAGAAAGCGGACATATGATTTATCCAAATATGAGAGAGTCTAAACTA 1572
QY 928 AATGAAATGAAATCAAGAGGGTAAATTTAGACAGATGAGGGGTTTATCAAACTCTGCC 987
DB 1573 AATGAAATGAAATCAAGAGGGTAAATTTAGACAGATGAGGGGTTTATCAAACTCTGCC 1632
QY 988 ATTATGCTACATGACAGGTTCTATGTACTGCAATCATGATGATGATGATGATGATGATGAT 1047
DB 1633 ATTATGCTACATGACAGGTTCTATGTACTGCAATCATGATGATGATGATGATGATGATGAT 1692
QY 1048 TGGGTGCTCCACAGGTTCTGCAAGTGCAGATCTGATATGATTAAGTCAATTTA 1107
DB 1693 TGGGTGCTCCACAGGTTCTGCAAGTGCAGATCTGATATGATTAAGTCAATTTA 1752
QY 1108 TAATTAACAAACACCTTTGTTCTGCTAG 1135
DB 1753 TAATTAACAAACACCTTTGTTCTGCTAG 1780

RESULT 6
US-09-004-422-46
Sequence 46, Application US/09004422
Patent No. 6337070
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,422
FILING DATE: January 8, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Mairen M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ. ID NO.: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL:
ANTI-SENSE:

FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: A/Okuda/57
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-09-004-422-46

Query Match 80.1%; Score 908.8; DB 4; Length 1783;
Best Local Similarity 98.7%; Pred. No. 3.7e-250;
Matches 916; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 208 AACTTATGCAACTAAAGCATCCGGATCATGAAAAAGAGAGACACTTGAAGACTGT 267
DB 853 AAATATCGAAAGAGAGTACTGAGGATCATGAAAAAGAGAGACACTTGAAGACTGT 912
QY 268 GAGACCAATGCCAATCCTTTGGGAGCAATAATCAACATTACTCTTTTCAACATGTC 327
DB 913 GAGACCAATGCCAATCCTTTGGGAGCAATAATCAACATTACTCTTTTCAACATGTC 972
QY 328 CACCACTGCAATAGGTGAGTCCCCCAATATGTAATCGAGAGAGTGTGCTTGA 387
DB 973 CACCACTGCAATAGGTGAGTCCCCCAATATGTAATCGAGAGAGTGTGCTTGA 1032
QY 388 ACAGGACTAAGAAATTTCCCAAGATTGAATCAAGAGATTGTTGGGGCAATAGCTGT 447
DB 1033 ACAGGACTAAGAAATTTCCCAAGATTGAATCAAGAGATTGTTGGGGCAATAGCTGT 1092
QY 448 TTTATGAAGAGAGATGCGAAGATGCTGAGGTTGATGATACATCAGCAAT 507
DB 1093 TTTATGAAGAGAGATGCGAAGATGCTGAGGTTGATGATACATCAGCAAT 1152
QY 508 GACCAAGGATCAGGATGATGAGAGACAAAGATCCACTAAAAGCATTTGATGAAATC 567
DB 1153 GACCAAGGATCAGGATGATGAGAGACAAAGATCCACTAAAAGCATTTGATGAAATC 1212
QY 568 ACCAACAAGTAAATTTGTGATGTAAGATTAACCAACCAATTTGAAGCTGTGGGAAA 627
DB 1213 ACCAACAAGTAAATTTGTGATGTAAGATTAACCAACCAATTTGAAGCTGTGGGAAA 1272
QY 628 GAATTCGTAACCTTAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 687
DB 1273 GAATTCGTAACCTTAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1332

QY 688 CTAGATGTGAGACATACAAATGCTGAGCTTTTACTGATGAAATGAGAGACACTT 747
DB 1333 CTAGATGTGAGACATACAAATGCTGAGCTTTTACTGATGAAATGAGAGACACTT 1392
QY 748 GACTTATGATTTTATGTCACAAATCTGATAGTAAAGTCACAAATGCTGAGAGAC 807
DB 1393 GACTTATGATTTTATGTCACAAATCTGATAGTAAAGTCACAAATGCTGAGAGAC 1452
QY 808 AACGTCAAG 867
DB 1453 AACGTCAAG 1512
QY 868 ATGATAGTGTGAAAAACGGACATATGATATCCAGATGAAAGAGAGAGAGAGAGAG 927
DB 1513 ATGATAGTGTGAAAAACGGACATATGATATCCAGATGAAAGAGAGAGAGAGAGAG 1572
QY 928 AATGAAATGAAATCAAGAGGTTAAATTTGAGAGAGATGGGGTTTATCAATCTTCC 987
DB 1573 AATGAAATGAAATCAAGAGGTTAAATTTGAGAGAGATGGGGTTTATCAATCTTCC 1632
QY 988 ATTATGCTACAG 1047
DB 1633 ATTATGCTACAG 1692
QY 1048 TGGGTGTCTCCAAAGGAGTCTGACAGTGCAGATGCAATGATGATTAAGTATTTTA 1107
DB 1693 TGGGTGTCTCCAAAGGAGTCTGACAGTGCAGATGCAATGATGATTAAGTATTTTA 11752
QY 1108 TAATTAATAAACACCTTTGTTCTGCTAG 1135
DB 1753 TAATTAATAAACACCTTTGTTCTGCTAG 1780

RESULT 7

US-08-229-781-28
Sequence 28, Application US/08229781
Patent No. 5589174
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,781
FILING DATE: April 19, 1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SRO ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1728 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1728 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
ORIGINAL SOURCE: A/12uni/5/65
ORGANISM: A/12uni/5/65
US-08-630-918-28

Query Match 73.8%; Score 838; DB 1; Length 1728;
Best Local Similarity 95.8%; Pred. No. 6,5e-230;
Matches 862; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 208 AAGTTATGCAACTAAGCGATCCGGGATCATGAAAAACAGAGAACACTTGAGACTGT 267
DB 827 AATATATCGAAAAGABGTAGTTCAGGGATCATGAGACAGAACACTTGAGACTGT 886
QY 268 GAGACCAATGCCAATCTCTTTGGAGCAATAAATCAACATTACTCTTTCAATATGC 327
DB 887 GAGACCAATGCCAATCTCTTTGGAGCAATAAATCAACACTCTTTCAACATGTC 946
QY 328 CACCCACTGACATATBTGAGTCCCAATATGTAAATCGGAGAGTGTCTTAGCA 387
DB 947 CACCCACTGACATATBTGAGTCCCAATATGTAAATCGGAGAGTGTCTTAGCA 1006
QY 388 ACAGACTAAGAAATTTCCCAAGATTGAATCAAGAGATTGTTGGGGCAATAGCTGT 447
DB 1007 ACAGACTAAGAAATTTCCCAAGATTGAATCAAGAGATTGTTGGGGCAATAGCTGC 1066
QY 448 TTTATAGAGAGAGATGCGCAAGAAATGTTGACGTTGCTATGATACCTACAGCAAT 507
DB 1067 TTTATAGAGAGAGATGCGCAAGAAATGTTGATGTTGATGATACCTACAGCAAT 1126
QY 508 GACGAGGATCAGGATGTCGAGCAGACAAAGAAATCCACTAAAGGATTTGATGAAAC 567
DB 1127 GACGAGGATCAGGATGTCGAGCAGACAAAGAAATCCACTAAAGGATTTGATGAAAC 1186
QY 568 ACCAACAGGTAATTTCTGTGATGAAAAGATTAACACCCAAATTTGAAGCTGTTGGAAA 627
DB 1187 ACCAACAGGTAATTTCTGTGATGAAAAGATTAACACCCAAATTTGAAGCTGTTGGAAA 1246
QY 628 GAATTCGTACTTATBAGAAAACACTGAGAACTTGACAAAAGATGAGACGGGTTT 687
DB 1247 GAATTCGTACTTATBAGAAAACACTGAGAACTTGACAAAAGATGAGACGGGTTT 1306
QY 688 CTGATGCTGAGCAATGACATGCTGAGCTTTTGTGATGAAAATGAGAGACACTT 747
DB 1307 CTGATGCTGAGCAATGACATGCTGAGCTTTTGTGATGAAAATGAGAGACACTT 1366
QY 748 GACTTTCATGATCTTATATGCAAGAAATCTGTATAGTAAGTCAAGATGACGTGAGAC 807
DB 1367 GACTTTCATGATCTTATATGCAAGAAATCTGTATAGTAAGTCAAGATGACGTGAGAC 1426
QY 808 AAGCTCAAGAACTAAGAAATGATGTTTGAATTTTATACAAATGCTGATGATGC 867
DB 1427 AAGCTCAAGAACTAAGAAATGATGTTTGAATTTTATACAAATGCTGATGATGC 1486
QY 868 ATGAAATGCTGAAAACCGGACATATGATTTCCCAAGATGAGAGAGTCTAAACTA 927
DB 1487 ATGAAATGCTGAAAACCGGACATATGATTTCCCAAGATGAGAGAGTCTAAACTA 1546
QY 928 AATAGAAATGAATCAAGGGGTAAATGAGCAGATGAGGGGTTTATCAAAATCTTGC 987
DB 1547 AATAGAAATGAATCAAGGGGTAAATGAGCAGATGAGGGGTTTATCAAAATCTTGC 1606
QY 988 ATTTATGCTACAGTATGAGGTTCTATGTCACCTGCAATCATGATGCTGGGATCTCTTC 1047
DB 1607 ATTTATGCTACAGTATGAGGTTCTATGTCACCTGCAATCATGATGCTGGGATCTCTTC 1666

QY 1048 TGGGTGCTCTCAACGGGCTCTGCACTGAGGATGCAATATGATTAAGTATTTA 1107
DB 1667 TGGATGCTCTCAACGGGCTCTGCACTGAGGATGCAATATGATTAAGTATTTA 1726
QY 1108 TA 1109
DB 1727 TA 1728

RESULT 9
US-09-004-422-28
Sequence 28, Application US/09004422
Patent No. 6337070
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,422
FILING DATE: January 8, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1728 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
ORIGINAL SOURCE: A/12uni/5/65
ORGANISM: A/12uni/5/65
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:

CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-09-004-422-28

Query Match 73.8%; Score 838; DB 4; Length 1728;
Best Local Similarity 95.6%; Pred. No. 6,5e-230;
Matches 862; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 208 AAGTATGCAAACTAAACGATCCGGATCATGAAAACAGAAAGACACTTGAGACTGT 267
DB 827 AAATATCGAAAAGAGGTAGTTCAGGATCATGAAAGACAGAAACCTTGGGAACTGT 886
QY 268 GAGACCAAAATGCCAACTCCTTGGGAGCAATAATACACATTACCTTTTACAAATGTC 327
DB 887 GAGACCAAAATGCCAACTCCTTGGGAGCAATAATACACACTACCTTTTACAAATGTC 946
QY 328 CACCCACTGCAATAGTGAAGTCCCAATATGTAATAATCGAGAGTGGCTTGA 387
DB 947 CACCCACTGCAATAGTGAAGTCCCAATATGTAATAATCGAGAAATGGCTTGA 1006
QY 388 ACAGGACTAAGGAATGTTCCCGATTTGAATCAAGAGATGTTTGGGCAATAGCTGT 447
DB 1007 ACAGGACTAAGGAATGTTCCCGATTTGAATCAAGAGATGTTTGGGCAATAGCTGT 1066
QY 448 TTATATGAGAGAGATGGCAAGATGTTGAGGTTGATGATACATCACAGCAAT 507
DB 1067 TTATATGAGAGAGATGGCAAGATGTTGATGTTGATGATACATCACAGCAAT 1126
QY 508 GACCAAGGATCAAGGATGATGACAGACAAAGAAATCCACTCAAAAGCATTTGATGATC 567
DB 1127 GACCAAGGATCAAGGATGATGACAGACAAAGAAATCCACTCAAAAGCATTTGATGATC 1186
QY 568 ACCAACAAGTAAATCTGATGATGAAAAGATTAACACCAATTTAGCTGTTGGAAA 627
DB 1187 ACCAACAAGTAAATCTGATGATGAAAAGATTAACACCAATTTAGCTGTTGGAAA 1246
QY 628 GAATTCGTAAGTGAAGAAAGACAGCACTTAACAAAAGATGGAAGCGGCTT 687
DB 1247 GAATTCGTAAGTGAAGAAAGACAGCACTTAACAAAAGATGGAAGCGGCTT 1306
QY 688 CTAGATGTTGACATACAAATGCTGAGCTTTAGTTCTGATGAAAATGAGAGCACTT 747
DB 1307 CTAGATGTTGACATACAAATGCTGAGCTTTAGTTCTGATGAAAATGAGAGCACTT 1366
QY 748 GACTTTCATGATCTAATGTCAGAAATCTGTATAGTAAGTGAAGTGAAGTGAAGAC 807
DB 1367 GACTTTCATGATCTAATGTCAGAAATCTGTATAGTAAGTGAAGTGAAGTGAAGAC 1426
QY 808 AACGTCAAGAACTGGAATGATGTTTGAATTTATCACAATGATGATGATGATG 867
DB 1427 AACGTCAAGAACTGGAATGATGTTTGAATTTATCACAATGATGATGATGATG 1486
QY 868 ATGATAGTGTGAAAAACGGGACATATGATTTCCAGTATGAGAGAGATCTAAACTA 927

DB 1487 ATGATAGTGTGAAAAACGGGACATATGATTTATCCAGTATGAGAGAGATCTAAACTA 1546
QY 928 AATGAAATGAAATCAAAAGGGGTAAATTTGAGCAAGATGGGGTTTATCAATCTTGGC 987
DB 1547 AATGAAATGAAATCAAAAGGGGTAAATTTGAGCAAGATGGGGTTTATCAATCTTGGC 1606
QY 988 AATTATGCTAGATGACAGGTTCTATGCTACTGCAATCATGATGATGATGATGATG 1047
DB 1607 AATTATGCTAGATGACAGGTTCTATGCTACTGCAATCATGATGATGATGATGATG 1666
QY 1048 TGGGTGCTCCACAGGTTCTGCTGAGTGCAGATCTGCAATGATGATGATGATG 1107
DB 1667 TGGGTGCTCCACAGGTTCTGCTGAGTGCAGATCTGCAATGATGATGATGATGATG 1726
QY 1108 TA 1109
DB 1727 TA 1728

RESULT 10
US-08-686-968C-226
Sequence 226, Application US/08686968C
Patent No. 6221361
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
FILE REFERENCE: 39119-H/JML
CURRENT APPLICATION NUMBER: US/08/686, 968C
NUMBER OF SEQ ID NOS: 231
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 226
LENGTH: 1721
TYPE: DNA
ORGANISM: Swinepox virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1707)
US-08-686-968C-226

Query Match 40.6%; Score 461.2; DB 3; Length 1721;
Best Local Similarity 70.5%; Pred. No. 3.7e-122;
Matches 616; Conservative 0; Mismatches 258; Indels 0; Gaps 0;

QY 226 GATCCGGGATCATGAAAACAGAAAGACACTTGAACTGTGAAACCAATGCCAACT 285
DB 844 GATCTGCTGATTTATCTTTTCAATGATACACAGTCCAGATTTGAATGACATTTGCAACA 903
QY 286 CTTTGGGAGCAATAATACAACTTACCTTTTCAATGTCACCCACTGACATAGT 345
DB 904 CCCAAGGCTGATATAAACCAGCCCTTCATTTAGAAATATCATCCAGTCAATTTGA 963
QY 346 GATGCCCCAATATGTAATTCGGAAGATGGTCTTACCAACGACTAAGAAATGTT 405
DB 964 GATGCCCCAATATGTAATTCGGAAGATGGTCTTACCAACGACTAAGAAATGTT 1023
QY 406 CCCAGATTTGAATCAAGAGATGTTTGGGCAATAGCTGGTTTATAGAGAGATGG 465
DB 1024 CCGTCTATTCATCTTAAGAGCTGTTTGGAGCAATGCTGCTTTATGAGGGGGATGG 1083
QY 466 CAAGAAATGTTGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATG 525
DB 1084 ACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1143
QY 526 GCAGCAGCAAAAGATCCACTCAAAAGCATTTGATGATGATGATGATGATGATGATG 585
DB 1144 GCAGCAGCAAAAGATCCACTCAAAAGCATTTGATGATGATGATGATGATGATGATG 1203
QY 586 GTGATGAAAAGATTAACACCAATTTGATGATGATGATGATGATGATGATGATGATG 645
DB 1204 GTTATGAAAAGATTAACACCAATTTGATGATGATGATGATGATGATGATGATGATG 1263

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QY 646 AAAAGACTGGAGACTTGAACAAAGATGAGAGCGGTTTCTAGATGTGACATAC 705
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1264 AAAAGATAGAGATTTAAACAAAAGCTGATGATGTTTCTGATGTTTGACATAC 1323
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 706 AATGCTGAGCTTTTATTTCTGATGAGAAATGAGAGACACTTCACTTCAATTCAT 765
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1324 AATGCCGAAGCTTTGTTTCTATGAGAAATGAGAAAGCTTGGATATATCAGATTCAT 1383
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 766 GTCAAGATCTGTATAGTAAGTCAGATTCAGCTGAGAGACACGTCAGAAAGCTAGGA 825
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1384 GTCAAGAACTATATAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1443
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 826 AATGATGTTTGAATTTTATCAAAATGTGATGATGATGATGATGATGATGATGATG 885
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1444 AATGCGCTGCTTGAATTTTACCAAAATGTGATGATGATGATGATGATGATGATGATG 1503
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 886 GGGACATGATGATTTATCCCAAGATGAGAGAGCTTAACCTAAATGAGAAATGAAATCMA 945
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1504 GGGACTATGATTTACCAAAATGATGATGATGATGATGATGATGATGATGATGATG 1563
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 946 GGGGTAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1005
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1564 GGGGTAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1623
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1006 GGTCTATGCTACATGCAATCATGATGAGCTGGATCTCTTCTGGGAGTGTCCCAAGGG 1065
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1624 AGTTCAATGCTACTGTAGTCTCTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1683
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1066 TCTCTGAGAGTGCAGATCTGTCATATGATGATGATGATGATGATGATGATGATG 1099
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1684 TCTTTACAGTGCAGATATGATATTTAAATTAGG 1717
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 11
US-08-453-848-8
; Sequence 8, Application US/08453848
; Patent No. 5858368
; GENERAL INFORMATION:
; APPLICANT: Smith, Gale Eugene
; APPLICANT: Volnovitz, Franklin
; APPLICANT: Wilkinson, Bithanie Eident
; APPLICANT: Voznesensky, Andrei I.
; APPLICANT: Hackett, Craig Stanway
; TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA
; TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; City: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA
; APPLICATION NUMBER: US/08/453,848
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/120,607
; FILING DATE: 13-SEPT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 1,284
; REFERENCE/DOCKET NUMBER: MGS101CIP
; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ. ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1766 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Influenza virus
; INDIVIDUAL ISOLATE: A/Texas/36/91 rHA
; FEATURE:
; NAME/KEY: polyhedrin mRNA leader (partial)
; LOCATION: 1 to 18
; FEATURE:
; NAME/KEY: coding region for AcNPV 61k protein signal
; NAME/KEY: peptide
; LOCATION: 19 to 72
; FEATURE:
; NAME/KEY: SmaI restriction site
; LOCATION: 76 to 81
; FEATURE:
; NAME/KEY: KpnI restriction site
; LOCATION: 82 to 87
; FEATURE:
; NAME/KEY: SmaI restriction site
; LOCATION: 88 to 93
; FEATURE:
; NAME/KEY: coding region for mature rHA
; LOCATION: 73 to 1734
; FEATURE:
; NAME/KEY: KpnI restriction site
; LOCATION: 1744 to 1749
; FEATURE:
; NAME/KEY: BglII restriction site
; LOCATION: 1750 to 1755
; FEATURE:
; NAME/KEY: universal translation termination signal
; LOCATION: 1756 to 1766
; US-08-453-848-8

Query Match 39.7%; Score 451; DB 2; Length 1766;
Best Local Similarity 70.0%; Pred. No. 3,1e-119;
Matches 607; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

QY 226 GGATCGGGATCATGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 285
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 877 GGTCAGAGATCATGCACTCAAAAGCATCATGATGATGATGATGATGATGATGATGATG 936
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 286 CCTTTGGAGACATTAATACACATTAACCTTTTCAAGATGTCACCCACTGACAAATAGCT 345
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 937 CCCAGGAGAGCTATAACAGTAGTCTTCTTCCAGAAATGTACACCCAGTCAACATAGGA 996
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 346 GAGTGGCCCAATATGTAAATGCGAGAGAGTGTCTTACCAACAGAGAGATGATGATGAT 405
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 997 GAGTGTCCAAAGATATGAGAGAGATGACAAATTAAGATGATGATGATGATGATGATG 1056
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 406 CCCGATTTGAATCAGAGAGATGTTTGGGCAATGATGTTTATAGAGAGAGAGATG 465
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1057 CCATCCATTCATCCAGAGAGTGTGTTTGGAGCCATTCGCGTTTCATTAAGAGAGAGATG 1116
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 466 CAAGATGTTGACGTTGTTATGATGATGATGATGATGATGATGATGATGATGATGATG 525
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1117 ACTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1176
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 526 GCAGCAGAAAGAAATCCATCAAAAGCATTTGATGATGATGATGATGATGATGATGATG 585
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1177 GCTGCGGACCAAAAAGACACACAAATGCCATTAAGGAGATGATGATGATGATGATGATG 1236
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 586 GTGATGAAAGATATAACACCCATTTGAAGCTGTTGGAAGAGAAATTCGTAACCTTAGAG 645
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db	1237	GTATCGAAGAAATGAAACATCTCANTTCACTACTGTGGCCAAAGATTAAACAATTAGAA	1236
OY	646	AAAAGACTGGAGAACTTGGAACAAAAAGATGGAAGACGGGTTTCTAGATGTGGACATAC	705
Db	1297	AGAAAGATGAGAAAACCTTAATATAAAAAAGCTTGATGATGGATTCTGGACATTGGACATAT	1356
OY	706	AATCGTGAAGCTTTAGTCTGTGATGGAATATGAGAGACACTGACTTTCATGATTTCTAT	765
Db	1357	AATCGAATATGTTGGTGTCTACTGGAAAAATGGAAGACCTTTGGATTTCATGACTCAAT	1416
OY	766	GTCAGAAATCTGTATAGTAAAGTCAGATGACGTGAGACAGACAAGTCGAAGAATAGGA	825
Db	1417	GTCGAAGATCTGTATGAGAAAAGTAAAAAGCCAAATTGAAGATTAATGCCAAAAGAAATAGG	1476
OY	826	AATGAGATGTTTGAATTTTATCACAAATGATGATGATGATGCATGAATAGTGTGAAAAAC	885
Db	1477	AACGGGTGTTTGAATTTCTATCACAAAGTAAACATGAATGCATGAAAGTGAATAAT	1536
OY	886	GGGACATATGATTTATCCCAAGTATGAGAAAGAGTCTAACTAAATAGAAATCAATCAA	945
Db	1537	GGAACTTATGACTATCCAAATATATCCGAACAAATCAAAGTTTAAACAGGGGAAATATGAT	1596
OY	946	GGGGTAAATATGACAGCAGCATGGGGTTTATCAAAATCCCTGGCATTTTATGTACAGTGA	1005
Db	1597	GGAGTGAATTTGGAATCAATGGAGCTATATAGATTCTGGGCACTTACTCAACTGTGCC	1656
OY	1006	GGTTCTATGTCATGGCAATCATGATGAGCGTGGGATCTCTTTCTG6G6TGCCTCCACGGG	1065
Db	1657	AGTTACACGTGGCTTTGGTCTCCCTGGGGGSCATACGCTTCTGGATGTGTTAATGGG	1716
OY	1066	TCTCTGACGTGACGATCTCGATATNGA	1092
Db	1717	TCCTTGCAGTCCAGAAATATGAAATCGA	1743

RESULT 12
US-09-169-027-8

; Sequence 8, Application US/09169027
; Patent No. 6245532

; GENERAL INFORMATION:

APPLICANT: Smith, Gale Eugene
APPLICANT: Volynovitz, Franklin
APPLICANT: Wilkinson, Betshale Eident
APPLICANT: Voznesensky, Andrei I.
APPLICANT: Hackett, Craig Stanway
TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA
TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES
NUMBER OF SEQUENCES: 31

CLASSIFICATI

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/453,848

FILING DATE: 30-MAY-1995
APPLICATION NUMBER: 08/1

FILING DATE: 13-SEPT-1993

ATTORNEY/AGENT INFORMATION:

```
; . NAME: Pabst, Patrea L.
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1 REGISTRATION NUMBER: 31,284
2 REFERENCE/DOCKET NUMBER: MG510C1P
3 TELECOMMUNICATION INFORMATION:
4 TELEPHONE: (404)-873-8794
5 TELEFAX: (404)-873-8795
6 INFORMATION FOR SEQ ID NO: 8:
7 SEQUENCE CHARACTERISTICS:
8   LENGTH: 1766 base pairs
9   TYPE: nucleic acid
10  STRANDEDNESS: single
11  TOPOLOGY: linear
12  MOLECULE TYPE: DNA (genomic)
13  HYPOTHETICAL: NO
14  ANTI-SENSE: NO
15  ORIGINAL SOURCE:
16  ORGANISM: Influenza virus
17  INDIVIDUAL ISOLATE: A/Texas/36/91 rHA
18  FEATURE:
19    NAME/KEY: polyhedrin mRNA leader (partial)
20    LOCATION: 1 to 18
21  FEATURE:
22    NAME/KEY: coding region for AcNPV 61K protein signal
23    NAME/KEY: peptide
24    LOCATION: 19 to 72
25  FEATURE:
26    NAME/KEY: SmaI restriction site
27    LOCATION: 76 to 81
28  FEATURE:
29    NAME/KEY: KpnI restriction site
30    LOCATION: 82 to 87
31  FEATURE:
32    NAME/KEY: SmaI restriction site
33    LOCATION: 88 to 93
34  FEATURE:
35    NAME/KEY: coding region for mature rHA
36    LOCATION: 73 to 1734
37  FEATURE:
38    NAME/KEY: KpnI restriction site
39    LOCATION: 1744 to 1749
40  FEATURE:
41    NAME/KEY: BglII restriction site
42    LOCATION: 1750 to 1755
43  FEATURE:
44    NAME/KEY: universal translation termination signal
45    LOCATION: 1756 to 1766
46 US-09-169-027-8

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Query Match

Best Local Similarity /0.0%; Pred No. 3,1e-119;
Matches 607; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

Oy	226	GGATCCGGGATCATGAAACACAGAGAACCTGTGAGACGTCGAGACCAATGCCAACT	285
Db	877	GGGTCAGGATCTCTACCTCAACGCCATCAATGATTAATGACGGGAAGTGTCAACAA	936
Oy	286	CCCTTGGGAGACATAAATACACATTAACCTTTTACATATGCCACCACGACCAATAGCT	345
Db	937	CCCCAGGAGCTATAACACGATGCTTCTCTCCAGATGTACACCCAGTCACAAATAGSA	996
Oy	346	GAGTCCCCCAATATGTAAATCGAGAGTGTCTTTAGCAACAGAGCTAAAGATGTT	405
Db	997	GAGTGTCCAAAGATGTCTAGAGAGTACAAAATTAAGATGTTTACAGAGCTAAAGAACTC	1056
Oy	406	CCCCAGATGGATCAAGAGAGATGTTTGGGCACTACCTGGTTTTATAGAGAGAGATG	465
Db	1057	CCATCCATTTCAATCCAGAGGTTTGTTTGGAGCCATTCCGGTTTTCAATGAAGGGGGGGTG	1118
Oy	466	CAAGGATGGTTGAGCGTTGGTATGCGATACCATACAGCAATATCCAGAGGATCAGGGAT	525
Db	1117	ACTGGAATGATAGATGGATGGATGTATCATCATGATATACACAGAGATCTGGCTAT	1176
Oy	526	GCAGCGACACAAGGATCCACTCAAAAGGCATTTGATGGATCCCAACAGTAAATCTT	585

Db 1177 GCTGCGGACCAAAAAGCACCACAAAATGCCATTACGGGATATCAAAACAGTGAAATCT 1236
QY 586 GTGATTTGAAAAGATTAACACCAATTTGAAGCTGTGGGAAAGATTTGGTAATCTAGAG 645
Db 1237 GTATGAGAAAATGAAACACTCAATTCACAGCTGTGGGCAAAAGATTTCAAGAAATAGAA 1296
QY 646 AAAAGACTGGAGAACTTGAACAAAAGATGGAAGAGGGGTCTAGATGTGTGACATAC 705
Db 1297 AGAAGATGGAACCTTAATAAATAAGTATGATGATGATTTGTGGCATTGTGACATAT 1356
QY 706 AATGCTGAGCTTTAATTTCTGATGAAATGAGAGCACTTGACTTTCAATTTCTAAT 765
Db 1357 AATGCAAGAAATTTGTTTCTTACTAGAAAATGGAAGCACTTTGGATTTTCAATGACTCAAT 1416
QY 766 GTCAAGATCTGTATAGTAAGTCAGATGACAGTCAAGCAAGCAAGCAAGCAAGCA 825
Db 1417 GTCAAGATCTGTATAGTAAGTCAGATGAAAGCAATTTGAAGATATGCAAGCAAGCAAG 1476
QY 826 AATGATGTTTGAATTTATCAAAATGTATGATGAATGATGATGATGATGATGATGATG 885
Db 1477 AAGGGGTTTGAATTTATCAAAATGTATGATGAATGATGATGATGATGATGATGATG 1536
QY 886 GGCATATGATGATTTCCAAATGTGAAGAGAGCTTAACATAATGAAATGAAATCAAA 945
Db 1537 GGCATATGATGATTTCCAAATGTGAAGAGAGCTTAACATAATGAAATGAAATCAAA 1596
QY 946 GGCATATGATGATTTCCAAATGTGAAGAGAGCTTAACATAATGATGATGATGATGATG 1005
Db 1597 GGCATATGATGATTTCCAAATGTGAAGAGAGCTTAACATAATGATGATGATGATGATG 1656
QY 1006 GGTATGATGATGATTTCCAAATGTGAAGAGAGCTTAACATAATGATGATGATGATGATG 1065
Db 1657 AGTTCACTGATGCTTTTGTCTCCCTGGGGGCAATGATGATGATGATGATGATGATG 1716
QY 1066 TCTCTGCAAGCAGAGTTCTGCAATATGA 1092
Db 1717 TCTTTGCAAGCAGAGTTCTGCAATATGA 1743

RESULT 13

US-09-197-679A-1
Sequence 1, Application US/9197679A
Patent No. 6287570

GENERAL INFORMATION:

APPLICANT: Foley, Patricia L.
TITLE OF INVENTION: Vaccine Against Swine Influenza
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Hendricks and Associates
STREET: P.O. Box 2509
CITY: Fairfax
STATE: Virginia
COUNTRY: USA
ZIP: 22031

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/197,679A
FILING DATE: 23-Nov-6287570-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hendricks, Glenna
REFERENCE/DOCKET NUMBER: foley
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 425-8405
TELEFAX: (703) 425-8406
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1724 base pairs
TYPE: nucleic acid

STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-197-679A-1

Query Match 39.5%; Score 448.6; DB 3; Length 1724;
Best Local Similarity 70.3%; Pred. No. 1.3e-118;
Matches 615; Conservative 0; Mismatches 259; Indels 1; Gaps 1;

QY 226 GATCCGGGATCATGAAACAGAGGACACTTGGAGACCTGTGAGACCAATGCCAACT 285
Db 835 GATCTGTGATTTATTCATTTTCAATTCAGATACACGCTCAGATTTGTATATGACCTGTCAACA 894
QY 286 CCTTTGGAGACATTAATACACATTAACCTTTTCAAGATGCAACCCACTGACAAATAGT 345
Db 895 CCCAAAGGTCTATTAACACACACCTCCCTTCAGAAATATCATCCAGATTCACACAAATGGA 954
QY 346 GAGTCCCCCAATATGTAATGCGAGAGATGTGCTTACACAGAGACTAAGGAATGTT 405
Db 955 GAATGTCCAAAATATGTCACAAAGATGAGAAATGCAATGCTACAGAGATTAAAGGAATTC 1014
QY 406 CCCCAAGATTGATCAAGAGATTTGGGGCAATAGCTGTTTATAGAAAGAGATGG 465
Db 1015 CCGTCTATTCAATCTAGAGGCGCTTTTGGAGCCATTGCTGCTTTATGAGGGGGGTGG 1074
QY 466 CAAGATGTTGACGGTGTGATGATATACATCAGACGAATGACAGGATCAGGGAT 525
Db 1075 ACAGAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1134
QY 526 GCAGCAGCAAAATCCATCAAAAGCATTTGATGATGATGATGATGATGATGATGATGATG 585
Db 1135 GCAGCAGCAGCAAAATCCATCAAAAGCATTTGATGATGATGATGATGATGATGATGATG 1194
QY 586 GTGATTTGAAAAGATTAACACCAATTTGAAGCTGTTGGGAAAGATTTGGTAATCTAGAG 645
Db 1195 GTTATTTGAAAAGATTAACACCAATTTGAAGCTGTTGGGAAAGATTTGGTAATCTAGAG 1254
QY 646 AAAAGACTGGAGACTTGAACAAAAGATGGAAGAGCGGTTCTAGATGTGTGACATAC 705
Db 1255 AAAAGACTGGAGACTTGAACAAAAGATGGAAGAGCGGTTCTAGATGTGTGACATAC 1314
QY 706 AATGCTGAGCTTTTACTTCGATGAAAGATGAGAGACCTTACATGATGATGATGATG 765
Db 1315 AATGCTGAGCTTTTACTTCGATGAAAGATGAGAGACCTTACATGATGATGATGATGATG 1374
QY 766 GTCAAGAAATCTGTATAGTAAGTCAGAAATGACAGTGAAGACGTCAAAGAACTAGGA 825
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QY 826 AATGATGTTTGAATTTATCAAAATGTGATGATGATGATGATGATGATGATGATGATG 885
Db 1435 AATGATGTTTGAATTTATCAAAATGTGATGATGATGATGATGATGATGATGATGATG 1494
QY 886 GGCATATGATGATTTCCAAATGTGAAGAGAGCTTAACATAATGAAATGAAATCAAA 945
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QY 946 GCGGTAAATTTGAGCAGCATGGGGTTTATCAATCTTGGCCATTTATGCTTACAGTACGA 1005
Db 1555 GCGGTAAATTTGAGCAGCATGGGGTTTATCAATCTTGGCCATTTATGCTTACAGTACGA 1614
QY 1006 GGTCTATGTCAC-TGGCAATCATGATGGCTGGGATCTCTTCTGSGGTGCTCAACGG 1064
Db 1615 AGTTCAATTTGATCTTGTAGTCCCTGGAGCAATCACTTTCTGATGATGCTCAATGG 1674
QY 1065 GTCCTGAGTGCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1099
Db 1675 GTCCTTACAGTGCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1709

RESULT 14
US-08-229-781-27
Sequence 27, Application US/08229781
Patent No. 5589174
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,781
FILING DATE: April 19, 1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1754 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: A/Sultia/1/89
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:

PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-229-781-27

Query Match 39.5%; Score 447.8; DB 1; Length 1754;
Best local Similarity 69.8%; Pred No. 2.6e-118;
Matches 605; Conservative 0; Mismatches 262; Indels 0; Gaps 0;

QY	226	GGATCCGGGATCATGAAAAAGAGAACACTTGAAGCTGTGACCAATGCCAACT	285
DB	855	GGGTGAGAAATCATCACTCAACGATCAATGATGATGACGCAATGTCAACA	914
QY	286	CCCTTGGGAGCAATAATCAATCTTTTCACAAATGTCACCCACTACATATGT	345
DB	915	CCCCAGGAGCTATAACAGTGTCTCTCCCAAGATGACACCCAGTCACATAGGA	974
QY	346	GAGTGCCCCCAATATGTAATAATCGGAGAAAGTGGCTTAGACACAGCACTAAGGAT	405
DB	975	GAGTGCCAAAGTATGTCTCAGAGGTACAAAATTAGAGATGTTACAGACTAGGACATC	1034
QY	406	CCCCAGATTGAATCAAGAGATTTGTTGGGCAATAGCTGTTTATAGAGAGAGATG	465
DB	1035	CCATCCATTCAATCCAGAGGTTTGTGGAGCAATTCGCGGTTTCATTGAAGGGGGTGC	1094
QY	466	CAGGAATGTTGAGGTTGGTATGATACATCAACCAATGACAGGATCAGGAT	525
DB	1095	ACTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1154
QY	526	GCAGCAGACAAAGATCCACTCAAAAGCATTGATGATGATGATGATGATGATGAT	585
DB	1155	GCTGGGATCAAAAAAGCACCAAAATGCCATTAAAGCAATTAACCAAGCTAATCT	1214
QY	586	GTGATTGAAAGATTAACACCAATTTGAGCTGTTGGAAAGATTCGTAACCTAGAG	645
DB	1215	GTAAATCGAAGAAATGAAACCTCAATTCACAGCTGTTGGCAAAAGATTCAACAAAT	1274
QY	646	AAAGACTGGAGAACTTGAACAAAGATGGAAGCGGTTCTAGATGTGACATAC	705
DB	1275	AGAAAGATGGAATTAATTAATAAAGTTGATGATGATGATGATGATGATGATGAT	1334
QY	706	AATCTGAGCTTTAGTCTGATGGAATGAGAGACACTTGCATTGATGATTAAT	765
DB	1335	AATGAGAAATTTGTTGTTCTACTGAAATGAAAGACTTTGGATTTCATGACTCAAT	1394
QY	766	GTCAAGAAATCTGTATATGTAAGTCAAGTGCAGCTGAGAGACAACGTCAAGAACTAGGA	825
DB	1395	GTGAAGAAATCTGTATGAGAAAGTAAAGCCAAATTAAGAAATTAAGCCAAAGAAATAGGA	1454
QY	826	AATGATGTTTGAATTTTATCACAATGTGATGATGATGATGATGATGATGATGATGAT	885
DB	1455	TACGGGTGTTTGAATTTTATCACAATGTGATGATGATGATGATGATGATGATGATGAT	1514
QY	886	GGGACATATGATTTATCCCAAGATGAAAGAGCTTAACATTAATTAAGAAATGAAT	945
DB	1515	GGAATTTATGATTTATCCCAAGATGAAAGAGCTTAACATTAATTAAGAAATGAAT	1574
QY	946	GGGTAATAATGAGCAGCATGGGGTTTATCAAAATCCCTTGCCATTTATGCTAGAGTA	1005
DB	1575	GGAGTGAATAATGAGCAGCATGGGGTTTATCAAAATCCCTTGCCATTTATGCTAGAGTA	1634
QY	1006	GGTTTATGTCACATGCAATATGATGATGATGATGATGATGATGATGATGATGATGAT	1065
DB	1635	AGTTCACTGCTGCTTTGCTCCCTGGGGCAATGAGCTTCTGAGATGCTCTAATGGG	1694
QY	1066	TCTCTGAGTGCAGGATCTGCATATGA	1092
DB	1695	TCTTTCAGTGTAGATATGATCTGA	1721

RESULT 15
US-08-630-918-27
Sequence 27, Application US/08630918
Patent No. 5631350
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKINO et al.
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,918
FILING DATE: April 5, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Mairen M. Cheek, Jr.
REGISTRATION NUMBER: 38,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1754 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
ORIGINAL SOURCE:
ORGANISM: A/Suita/1/89
US-08-630-918-27

Query Match 39.5%; Score 447.8; DB 1; Length 1754;
Best Local Similarity 69.8%; Pred. No. 2.6e-118;
Matches 605; Conservative 0; Mismatches 262; Indels 0; Gaps 0;

QY 226 GGATCGCGGATCATGAAGACAGAGAACACTTGAGAACCAATGCCAAACT 285
DB 855 GGGTCAGAGATCATCATCAACCAACATGATGATGATGACGCGAAGTGTCAACA 914
QY 286 CCTTTGGAGCATATAATACATTTACTTTTCCATGTCACCCACTGCATAGGT 345
DB 915 CCCAGGGGAGCTATAACAGTAGTCTTCTTCCAGAAATGTACACCCAGTCACAAATAGA 974
QY 346 GAGTCCCCCAATATATGAATCGAGAGAGTTGCTTACCAACAGAGACTAAGATGTT 405
DB 975 GAGTGTCCAAATATGTCAGAGATCAAAATTAAGATGTTACAGAGACTAAGAGATATC 1034
QY 406 CCCAGATTGAATCAATAGATTTGTTGGGCAATAGCTGTTTATAGAGAGAGATG 465
DB 1035 CCATCCATTCATCAATAGATTTGTTGGAGCCATTCGCGGTTTCATTGAAGGGGGTGG 1094
QY 466 CAAGGAATGCTGAGGTTTGGATGATACCATCAGAGAAATGACAGGATCAGGATAT 525
DB 1095 ACTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1154

QY 526 GCACAGACAAAGATTCACACTCAAAAGCACTTGTGATGATATCCAAACAGTAATTC 585
DB 1155 GCTGCGGATCAAAAAGACACACAAAATGCCATTAAAGGAATTTCAACAAAGGATTC 1214
QY 586 GTGATTGAAGAAGATAAACAACCCAAATTTGAAGCTGTTGGGAAGAATTCGTTACTAGAG 645
DB 1215 GTATCGAGAAAATGAACTCAATTCACAGCTGTGGGCAAAAGATTCACAAATTTAGAA 1274
QY 646 AAAAGCTGGAACACTTGAACAAAAGATGAGAGACGGGTTTCTAATGTGTGACATAC 705
DB 1275 AGAAGATGGAATATCTTAATATAAAGTTGATGATGATTTCTGACATTTGGACATAT 1334
QY 706 AATGCTGACTTTTACTTCTGATGAAATAGAGAGACACTTTCATGATTTCTAAT 765
DB 1335 AATGCAGAATTTGTTGTTTCTACTGAAATGAAGACATTTTGAATTTTCTATGCTAAAT 1394
QY 766 GTCAAGAAATCTGTATAGTAAGTACAGATGACAGCTGAGAGACACGTCAAAAGACTAGGA 825
DB 1395 GTCAAGAAATCTGTATAGTAAGTACAGATGACAGCTGAGAGACACGTCAAAAGACTAGGA 1454
QY 826 AATGATGTTTGAATTTTATCAAAATGATGATGATGATGATGATGATGATGATGATGATGAT 885
DB 1455 TACGGGTGTTTGAATTTTCAACCAAGTAAACAAATGAATGCAATGGAAGTGAATAAAT 1514
QY 886 GGCACATATGATTTATCCCAAGTATGAAGAAGTCTAACTAAATGAATGAATCAAA 945
DB 1515 GGAATCTTATGATCTATCCAAATATTTCCGAGAAATCAAAAGTTAAACAGGAAAAATTTGAT 1574
QY 946 GGGGTAAATTTGAGCAGATGGGGGTTTATCAAAATCTTGCCATTTATGCTACAGTAGCA 1005
DB 1575 GGAGTGAATTTGGAATTCATCAATGAGGAGTCTATCAGATTTGCGCATCTACCACTGTCGCC 1634
QY 1006 GGTCTATGTCTACTGCAATCATGATGCTGGATCTTTCTTGGGTGCTGCTCAACGGG 1065
DB 1635 AGTTCACTGTGCTTTTGTGCTCCCTCGGGGGAATCAGCTTGATGATGCTTCTAATGGG 1694
QY 1066 TCTCTCAGTCGAGATGTCATATGA 1092
DB 1695 TCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1721

Search completed: August 10, 2003, 16:15:38
Job time : 59.7644 secs

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BenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 19:11:43 ; Search time 1741.95 seconds
(without alignments)
15836.045 Million cell updates/sec

Title: US-09-918-568-49

Perfect score: 1135
Sequence: 1 CTAGCAAGAGCGGGTTAT.....AACACCCCTGTTCTGCTAG 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:
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2: em_esthum:*
3: em_estlin:*
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5: em_estov:*
6: em_estp1:*
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9: gb_est1:*
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14: gb_est5:*
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17: em_gss_hum:*
18: em_gss_lin:*
19: em_gss_pln:*
20: em_gss_vri:*
21: em_gss_fun:*
22: em_gss_man:*
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25: em_gss_rok:*
26: em_gss_phg:*
27: em_gss_vri:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	62.2	5.5	1101	29	CNS00396	AL063821 Drosophila
3	55	4.8	639	29	CNS0170D	AL108367 Drosophila
4	54.2	4.8	994	18	BX414650	BX414650 BX414650

5	52.8	4.7	1101	29	CNS0006J	AL062049 Drosophila
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7	52.2	4.6	1167	13	BX463903	BX463903 BX463903
8	51.8	4.6	847	29	CNS023EX	AL200130 Tetradon
9	50.2	4.4	1101	29	CNS0182P	AL108811 Drosophila
10	49.6	4.4	468	29	CNS06XGD	AL141969 t7 end of
11	49.4	4.4	918	29	CNS006MW	AL065768 Drosophila
12	48.8	4.3	1201	13	BX406178	BX406178 BX406178
13	48.6	4.3	938	29	CNS006TJ	AL065906 Drosophila
14	48.4	4.3	1201	13	BX461128	BX461128 BX461128
15	47.8	4.2	300	9	A0087765	A0087765 A0087765
16	47.6	4.2	1200	29	CNS016CO	AL106578 Drosophila
17	47.4	4.2	1101	29	CNS0106X	AL098595 Drosophila
18	47	4.1	1101	29	CNS000D1	AL065414 Drosophila
19	46.8	4.1	1200	13	BX414560	BX414560 BX414560
20	46.2	4.1	1106	13	BX438107	BX438107 BX438107
21	46	4.1	1001	13	BX329654	BX329654 BX329654
22	46	4.1	1101	29	CNS008E1	AL069797 Drosophila
23	46	4.1	1201	9	AL536104	AL536104 AL536104
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25	45.8	4.0	1101	29	CNS016HF	AL106749 Drosophila
26	45.8	4.0	1101	29	CNS017FX	AL108171 Drosophila
27	45.6	4.0	516	28	A0879779	A0879779 HS_4821_A
28	45.2	4.0	781	29	AG171177	AG171177 Pan trogl
29	45.2	4.0	932	9	AL514901	AL514901 AL514901
30	45.2	4.0	941	28	AZ682404	AZ682404 ENT1016TF
31	45.2	4.0	1044	13	BX415231	BX415231 BX415231
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33	44.6	3.9	963	29	CNS006X1	AL066049 Drosophila
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35	44.6	3.9	1001	29	CNS01400	AL103554 Drosophila
36	44.4	3.9	930	29	CNS01644	AL106270 Drosophila
37	44.4	3.9	1100	29	CC206010	CC206010 CH261-159
38	44.2	3.9	1101	29	CNS0039W	AL063937 Drosophila
39	44	3.9	630	14	CB271310	CB271310 taa2ic05
40	44	3.9	644	14	CD567533	CD567533 lab78g10
41	44	3.9	917	28	BH166948	BH166948 ENT5758TF
42	44	3.9	1201	13	BX461310	BX461310 BX461310
43	43.8	3.9	467	13	B0497794	B0497794 PFE50a08
44	43.8	3.9	859	29	CNS00KLL	AL077728 Drosophila
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ALIGNMENTS

RESULT 1
LOCUS BX376097/c. 1201 bp mRNA linear EST 08-MAY-2003
DEFINITION BX376097 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DC022YM12 5-PRIME, mRNA sequence.

ACCESSION BX376097
VERSION BX376097
KEYWORDS BX376097.1 GI:30434756
SOURCE EST.
ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 1201)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE Li, W.-B., Gruber, C., Jesse, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished
Contact: Genoscope
Genoscope, Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2866.f
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0DC022B6060P1.
Location/Qualifiers
1. 1201

FEATURES
source

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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0DC0221M2"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/notes="1st strand cdna was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cdna was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT
ORIGIN
79 a      152 c      66 g      270 t      634 others

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Query Match	5.9%;	Score 67.2;	DB 13;	Length 1201;
Best Local Similarity	14.6%;	Pred. No. 0.00023;		
Matches 123;	Conservative 256;	Mismatches 464;	Indels 2;	Gaps 1

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Db 1010 MNNMNMNMMMNKMKNNNKMTNTTKTWMKKRTTYMMNMNMNMNVKRMKM 951

TABLE II.

[illegible]

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DB 890 GGGGMMWYGRGGVMMMGSTGKLTNGKNNNNMGKMMGMMNNTDMMKTTETKMMNMHTM 831

OY 290 TGGGAGCAATTAATCAACATTACTTTTCACAATGTCCACCCAGTACCAATAGTGATG 349

Db 830 TKGNGKTHMGKMMNNMVKKMTMMNVGAAAAAADAAGGGAIAAAAAAGAAAAAKAKAKAK 771

QY 350 GCCCAATATGTAAATCGGAGAAGTTGCTTACCAACAGGACTTAAGCAATGTTCGCC 409

Db 770 HMMNMGKTMGMIMMGTCGMMGKGTCHMTMTMKYMMMMMMMMMMGKKNMNMKGRKNMM 711

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      | :: :: : | | :: :: : | :: :: :
710 AMMKMKMTMTMTGMMMTMTMGCKKTYMTKBNBKMKKAGKKANANMKNNKNNANN 651
Db

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Dy
650 GAAAGCGTACCGGTTGGTAGGGAATCAACAGCAGTAATGCACGAGGATCAGGGTATGCG 529

Dd
650 NGKANNMKKKTKKRNMMKKNMKNNNNNNMKNMNMKMGKNNMGKAKANNMKM--KMNN 593

Qy 530 CAGCAAGAATCCACTCAAAAGGACTTTTCATGGAATCACCACACAGGTAAATTCTGTGA 589
Db 552 NKMMNNNNMKKKKKNNMKNNMKKKNNNNNNKKKKMMNNNNNNMKKKKKNNNNNAGK 533

OY 590 TTGAAAGATTAACACCCCAATTGTGAAGCTGGCGAAGAGATTGCGTAACTTAGAGAAA 649
::
DB 532 KKKKMMNN 473
:: ::

650 GACTGAGAACTTGCACAAAGATGGAAGCGGTTTCTAGATGTGTGCACATACATG 709

DD 4 12 .MMMMMNCNMMNANMMMAK NNAAMNAAAAAAGKGGKNNKRAAAAANAAANNAKKKAAANA 413

QY 710 CTGAGCTTTTGAATTCTGATGGAATAAGAGAGACACTTGACTTTCATGATCTTAATGTCA 769

Db 412 ACNNCCMNACMNNKAKKNNKKNNNNNNNNNNMMKANKNAKKAKECNCNANNNNKNAAKKA 353

Oy 770 AGAATCTGTATAGTAAGTCAGAAATGCAGCTGACAGACAACGTCAAAGAATACTAGGAATG 829

Dy . 830 GATGTTTGAATTATCACAACCTGGATGCATGCAATAGTGTTAAAAAACCAGA 889

Db 352 AKANNAANAANNAACANANNCKNNCCAKAAAANNNANCANNAAKKAANKNAAATA 293

292 CACGAGKAKNNKRAAAAKANANNNNNCANANANAKNNKACAKANAKAACTAANANCCAKA 233

QY 890 CAAATGATATATCCCAAGTATGAGCAAGCTAACTAAATAGAAATGAATCAAGGGC 949
 Db 232 ATTAAGCTATAAAGAACCCNCCACAAACACATTAAGAAATAGTGACAAACCAAAAAATATACAG 173

QY	950	TAAA	954
Db	172	CAGA	168

	RESULT 2	
CNS0039C/c	1101 bp	DNA linear GSS 03-JUN-1999
LOCUS		
DEFINITION		Drosophila melanogaster genome survey sequence TET3 end of BAC # . prophemia of heart disease.

ACCESSION	AL063921
VERSION	AL063921.1
KEYWORDS	GI:4941778
SOURCE	GSS.
ORGANISM	<i>Drosophila melanogaster</i> (fruit fly)

REFERENCE
AUTHORS
TITLE
Direct Submission
Genoscope.
1 (bases 1 to 1101)
Ephydroidea: Drosophilidae, Drosophila.
Muscomorpha; Diptera, Brachycera; Neoptera; Endopterygota; Muscomorpha; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
Direct Submission

COMMENT
 bp 191 91006 ENVI cedex - FRANKLE (E-mail: segreter@genome.cns.it
 - Web : www.genome.cns.it)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila

The mammoaster BAC library was prepared by Kazutoyo Osoegawa and Aaton Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPcJ-98 and was constructed by partial

PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.bufiled.edu/drosophila_bac.htm.

```

/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR08K10"

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Query Match	5.5%	Score 62.2;	DB 29;	Length 1101;
Best Local Similarity	15 ref;	Read No. 0	0020.	
BASE COUNT	201 a	64 c	131 g	202 t
ORIGIN				503 others

QY 420 AAGAGATGTTGGGCAATAGCTGTATTATACGAAGCATGCACAAAGATGGTGA 479
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
Db 1099 ARRGDDTWDRTRKDEMDWTkwmtwmkDRADDPRNAGDADRAMDGCGTMTATATMWWW 1040

Db 1039 WWWATWDTWMDKMMWATAAKTIDTAWTWMRTAMRADMAGRDAGACRDRDAATTDADGAG 980

OY 540 ATCCACTCAAAAGGCAATTTTGATGCAATCACCAACAAAGTAAATTCGTGATTTGAAAAAT 599

Dy 600 AACACCCCAATTGAAGCTGTGGGAAATTCGTAATTGAGAAAAAAGACTGGAGA 659
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 919 DDDGAGDKDDGGKADDDTDTGKTDDDKDKMDMDMKRAGTWDGATWMAAATDMMWGM 860

QY 660 CTTCGAACAAAAGATGCGAAGCAGCGCTTCTCATGTGTGGACATACAATGCTGAGCTTTT 719
.: ::::||||::: :::: :::::| |:::| :::: ::::| :||:

[illegible]

RESULT 5				
CNS0006J				
LOCUS	CNS0006J	1101 bp	DNA	linear
DEFINITION	Drosophila melanogaster genome survey sequence Tetr3 end of BAC #			
	BACR01M22 of Rpci-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.			
ACCESSION	AL062049			
VERSION	AL062049.1	GI:4938511		
KEYWORDS	GSS.			
SOURCE	Drosophila melanogaster (fruit fly)			
ORGANISM	Drosophila melanogaster			
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peiryocta;			
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
	Ephydroidea; Drosophilidae; Drosophila.			
REFERENCE	1 (bases 1 to 1101)			
AUTHORS	Genoscope.			
TITLE	Direct Submission			
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :			

COMMENT
 Web: www.genoscope.cns.fr/17
 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazuhiro Oseegawa and Aaron Mammosser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPc1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES	SOURCE	LOCATION/QUALIFIERS
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		/organism="Drosophila melanogaster"
		/mol_type="genomic DNA"
		/db_xref="taxon:7227"
		/clone="BACR01M22"
		/clone_lib="RPC1-98"
		/note="end : TET3"
BASE COUNT		333 a 162 c 148 g 177 t 281 others
ORIGIN		

Query Match	4.78	Score 52.8	DB 29	Length 1101
Best Local Similarity	25.78	Pred. No. 0.35		
Matches 151	Conservative 165	Mismatches 268	Indels 4	Gaps 2

OY 453 AGAAGGAGATGGCAAGGATGGTTGACGGTTGGATGGATACATCAGACAAATGACCA 512
 Db 496 RRAATGRRARATRRARAGTTTMTTGAIAAAAAAAAAAAATTTAAAGCAAAAAAAAAAAATA 555
 OY 513 GCGATCAGGCTATGACGACGACAAAGATCCACTCAAAAGCATTTTATGATGATCCAA 572
 Db 556 TKAATATTTTTRRRTRAGTATTTTDTAKAAAAAAAAAAAAATTTAGAAAAACAAAAA 615
 OY 573 CAAGTAAATTTCTGATTTGAAAAGATTAACACCCAAATTTGAAGCTTTGGGAAGATT 632
 Db 616 AARAAGTGTGTAAGCAAAAAAAAAAAAAAATATAAAKAKAAAAAGGAAAAAAAAATTA 675
 OY 633 CGGAATCTTGAGAAAGACATGCAACTGTGACAAAAAGTGGAAAGCGGTTCTTGA 692
 Db 676 AAKAAWTGTTATTAIAAAAAAAAAAAAAAARAGGAKRGGKRRGARARRGGGGAATTA 735
 OY 693 TGTGTGACATACAAATGCTGAGCTTTTAGTTCTGTGAAAATGACAGCACTTGACT 752
 Db 736 KTRKKKTKTKRRAAGRRARABAMGAAAAAARAADAATKTGTAKAAWRTAAWKD 795
 OY 753 TCATGATTTAATGTCACAGATCTGTATATGTAAGTCAGATGCACTGACGACACACT 812
 Db 796 WKATDAAKAAARERDWTATAKAKDKTKWGAANAATGAMGAAARGWRGKKGDTGRAR 855
 OY 813 CAAGAAGACAGAGAAGATGCTTTTGATATTTATCACAAATGATGATGATGAATGCATGA 872
 Db 856 ARAGAGGOWDKAMWMAAAWMAATTAATTAATTAADRRARAKMDRPAALAADRDND - KGRA 914
 OY 873 TAGTGTGAAAAACGGACATGATGATTAATCCCAAGTATGAAGAGAGCTAACTAAATG 932
 Db 915 GWTGTRRRARARTRKAARAKRGAAGAKAKARRAGAMMDGKKKWKMDAAMAAKAKGT 974
 OY 933 AAATGAATCAAGGGGTAAATTTGAGCAGCAGTGGGGGTTTATCAATCCTTGCCATTTA 992
 Db 975 GDMKKRARK --- AKTGMRKARADKDBRAAADDTFMRTKAMWMTDMWATATKDKDTDKA 1033
 OY 993 TGTCTACAGTACGAGGTTTATGTCTACCTGGCAATATATGATGCTGGGAT 1040
 Db 1032 KKKRAKTTTTRDRAKAKAKDDTATTAATAWMDADKKKADKANR 1079

RESULT 6	
CNS005TE/c	
LOCUS	997 bp
DEFINITION	DNA linear GSS 03-JUN-1999
	Drosophila melanogaster genome survey sequence Tc73 end of BAC #
	BACR12K22 of RPC1-98 library from Drosophila melanogaster (fruit
	fly), genomic survey sequence.
ACCESSION	AL060767
VERSION	AL060767.1
KEYWORDS	GI:4943573
SOURCE	GSS.
ORGANISM	Drosophila melanogaster (fruit fly)
	Drosophila melanogaster
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
	Ephyroidae; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 997)
TITLE	genoscope.
AUTHORS	Direct Submission
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage

COMMENT

determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP *Drosophila melanogaster* BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoosier in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's


```

ACCESSION AL419699
VERSION AL419699.1
KEYWORDS GSS.
SOURCE picchia farinosa
ORGANISM picchia farinosa

REFERENCE
AUTHORS Bolotin-Fukuhara, J., Bon, E., Brothier, P., Casarogola, S., de Montigny, J., Dujon, B., Durrien, P., Lepingle, A., Llorente, B., Malpertuy, A., Neugejlise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekala, F., Toffano-Moche, C., Wesolowski-Louvel, M., Winkler, P. and Weissenbach, J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 20584711
PUBMED 11152876
REFERENCE 2 (bases 1 to 468)
AUTHORS de Montigny, J., Stehner, C., Souciet, J., Tekala, F., Dujon, B., Winkler, P., Artiguenave, F. and Potier, S.
TITLE Genomic exploration of the hemiascomycetous yeasts: 15. Picchia sorbitophila
JOURNAL FEBS Lett. 487 (1), 87-90 (2000)
MEDLINE 20584725
PUBMED 11152890
REFERENCE 3 (bases 1 to 468)
AUTHORS Direct Submission
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: segref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
COMMENT This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Picchia angusta, Debaryomyces hansenii var. hansenii, Picchia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
FEATURES
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/clone_lib="XAXOAA"
/feature="end : 77"
misc_feature <13..>159
/note="similar to Saccharomyces cerevisiae ORF YLR127c [ APC2 ; component of the anaphase promoting complex ]"
/evidence="not experimental"
BASE COUNT 124 a 59 c 212 t 18 others
ORIGIN
Query Match 4.4%; Score 49.6; DB 29; Length 468;
Best Local Similarity 50.5%; Pred. No. 1.6;
Matches 104; Conservative 6; Mismatches 96; Indels 0; Gaps 0;

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Db 137 TGATACCTAATCARGAAAACTGMAAATTCAGACCATGATATCCAAAGTAAAG 78
Qy 915 AGAGTCTAAACTAATAGAAATGAA 940
Db 77 ATGATATGATACCAAGATATCAAA 52

RESULT 11
CNS0006MW
LOCUS 918 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC #
BAC14F09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL065768.1
VERSION GI:4944648
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 918)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Hammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm
FEATURES
source 1..918
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/mol_type="genomic DNA"
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/db_xref="taxon:14609"
/clone_lib="RPCI-98"
/clone_lib="RPCI-98"
/feature="end : 77"
BASE COUNT 251 a 169 c 125 g 130 t 243 others
ORIGIN
Query Match 4.4%; Score 49.4; DB 29; Length 918;
Best Local Similarity 21.3%; Pred. No. 2;
Matches 60; Conservative 114; Mismatches 108; Indels 0; Gaps 0;

```



```

Qy      930 TAGAATGAAATCAAGGGCTAAAAATTGAGCAGCATGGGGT 971
      :::| || |:::|:::|:::|:::|
Db      877. RDRGRAGAAAAAWKARAKDGRKAKKKAGCTDKDGCWGDKK 918

```

RESULT 12	1201 bp	mRNA	linear	EST 13-MAY-2003
LOCUS BX406178/c				
DEFINITION BX406178 Homo sapiens FETAL LIVER cDNA clone				
ACCESSION C50DM010YV1.1 3-PRIME, mRNA sequence.				
VERSION BX406178.1	GI:30639385			
KEYWORDS	EST.			
SOURCE Homo sapiens (human)				

REFERENCE	1 (bases 1 to 1201)
AUTHORS	Li, W. B., Gruber, C., Jesse, J. and Polayres, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	unpublished
COMMENT	Contact: Genoscope

COMMENT	FEATURES
<p>Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: secref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. Contact: Feng Liang Email: lliang@lifestech.com URL : http://fulllength.invitrogen.com Faraday Avenue Genoscope sequence ID : CS0AM010CC06NP1.</p>	<p>Location/Qualifiers</p>

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDDM0101N1"
/lisue_type="FETAL LIVER"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT      239 a      246 c      241 g      220 t      255 others
ORIGIN

```

	Query Match	4.3%	Score 48.8	DB 13	Length 1201
	Best Local Similarity	25.0%	Pred. No. 2.8		
	Matches	70	Conservative	100	Mismatches 110
					Indels 0
					Gaps 0
QY	637	AACTTAGAGAAAAGCTGGAGAACTTGACAAAAAGATGAAGACGGGTTCTTAGATGTC	696		
Db	1193	AAAAAAAAAAAAAAAAATWFMATATKTTTTTTTAMDATADAMRARNRNRNTATTTTDDTT	1134		
QY	697	TGCACATACAAATGCTGACCTTTTGGTTGGTATGGAATGAGAGACCTTGACCTTCAT	756		
Db	1133	TTTTRDBDDDDRRDTRDRTDNTFADNWDADARARARARARARATWDRTTAAWWRRTD	1074		
QY	757	GATTCATATGTCAGAAATCTGTATAGTAAGTCAGAAATGCAGCTGAGAGACAACGTCAA	816		
Db	1073	WDTWAKADTTTAAADRDATATRRDTRDDEDTARATADAMRWMBADMRWRTAAATWWRBARA	1014		
QY	817	GAACCTAGAGAAATGAGCTGTTTGATTTTATACAAATGTAGATGAGATGAATGATG	876		
Db	1013	TWMAAMARRAATBRADDTADRRRRKTKTTTDDDRDTRDADKADTPRAAGDCDRTTRRGV	954		
QY	877	GTGAAAAACGGACATATGATTAATCCCAAGATGACAGAG	916		
Db	953	AVDRTWMDMAAATTDTWBRKTDADADVRGGTAAADDAAD	914		

RESULT 13
CNS006TJ/c

LOCUS CNS00061J 938 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14J11 of RPCT-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL065906
VERSION AT065906.1 GI:4944874
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 938)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

COMMENT

JOURNAL
Submitted (02-JUN-1999) Genoscope - Centre National de Séquençage
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT
- Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org/TheBDGP/Drosophila_melanogaster_BAC_library was prepared by Kazuhiro Oosagawa and Aaron Mamosser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw^{sp}, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES	
source	Location/Qualifiers
1. 938	
	/organism="Drosophila melanogaster"
	/mol_type="genomic DNA"
	/db_xref="taxon:7227"
	/clone="BACR14J11"
	/clone_1lb="RPC1-98"
	/note="end : T7"
BASE COUNT	86 a 98 c 85 g 334 t 335 others
ORIGIN	

Query Match	4.38;	Score 48.6;	DB 29;	Length 938;
Best Local Similarity	22.68;	Pred. No. 2.9;	.	.
Matches 106;	Conservative 148;	Mismatches 211;	Indels 5;	Gaps 1.

OY		36	TAAATTCGAGGAATTGGTCTTAGCAACAGCACTAAGCAATGTTCGCCAGATGATCA	421
Db		925	DKAADKADAKDAGRAAADAMAAARBDKKDXKDADDAKKAADDDBDARAARAKKKKKKA	866
OY		422	GAGAGTTGTTTGGGGCAATAGCTGGTTTTATAGAAG-----GAGATGGCAGGAATGCT	476
Db		865	KKKRKAADKKKKKKKKAKDKMKWKKKADDAADAAKKAASAAAAAMDKKRWKADDDPKA	806
OY		477	TGACGGTTTGATGGATACCATCACAGCAATGACCAGGATCGGGTATGCAGCAGACA	536
Db		805	AAXDKXADKADKKKAKAKDKDKDKADADAADDKAKKKDADAADDAADAAAARAAADR	746
OY		537	AGAATCCACTCAAAAAGCATTGATGTAATCCACAAGGTAAATTCTGTGATTGAAA	596
Db		745	AABKAGDAAYKAAAKRKKAARAKAKDKDKKAMMAVADADADADCKADKWMAADDD	686
OY		597	GATTAACAACCCATTGTGAGCTGTGGGAAAAGATTGGTAACCTTGAGAACAAAAGCTGA	656
Db		685	KAARKRAAAMWMAADADDAKARTPADANAKAKAKOKKXAALAAADKKAAARARAGAKXD	626
OY		657	GAACTTGAACAAAAAGATGCAAGACGGSTTCTTAGATGTGTGCACATACAAATGCTGAGCT	716
Db		625	RKDAGTAATKAAAAAAAKKKAKKDDTTDTITWTWATAIDTKKTDDSWTKKDATATATRGAKT	566
OY		717	TTTAGTCTGATGAGAAATGAGAGACACTTGAACCTTCATGATCTTAATGTCAAGAACT	776

OY 923 AACTAATAGAAATGAATCA 943
| | | | | | | | | | | |
Db 376 ACATTAAGAGAAAAATATTTA 396

Search completed: August 10, 2003, 10:57:45
job time : 1743.95 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search,
using sw model

Run on: August 9, 2003, 18:20:24 ; Search time 182.31 Seconds
(without alignments)
12843.535 Million cell updates/sec

Title: US-09-918-568-49

Perfect score: 1135
Sequence: 1 CTAGCAAAAGCGGGCTAT.....AACACCTTCTTCTGCTAG 1135

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications - NA:*

- 1: /cgn2_6/p/odata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/p/odata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/p/odata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/p/odata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/p/odata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/p/odata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/p/odata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/p/odata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/p/odata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/p/odata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/p/odata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/p/odata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/p/odata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/p/odata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/p/odata/1/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/p/odata/1/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/p/odata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DE	ID	Description
1	1135	100.0	1135	5	US-09-918-568-49	Sequence 49, Appl
2	908.8	80.1	1783	5	US-09-918-568-46	Sequence 46, Appl
3	838	73.8	1728	5	US-09-918-568-28	Sequence 28, Appl
4	447.8	39.5	1754	9	US-09-918-568-27	Sequence 27, Appl
5	400	35.2	400	9	US-09-918-568-33	Sequence 33, Appl
6	397	35.0	409	9	US-09-918-568-34	Sequence 34, Appl
7	382.4	33.7	410	9	US-09-918-568-35	Sequence 35, Appl
8	379.6	33.4	394	9	US-09-918-568-36	Sequence 36, Appl
9	263	23.2	1777	9	US-09-918-568-54	Sequence 54, Appl
10	252.6	22.3	1110	9	US-09-918-568-57	Sequence 57, Appl
11	251.6	22.2	442	9	US-09-918-568-29	Sequence 29, Appl
12	241.8	21.3	429	9	US-09-918-568-32	Sequence 32, Appl
13	233.6	20.6	424	9	US-09-918-568-30	Sequence 30, Appl
14	233.6	20.6	424	9	US-09-918-568-31	Sequence 31, Appl
15	233.6	20.6	1711	13	US-10-099-619-1	Sequence 1, Appl
16	125.2	11.0	334	9	US-09-918-568-38	Sequence 38, Appl

17	123.6	10.9	329	9	US-09-918-568-39	Sequence 39, Appl
18	123.6	10.9	334	9	US-09-918-568-40	Sequence 40, Appl
19	121	10.7	329	9	US-09-918-568-37	Sequence 37, Appl
20	118.8	10.5	329	9	US-09-918-568-41	Sequence 41, Appl
21	44.4	3.9	1115	14	US-10-184-644-440	Sequence 440, App
22	44.4	3.9	1115	14	US-10-184-634-440	Sequence 99638, A
23	42.4	3.7	719	13	US-10-027-632-99638	Sequence 99639, A
24	42.4	3.7	719	13	US-10-027-632-99639	Sequence 126, App
25	41.8	3.7	3423	14	US-10-037-270-126	Sequence 41, Appl
26	41.8	3.7	3441	9	US-09-880-192-41	Sequence 126, App
27	41.8	3.7	3444	13	US-10-114-893-126	Sequence 126, App
28	41.6	3.7	475	11	US-09-918-995-23463	Sequence 23463, A
29	41.4	3.6	25574	11	US-09-764-891-8307	Sequence 8307, Ap
30	41.4	3.6	25576	11	US-09-764-891-8306	Sequence 8306, Ap
31	40.8	3.6	4239	10	US-09-070-927A-450	Sequence 450, App
32	40	3.5	471	11	US-09-918-995-22350	Sequence 22350, A
33	40	3.5	1777	13	US-10-042-417-51	Sequence 51, Appl
34	40	3.5	2843	11	US-09-822-846-421	Sequence 421, App
35	40	3.5	3058	14	US-10-106-698-468	Sequence 468, App
36	39.8	3.5	1257	9	US-09-877-065-2	Sequence 2, Appl
37	39.2	3.5	1955	8	US-08-781-986A-598	Sequence 598, App
38	39.2	3.5	2232	10	US-09-925-637-71	Sequence 71, Appl
39	39.2	3.5	2232	14	US-10-084-205-71	Sequence 71, Appl
40	39.2	3.5	2235	9	US-09-815-242-8697	Sequence 8697, Ap
41	38.8	3.4	678	13	US-10-027-632-212662	Sequence 212662,
42	38.6	3.4	2000	10	US-09-938-842A-3817	Sequence 3817, Ap
43	38	3.3	1214	13	US-10-027-632-30819	Sequence 30819, A
44	38	3.3	271990	14	US-10-195-144-87	Sequence 87, Appl
45	37.8	3.3	2000	10	US-09-938-842A-4130	Sequence 4130, Ap

ALIGNMENTS

RESULT 1
US-09-918-568-49
Sequence 49, Application US/09918568
Patent No. US2002005482A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Menderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-721-8200
 TELEFAX: 202-721-8250
 TELEX: <unknown>
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1135 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to genomic RNA
 HYPOTHEetical: <unknown>
 ANTI-SENSE: <unknown>
 FRAGMENT TYPE: <unknown>
 ORIGINAL SOURCE:
 ORGANISM: A/Okuda/57
 STRAIN: <unknown>
 INDIVIDUAL ISOLATE: <unknown>
 DEVELOPMENTAL STAGE: <unknown>
 HAPLOTYPE: <unknown>
 TISSUE TYPE: <unknown>
 CELL TYPE: <unknown>
 ORGANELLE: <unknown>
 IMMEDIATE SOURCE:
 LIBRARY: <unknown>
 CLONE: <unknown>
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: <unknown>
 MAP POSITION: <unknown>
 UNITS: <unknown>
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION:
 PUBLICATION INFORMATION:
 AUTHORS:
 TITLE:
 JOURNAL:
 VOLUME:
 ISSUE:
 PAGES:
 DATE:
 DOCUMENT NUMBER:
 FILING DATE:
 PUBLICATION DATE:
 RELEVANT RESIDUES IN SEQ ID NO:
 SEQUENCE DESCRIPTION: SEQ ID NO: 49:
 US-09-918-568-49

Query Match 100.0%; Score 1135; DB 9; Length 1135;
 Best Local Similarity 100.0%; Pred. No. 5.6e-300;
 Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTACCAAGAGGAGGTTATACCATAGAAAACCAAAAGCAAAACATGGCCATCATTTAT	60
DB	1	CTACCAAGAGGAGGTTATACCATAGAAAACCAAAAGCAAAACATGGCCATCATTTAT	60
QY	61	CTCATTCCTCTGTTACAGCAGTGAAGGAGGACGATATGATGATGATGATGATGATGAT	120
DB	61	CTCATTCCTCTGTTACAGCAGTGAAGGAGGACGATATGATGATGATGATGATGATGAT	120
QY	121	AATTCACAGAGAGGTTGACACATTTAGAGCGGAACGTCACGTGACTGATCCCAAG	180
DB	121	AATTCACAGAGAGGTTGACACATTTAGAGCGGAACGTCACGTGACTGATCCCAAG	180
QY	181	GACATCTTGAAGAGCCCATACGGAAGTTATGCAACTAAGCGATCCGGGATCATG	240
DB	181	GACATCTTGAAGAGCCCATACGGAAGTTATGCAACTAAGCGATCCGGGATCATG	240
QY	241	AAACAGAGGAGACATTTGAGACGTGAGACCAATCCCAACTCTTTGGGAGACATA	300
DB	241	AAACAGAGGAGACATTTGAGACGTGAGACCAATCCCAACTCTTTGGGAGACATA	300

QY	301	AATACACATTTACCTTTTACACATGTCCACCACCTGACATATAGTGTGCCCCAAATAT	360
DB	301	AATACACATTTACCTTTTACACATGTCCACCACCTGACATATAGTGTGCCCCAAATAT	360
QY	361	GTAATAATCGAGAGTGTGCTTACACAGAGCTAAGAAATGTTCCCAATGGAATCA	420
DB	361	GTAATAATCGAGAGTGTGCTTACACAGAGCTAAGAAATGTTCCCAATGGAATCA	420
QY	421	AGAGATTTGTTGGGGCAATACCTGTTTATAGAGAGAGATGCGCAAGAAATGTTGAC	480
DB	421	AGAGATTTGTTGGGGCAATACCTGTTTATAGAGAGAGATGCGCAAGAAATGTTGAC	480
QY	481	GCTTGATGATGATACATACAGCAATGACAGGATGAGGTTATGACAGCAAGAAAT	540
DB	481	GCTTGATGATGATACATACAGCAATGACAGGATGAGGTTATGACAGCAAGAAAT	540
QY	541	TCACACTCAAAAGGCAATTTGATGGAATCAACCAAGTAATTTCTGTGATGAAAGATA	600
DB	541	TCACACTCAAAAGGCAATTTGATGGAATCAACCAAGTAATTTCTGTGATGAAAGATA	600
QY	601	AACACCAATTTGAGAGTGTGGGAAAGAAATGCGTACCTAGAGAAAGAGCTGAGAAC	660
DB	601	AACACCAATTTGAGAGTGTGGGAAAGAAATGCGTACCTAGAGAAAGAGCTGAGAAC	660
QY	661	TTGAACAAAAGATGAGAGAGCGGTTTCTAGATGTGACATCAATGCTGAGCTTTTA	720
DB	661	TTGAACAAAAGATGAGAGAGCGGTTTCTAGATGTGACATCAATGCTGAGCTTTTA	720
QY	721	GTTCTGATGAGAAATGAGAGACCTTGATGATTTCAATGTTAATGTCAGAAATCTGAT	780
DB	721	GTTCTGATGAGAAATGAGAGACCTTGATGATTTCAATGTTAATGTCAGAAATCTGAT	780
QY	781	AGTAAAGTCAGATGACAGTGGAGACAGCAACGCAAGAACTAGAAATGATGTTTGA	840
DB	781	AGTAAAGTCAGATGACAGTGGAGACAGCAACGCAAGAACTAGAAATGATGTTTGA	840
QY	841	TTTTATCACAATGTGATGATGAATGATGATGATGATGATGATGATGATGATGAT	900
DB	841	TTTTATCACAATGTGATGATGAATGATGATGATGATGATGATGATGATGATGAT	900
QY	901	CCCAAGTATGAAGAGAGCTTAACCTAATGAAATGAAATGAAATGAAATGAAATGAGC	960
DB	901	CCCAAGTATGAAGAGAGCTTAACCTAATGAAATGAAATGAAATGAAATGAAATGAGC	960
QY	961	AGCATGGGGGTTTATCAATCTTGGCATTTATGCTACAGAGAGGTTCTATGTCAC	1020
DB	961	AGCATGGGGGTTTATCAATCTTGGCATTTATGCTACAGAGAGGTTCTATGTCAC	1020
QY	1021	GCAATCATGATGAGGCTGAGATCTTTTGGGTTGCTCACAAGCGGTCCTGACAGT	1080
DB	1021	GCAATCATGATGAGGCTGAGATCTTTTGGGTTGCTCACAAGCGGTCCTGACAGT	1080
QY	1081	ATTCGATATGATTAATGATGATTAATTAATAAACCCTTTGTTGCTGAG	1135
DB	1081	ATTCGATATGATTAATGATGATTAATTAATAAACCCTTTGTTGCTGAG	1135

RESULT 2
 US-09-918-568-46
 Sequence 46, Application US/09918568
 Patent No. US20020054882A1
 GENERAL INFORMATION:
 APPLICANT: Yoshinobu OKUNO et al.
 TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESS: Wenderoth, Lind & Ponack, L.L.P.
 STREET: 2033 K Street, N.W., #800
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.

```

ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-121-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/Oluca/57
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUE: IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-918-568-46

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Query Match	80.1%	Score 908.8	DB 9	Length 1793
Best Local Similarity	98.7%	Pred. NO. 5.4e-28		
Matches 916	Conservative 0	Mismatches 12	Indels 0	Gaps 0
QY	208	AAGTTATGCAACACTTAACGSGATCCCGGATCTATGAAACAGAGGAGACACTTGAGAACTGT	267	
Db	853	AAATPATCGAAGAGAGGTACTTTCAGCGATCATGAAACAGAGGAGACCTTGAGAACTGT	912	
QY	268	GAGACCAAAATGCCAAACTCCTTTGGGAGCAATAATACACATTACCTTTTACAATGTC	327	
Db	913	GAGACCAAAATGCCAAACTCCTTTGGGAGCAATAATACACATTACCTTTTACAATGTC	972	
QY	328	CACCCACGCAAAATAGGTGAGTGGCCCCCAATATGTAAATGCGGAAAGTGGCTGTGACA	387	
Db	973	CACCCACGCAAAATAGGTGAGTGGCCCCCAATATGTAAATGCGGAAAGTGGCTGTGACA	1032	
QY	388	ACAGGACTAAAGAAATGTTTCCCAAGATGTAATCAAGAGAGATGTTTGGGGCAATAGCTGGT	447	
Db	1033	ACAGGACTAAAGAAATGTTTCCCAAGATGTAATCAAGAGAGATGTTTGGGGCAATAGCTGGT	1092	
QY	448	TTTATTAGAGGAGATGGCAAGAAATGTTGACGGTGTGTATGCATACATCACACAAT	507	
Db	1093	TTTATTAGAGGAGATGGCAAGAAATGTTGACGGTGTGTATGCATACATCACACAAT	1152	
QY	508	GACACGAGATFAGGGTATGACGACGACAAACAAATCCACTCAAAAGGCACTTTGATGGAAATC	567	
Db	1153	GACACGAGATFAGGGTATGACGACGACAAACAAATCCACTCAAAAGGCACTTTGATGGAAATC	1212	
QY	568	ACCAACAAGGTAATTCGTGTGATTGAAAGATTAACACCCCAATTTGAAGCTGTGGGAAA	627	
Db	1213	ACCAACAAGGTAATTCGTGTGATTGAAAGATTAACACCCCAATTTGAAGCTGTGGGAAA	1272	
QY	628	GAATTCGGTAACCTTAGAGAAAAGACTGAGAACTTGAACAAAAGATGGAAGACGGGTTT	687	
Db	1273	GAATTCGGTAACCTTAGAGAAAAGACTGAGAACTTGAACAAAAGATGGAAGACGGGTTT	1332	
QY	688	CTAGATGTTGTCGACATCAATGCTGAGCTTTTACTGTTGATGGAAATGAGAGGACACTT	747	
Db	1333	CTAGATGTTGTCGACATCAATGCTGAGCTTTTACTGTTGATGGAAATGAGAGGACACTT	1392	
QY	748	GACTTTCATGATTCATTAATGTCAGAATCTGTATAGTAAAGTCAGAAATGACAGCTGAGAGAC	807	
Db	1393	GACTTTCATGATTCATTAATGTCAGAATCTGTATAGTAAAGTCAGAAATGACAGCTGAGAGAC	1452	
QY	808	AACGTCAAAGAACTTAGGAATGATGTTTAAATTTATCACAATGTGATGATGAATGC	867	
Db	1453	AACGTCAAAGAACTTAGGAATGATGTTTAAATTTATCACAATGTGATGATGAATGC	1512	
QY	868	ATGAATAGTGTGAAGAAAACGGGACATATGATTTATCCCAAGTATGAGAGAGCTTAACCTA	927	
Db	1513	ATGAATAGTGTGAAGAAAACGGGACATATGATTTATCCCAAGTATGAGAGAGCTTAACCTA	1572	
QY	928	AATGAAATGAAATCAAAAGGGGTAAATTTGAGCAGATGGGGGTTTATCAAAATCCTTGCC	987	
Db	1573	AATGAAATGAAATCAAAAGGGGTAAATTTGAGCAGATGGGGGTTTATCAAAATCCTTGCC	1632	
QY	988	ATTATATGCTACAGTAGCAGTTCTATATGTCATGTGCATCATGATGAGTGGGATCTCTTTC	1047	
Db	1633	ATTATATGCTACAGTAGCAGTTCTATATGTCATGTGCATCATGATGAGTGGGATCTCTTTC	1692	
QY	1048	TGGGTGTGCTCCAAAGGGGTCTCTCAGTGCAGATCTGCATATGATTATAGTCATTTTTA	1107	
Db	1693	TGGGTGTGCTCCAAAGGGGTCTCTCAGTGCAGATCTGCATATGATTATAGTCATTTTTA	1752	
QY	1108	TAAATTAATAAACACCCCTGTGTTCTGCTAG	1135	
Db	1753	TAAATTAATAAACACCCCTGTGTTCTGCTAG	1780	

Patent No. US2002005482A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1728 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/12um1/5/65
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:

Query Match 73.8%; Score 838; DB 9; Length 1728;
Best Local Similarity 95.6%; Pred No. 1,2e-218;
Matches 862; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 28;
US-09-918-568-28
QY 208 AAGTATGCAAACTAAGCGATCCGGATCATGAAAGAGAAACACTTGAGAACTGT 267
DB 827 AAAATATCGAAAAGAGGTAGTTCAGGATCATGAAAGAGAAACACTTGAGAACTGT 886
QY 268 GAGACCAATGCCAACTCTTTGGAGCAATAATACAACTTACCTTTTACAAATGTC 327
DB 887 GAGACCAATGCCAACTCTTTGGAGCAATAATACAACTTACCTTTTACAAATGTC 946
QY 328 CACCCACATGCAATGAGTGGAGTCCCAATATGTAATGGAAGTGGCTTACGA 387
DB 947 CACCCACATGCAATGAGTGGAGTCCCAATATGTAATGGAAGTGGCTTACGA 1006
QY 388 ACAGGACTAAGGAATGTTCCCGATGCAATGCAAGAGATGTTGGGCAATAGCTGT 447
DB 1007 ACAGGACTAAGGAATGTTCCCGATGCAATGCAAGAGATGTTGGGCAATAGCTGT 1066
QY 448 TTTATGAGAGAGATGCGCAAGATGTTGACGTTGTATGATACCATCACAGCAAT 507
DB 1067 TTTATGAGAGAGATGCGCAAGATGTTGACGTTGTATGATACCATCACAGCAAT 1126
QY 508 GACCAAGGATCAGGATGATGACAGCAAGCAATCCACTCAAAAGGCTTTGATGATC 567
DB 1127 GACCAAGGATCAGGATGATGACAGCAAGCAATCCACTCAAAAGGCTTTGATGATC 1186
QY 568 ACCAACAAGTAAATTTGTTGATTAAGATAAACACCAATTTGAAGCTTTGGGAAA 627
DB 1187 ACCAACAAGTAAATTTGTTGATTAAGATAAACACCAATTTGAAGCTTTGGGAAA 1246
QY 628 GAATTCGATTAATTTAGAGAAAAGCTGAGAACTTGAAACAAAGATGGAAGACGGGTTT 687
DB 1247 GAATTCGATTAATTTAGAGAAAAGCTGAGAACTTGAAACAAAGATGGAAGACGGGTTT 1306
QY 688 CTAGATGCTGACATACATGCTGAGCTTTAGTCTGATGGAAGATGAGAGACACTT 747
DB 1307 CTAGATGCTGACATACATGCTGAGCTTTAGTCTGATGGAAGATGAGAGACACTT 1366
QY 748 GACTTTCATGATTTCAATGTCAGAATCTGTATAGTAAGTCAGAAATGCAAGTGAAGAC 807
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QY 808 AACGTCAAGAACTAGGAATGATGTTTAAATTTATCAAAATGATGATGAATGC 867
DB 1427 AACGTCAAGAACTAGGAATGATGTTTAAATTTATCAAAATGATGATGAATGC 1486
QY 868 ATGATAGTGTGAAGAAAGCGGACATATGATATCCCAAGTATGAAGAAAGTGTAAACTA 927
DB 1487 ATGATAGTGTGAAGAAAGCGGACATATGATATCCCAAGTATGAAGAAAGTGTAAACTA 1546
QY 928 AATAGAAATGAATCAAGGGGTAAATTTAGAGCAATGGGGGTTTATCAAACTCTTCC 987
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QY 988 ATTATGCTACAGTACAGGTTTATGCTACGTCGCAATCATGATGCTGGGATCTCTTC 1047
DB 1607 ATTATGCTACAGTACAGGTTTCTGCTACGTCGCAATCATGATGCTGGGATCTCTTC 1666

FILED DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/kumamoto/1/65
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-918-568-35

Query Match 33.7% Score 382.4; DB 9; Length 410;
Best Local Similarity 96.1%; Pred. No. 2.2e-94;
Matches 392; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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DB 3 CTTTGGAGCAATAATACACATTAACCTTTTCAACATGCCACCCAGTACATAGGTC 62
QY 347 AGTGGCCCAATATGTAAATCGAGAGTGGCTTTAGCAACAGAGAGCTAAGATGTC 406
DB 63 AATGCCCAATATGTAAATCGAGAGTGGCTTTAGCAACAGAGAGCTAAGATGTC 122
QY 407 CCCAGATTGAATCAAGAGATGTTGGGGCAATACCTGTTTATAGAGAGAGATGGC 466
DB 123 CCCAGATTGAATCAAGAGATGTTGGGGCAATACCTGTTTATAGAGAGAGATGGC 182

QY 467 AAGAAATGTTGACGGTGTATGATACATCAGCAATGACGAGGATCAGGTATG 526
DB 183 AAGAAATGATTGATGTTGATGATGATACATCAGCAATGATCAGGATAGGTTG 242
QY 527 CACGAGCAAAAGATCCACTCAAAAGAGCTTTGATGAAATCACAACAGATTAATGTC 586
DB 243 CACGAGCAAAAGATCCACTCAAAAGAGCTTTGATGAAATCACAACAGATTAATGTC 302
QY 587 TGATTGAAAAGATTAACACCCCAATTTGAAGCTGTTGGAAAGAAATTCGTAATTAGAGA 646
DB 303 TGATTGAAAAGATTAACACCCCAATTTGAAGCTGTTGGAAAGAAATTCGTAATTAGAGA 362
QY 647 AAGACTGGAGACTTGAACAAAAGATGAGAGCGGTTTCTAGATG 694
DB 363 AAGACTGGAGACTTGAACAAAAGATGAGAGCGGTTTCTAGATG 410

RESULT 8
US-09-918-568-36
Sequence 36, Application US/09918568
Patent No. US20020054882A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/kaisuka/2/65
STRAIN: <Unknown>

MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUOS IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-918-568-57

Query Match 22.38; Score 252.6; DB 9; Length 1110;
Best Local Similarity 56.6%; Pred. No. 1.2e-58;
Matches 512; Conservative 0; Mismatches 384; Indels 9; Gaps 2;

227 GATCCGGATCATGAAGAGAGAACACTTGAGAACCTGAGACCAATGCCAATCTC 286
215 GCTCCTCAAGGGGAAATATGCAACAAATATGATACCTGATTTCTGAAATGCAATCCTC 274
287 CTTTGGAGCAATTAATFACAACTTACCTTTTCAATGTCACCCACTGACATAGTG 346
275 CAATGGAACCATTCCTCAATGACAGCCCTTCAAAACGTAACAGATACATATGAG 334
347 AGTCCCAAAATFCTAAATCGAGAGTTGCTTTAGCAACAGACGTAAGAGTTTC 406
335 CATGCCCAAGTATGTAAAGCAAAACACCTGAAGTTGGCAACAGGAGTCCGGAATGTAC 394
407 CCGAGATTGATGATAGAGATTGTTGGGCAATAGCTGTTTATGAGAGAGATGGC 466
395 CAGGAAACAAACACTAGAGGCTATTCGGCGCAATAGCAGGTTTCATAGAAATGGTTGGG 454
467 AAGGAATGTTGACGGTTGGTATGATACCATCAACAGCAATGACACGAGATCAGGATATG 526
455 AAGGAATGATAGACGGTTGGTACGGTTTCAGGCATCAAAATTCAGAGGACAGAGCAAG 514
527 CAGCAGACAAAGATCTACTCAAAAGGCAATTTGATGATGATCCCAACAGTAATTTCTG 586
515 CAGCAGATCTTAAAGACTCAAGCAGCCATCGAACCAATCAATGGGAATTTGAACAGGG 574
587 TGATTTGAAGATTAAGACCAATTTGAGCTGTGGGAAGAATTTGGTAACCTTAGA 646
575 TAATCGAGAGAGAGAGAGAAATTCATCAAAATCGAAAGAAATTTCTAGAAGTAAAG 634
647 AAGACTGAGAACTTGACCAAAAGATGGAAGACGGGTTTCTAGATGTGACATACA 706
635 GAGGAATTCAGGACCTGAGAAATAGCTTGAAGCACTAAATATAGATCTGTGCTTACA 694
707 ATGCTGACCTTTTACTCTGATGAAATAGAGAGACCTTGACTTTTCATGATTTTAATG 766
695 ATGCGGAGCTTTCTGCTCTGAGAAATCAATCAATTTGACCTGACTCGGAAA 754
767 TCAAGATCTGTATAGTAAGTCAAGATGAGCTGAGAGACGTCACAAAGTAAAGTAAAG 826
755 TGAACAGAGCTTTTGAAGAAACAGAGAGGCACTGAGGGAATGCTGAAGAGATGGCA 814
827 ATGATGTTTGTGATTTTATCACAATGTGATGATGATGATGATGATGATGATGATGATG 886
815 ATGTTGCTTCAAAATATACCAACAAATGTGCAACAGCTTGCATAGATCAATCAGAAATG 874
887 GGCATATGATTTCCCAAGTATGAGAGAGAGATCTTAATTAATGAAATGAATCAAG 946
875 GTACTTATGACATGATTTATACAGAGAGACGATTAACCAACCGGTTTCAGATCAAG 934

947 GGGTAAATTTGAGCAGCATGGGGGTTTATCAATCCTTGCATTTATGATACAGTACAG 1006
935 GTGTTGACTGAACTGATGATACAAAGACGATGATCTGTGATTTCTTTGCCATATCAT 994
1007 GTTCTATGCTGCTGCAATCATGATGATGATGATGATGATGATGATGATGATGATGAT 1066
995 GCTTTTGG---CTTTGTTGTTGTTGCTGGGTTTCATCATGATGATGATGATGATGATGAT 1051
1067 CTCTGAGTGCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1126
1052 ACATGATGCTCAACATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1105
1127 TTCTG 1131
1106 TTCTG 1110

RESULT 11
US-09-918-568-29
Sequence 29, Application US/09918568
Patent No. US20020054882A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
AMTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/PR/8/34
STRAIN: <Unknown>

INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 29;
US-09-918-568-29

Query Match 22.2% Score 251.6; DB 9; Length 442;
Best Local Similarity 73.1% Pred. No. 1,4e-58;

Matches 323; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 313 CCTTTTCACAAATGCCACCACTGACAAATAGTGAGTGGCCCAATATGTAATCGAG 372
DB 1 CTTTCCAAATATACACCCAGTCACAAATAGAGAGTGGCCCAAAATACGTCAGAGATGCC 60
QY 373 AAGTTGGTTTACCAACAGGACTAAGGAATGTTCCCAAGTTGATCAAGAGATTGTTT 432
DB 61 AAATTGAGGATGTTACAGGACTAAGGAATGCCCTCCATTCATCAACAGGCTATATT 120
QY 433 GGGGCAATAGTGGTTTATAGAAAGGAGATGGCAAGGAATGTTGACGTTGATGGA 492
DB 121 GAGGCCATTCGCCGTTTATTGTAAGGGGATGACTGSAATGATGATGATGATGAT 180
QY 493 TACCATCAACGAATGACCAGGATCAGGATATGCAGACAGCAAAAGATCCACTCAAAAG 552
DB 181 TATCATCATCAGAAATGAACAGGATCAGGCTATGCAGCGATCAAAAAGCACACAAAT 240
QY 553 GCATTGATGATATACCAACAGGTAATTTCTGATGATGAAGATTAACACCAATTT 612
DB 241 GCCATTAAAGGGATACAAACAGGAACTCTGTTATCGAGAAATGAACACTCAATTC 300
QY 613 GAAGCTGTTGGGAAGATTCGTTAAGAGAAAGACGTGAGAACTGGAACAAAG 672
DB 301 ACAGCTGTGGTAAAGAAATTAACAAATTAAGGATGAAATTAATTAATAAAG 360
QY 673 ATGAAGACGGGTTCTAGATGTGACATACAAATGCTGAGCTTTTACTTCTGATGGA 732
DB 361 GTTGATGATGATTTCTGACATTTTGACATATATATGCAATTTGTTACTTACTGAA 420
QY 733 AATGAGAGACACTTGACTTTC 754
DB 421 AATGAAGAGACTCTGATTTCC 442

RESULT 12
US-09-918-568-32

Sequence 32, Application US/09918568
Patent No. US20020054882A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/228,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 429 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/Osaka/930/88
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:

AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-918-568-32

Query Match 21.3% Score 241.8; DB 9; Length 429;
Best Local Similarity 72.7%; Pred. No. 6.4e-56;
Matches 312; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 313 CCTTTACAGATGCTCCACCCACTGACATAGTGTAGTGGCCCAATATGTAAATCGGAG 372
1 CCTTTCAGATGTACACCCAGTCAATAGAGAGATGCCCAAGTATGTACAGAGTACA 60
QY 373 AAGTGGCTTACAGATGAGACTAGAGAAATGTTCCCAATTCATCAAGAGAGATTGTT 432
61 AATTAAGGATGTGTTTACGAGTAAGAGAACATCCCATTCATTCATCCAGAGGTTGTTT 120
QY 433 GGGGCAATAGCTGTTTATAGAGAGAGATGGCAAGAAATGTTGACGTTGCTATGGA 492
121 GGAGCCATTGCGGTTTCATAGAGAGGGGTGACTGAGTAATGATGATGATGATGAT 180
QY 493 TACCATCAGACAGATGACCCAGGATGAGGTTATGACAGACAAAGATCCACTCAAAAG 552
181 TATCATCATCAGATGATGACAGAGATGCTATGCTATGCTGCGGATCAAAAAAGCACAAAT 240
QY 553 GCATTGATGATCATCATCAACAAGTAATTTCTGATTTGAAAAGATTAACCCCAATTT 612
241 GCCATTAAAGGAAATTAACAAGGTAATTTCTGATTCGAGAAATGAACCTCAATTC 300
QY 613 GAAGCTGTTGGGAAAGATTGCTACTTATAGAGAAAGATGAGAGAACTGTAACAAAG 672
301 ACAGCTGTGGGCAAGATTTCAACAATTAAGAAAGAGATGAGAAACTTAATTAAGAA 360
QY 673 ATGAGAGAGGCTTTCAGATGTGAGCATACATCAATCTGAGCTTTAGTCTGATGAA 732
361 GTTGATGATGATTTTCAGACATTTGACATATTAATGACAGAAATTTGTTGTTCTACIGAA 420
QY 733 AATGAGAG 741
421 AATGAAGG 429
DB

RESULT 13
US-09-918-568-30

Sequence 30, Application US/49918568
Patent No. US2002005482A1
GENERAL INFORMATION:

APPLICANT: Yoshinobu KUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)

NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderpich, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.

ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/Bangkok/10/83
STRAIN: <Unknown>

INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>

IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>

FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:

AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-918-568-30

Query Match 20.6% Score 233.6; DB 9; Length 424;
Best Local Similarity 71.9%; Pred. No. 1.1e-53;
Matches 305; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 313 CCTTTACAGATGCTCCACCCACTGACATAGTGTAGTGGCCCAATATGTAAATCGGAG 372
1 CCTTTCAGATGTACACCCAGTCAATAGAGAGATGCCCAAGTATGTACAGAGTACA 60

Db 1 CCTTCCAGATGTCACCCAGTCACATAGAGAGTCCCAAGTAGCTCAGAGTACA 60
QY 373 AAGTTGCTTTAGCAACAGAGTAAAGATGTTCCCAAGTTGAATCAAGAGATGTTT 432
Db 61 AAATTAAGAGTGTGTTACAGAGTAAAGATGTTCCCAAGTTGAATCAAGAGTGTGTT 120
QY 433 GGGGCAATAGCTGTTTATAGAGAGAGATGCGCAAGATGTTGACGGTGTGATGA 492
Db 121 GGAGCATGTCGGGTTTCATTTAGAGGGGATGACATGATGATGATGATGATGAT 180
QY 493 TACCATCAGACAGATGACAGAGTATGCGACAGACAAATCCACTCAAAAG 552
Db 181 TATCATCTCAGATGACAGAGATGCTGCTATGCTGCGATCAAAAAGACACAAAT 240
QY 553 GCATTGTGATGATCACCACAGAGTAAATCTGTGATGAAAGATTAACACCCCAAT 612
Db 241 GCCATTAAAGGATTTACAAACAGAGTAACTCTGTATGAGAAATGAACACTCAATTC 300
QY 613 GAAGCTGTTGGGAAGATTCGGTAACTTAGAGAAAAAGACTGGAGACTTGAACAAAAG 672
Db 301 ACAGCTGTGGTAAAGATTCACAAATTAAGAAAAAGATGAAATCTTAATAAATAA 360
QY 673 ATGGAAGAGGGTCTTCTGATGATGACATACATGCTGACGCTTTACTGATGANA 732
Db 361 GTTGATGATGATTTCTTGACATTTGGACATTAATGCAGAATGTTGGTCTACTGAA 420
QY 733 AATG 736
Db 421 AATG 424

RESULT 14

US-09-918-568-31
Sequence 31, Application US/09918568
Patent No. US20020054882A1

GENERAL INFORMATION:

APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESSES:

ADDRESS: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/918, 568
FILING DATE: 02-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 424 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to genomic RNA

HYPOTHETICAL: <Unknown>

ANTI-SENSE: <Unknown>

FRAGMENT TYPE: <Unknown>

ORIGINAL SOURCE:

ORGANISM: A/Yamagata/120/86

STRAIN: <Unknown>

INDIVIDUAL ISOLATE: <Unknown>

DEVELOPMENTAL STAGE: <Unknown>

HAPLOTYPE: <Unknown>

TISSUE TYPE: <Unknown>

CELL TYPE: <Unknown>

CELL LINE: <Unknown>

ORGANELLE: <Unknown>

IMMEDIATE SOURCE:

LIBRARY: <Unknown>

CLONE: <Unknown>

POSITION IN GENOME:

CHROMOSOME/SEGMENT: <Unknown>

MAP POSITION: <Unknown>

UNITS: <Unknown>

FEATURE:

NAME/KEY:

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION:

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOURNAL:

VOLUME:

ISSUE:

PAGES:

DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

SEQUENCE DESCRIPTION: SEQ ID NO: 31:

US-09-918-568-31

Query Match 20.6%; Score 233.6; DB 9; Length 424;

Best Local Similarity 71.9%; Pred. No. 1.1e-53;

Matches 305; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 313 CCTTTCCAGATGTCACCCAGTCACATAGAGAGTCCCAAGTAGCTCAGAGTACA 372
Db 1 CCTTCCAGATGTCACCCAGTCACATAGAGAGTCCCAAGTAGCTCAGAGTACA 60
QY 373 AAGTTGCTTTAGCAACAGAGTAAAGATGTTCCCAAGTTGAATCAAGAGATGTTT 432
Db 61 AAATTAAGAGTGTGTTACAGAGTAAAGATGTTCCCAAGTTGAATCAAGAGTGTGTT 120
QY 433 GGGGCAATAGCTGTTTATAGAGAGAGATGCGCAAGATGTTGACGGTGTGATGA 492
Db 121 GGAGCATGTCGGGTTTCATTTAGAGGGGATGACATGATGATGATGATGATGAT 180
QY 493 TACCATCAGACAGATGACAGAGTATGCGACAGACAAATCCACTCAAAAG 552
Db 181 TATCATCTCAGATGACAGAGATGCTGCTATGCTGCGATCAAAAAGACACAAAT 240
QY 553 GCATTGTGATGATCACCACAGAGTAAATCTGTGATGAAAGATTAACACCCCAAT 612
Db 241 GCCATTAAAGGATTTACAAACAGAGTAACTCTGTATGAGAAATGAACACTCAATTC 300
QY 613 GAAGCTGTTGGGAAGATTCGGTAACTTAGAGAAAAAGACTGGAGACTTGAACAAAAG 672

Db 301 ACAGCTGTGGCAAAATTCAACAATTAGAAAAGAGTGAAGAAACTTAAATAAAAA 360
QY 673 ATGGAACAGCGGTTTATGATGTGTGCATACATGCGAGCTTTAGTTGATGAGAA 732
Db 361 GTTGATGATGATTTTGTGCAATTTTGACATATTAATGCAAGATTGTGGTCTACTGAA 420
QY 733 AATG 736
Db 421 AATG 424

RESULT 15
US-10-099-619-1
: Sequence 1, Application US/10099619
: Publication No. US2002016834A1
: GENERAL INFORMATION:
: APPLICANT: CLAESSENS, JOHANNES AJ
: APPLICANT: WALTER, FUCHS
: TITLE OF INVENTION: RECOMB
: FILE REFERENCE: 20010010US
: CURRENT APPLICATION NUMBER: US/10/099,619
: PRIOR FILING DATE: 2002-03-15
: PRIOR FILING DATE: 2001-03-15
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 1711
: TYPE: DNA
: ORGANISM: AVIAN INFLUENZA VIRUS
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (11)..(1705)
: OTHER INFORMATION: ISOLATE A/ITALY/445/99 (H7/N1)
US-10-099-619-1

Query Match 20.4%; Score 233.6; DB 13; Length 1711;
Best Local Similarity 56.4%; Pred. No. 2.5e-53;
Matches 493; Conservative 0; Mismatches 369; Indels 18; Gaps 2;

QY 232 GGGATCATGAAACAAAGAGACACTGTAGACCAAAATGCCAAACTCCTTG 291
Db 833 GGGATTCAGAGTGAATACAGTTGAGGCCAATGTGAAGAGATTGCTATCAGTGA 892
QY 292 GGGACATTAATACACATTTACTTTTCACATGTCACCCACTGACATAGTGAGTGC 351
Db 893 GGGACATTAATAGTAAATTTGCCCTTCAGAACATTAATAGCAGGGCAGTGAAGAAATGT 952
QY 352 CCCAATATGTAATAACCGAGAGTTGGTCTAGCAACAGAGCTAAGGAATGTTCCCGAG 411
Db 953 CCGAGATATGTTAAGAAAGAGACTGTGCTGCTGCAACAGGAGTGAAGAAATGTTCCCGAA 1012
QY 412 ATTGAATCA-----AGAGATTGTTGGGCAATAGCTGTTTATAGAA 456
Db 1013 ATTCAAAAAGATCGAGTGAGAGAGAGCGCTATTGTTGCTATAGCGGTTTCATTGAA 1072
QY 457 GAGAGATGCAAGCAATGTTGACGTTGATGATGATACATCAAGCAATGACAGGGA 516
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QY 517 TCAGGATATGACAGCAACAAAGATCCACTTATGATGAATCACCACAAAG 576
Db 1133 GAGGGAACGCTGCTCAATTACAAAGACCCCAATTCAGCAATTTATCAAGTAAACAGCAAAA 1192
QY 577 GTAAATTTCTGTGATTTAAAGATTAACACCAATTTGAAGCTGTGGGAAAGAAATCGGT 636
Db 1193 TTGAACCGGCTTATTAATAAAACTAACCAACCAATTTGAGTTAATAGCAATGAATTCACAT 1252
QY 637 AACTTAGAGAAAGATGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 696
Db 1253 GAGGTTGAAAGCAAAATTTGACATGATTAATTAATGAGACCAAGATTCACAGCAAGAGTG 1312
QY 697 TGACATACAAATGCTAGCTTTAGTTCTGATGAGAAATGAGAGACACTTGACTTCAT 756

Db 1313 TGGTCTATATACGGTGAACCTCTGTGTAGCAATGAGAGAACCGACATACATTTGATCTGACC 1372
QY 757 GATTCTATATGTCAGAAATCTGTATAGTAAGTCAAGATGCAAGCTGAGAGACACAGTCAAA 816
Db 1373 GACTCAGAAATGAAACAACTATAGCAACGAGTGAAGAGTACTACTGAGAGAAATGCTGAA 1432
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QY 877 GTGAAAAACGAGCATATGATTTATCCCAATGATGATGATGATGATGATGATGATGATGATGAT 936
Db 1493 ATTAGAAACAAACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1552
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Job time: 185.31 secs

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OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 18:45:33 ; Search time 2795.67 Seconds

(without alignments)
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Title: US-09-918-568-57

Perfect score: 1110

Sequence: 1 CTAGACGCAACACAGGCGAT.....TAAACACACCCCTGTTCTCG 1110

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1110	100.0	1110	6	AR181971	AR181971 Sequence
2	1110	100.0	1110	6	E08894	E08894 DNA encodin
3	1110	100.0	1110	6	I32536	I32536 Sequence 57
4	1110	100.0	1110	6	I43481	I43481 Sequence 57
5	868	78.2	1777	6	AR181968	AR181968 Sequence
6	868	78.2	1777	6	I32533	I32533 Sequence 54
7	868	78.2	1777	6	I43478	I43478 Sequence 54
8	867	78.1	1765	14	OR1N11	V01085 Hemagglutin
9	862.2	77.7	1736	14	AF348176	AF348176 Influenza
10	862.2	77.7	1736	14	AF348177	AF348177 Influenza
11	862.2	77.7	1765	14	OR1N16	V01103 Influenza v
12	860.6	77.5	1736	14	AF348178	AF348178 Influenza
13	860.6	77.5	1736	14	AF348179	AF348179 Influenza
14	860.6	77.5	1765	14	FLAHMA	J02135 Influenza A
15	860.6	77.5	1765	14	INA289703	AJ289703 Influenza
16	855	77.0	1765	14	FLAHM2	M55059 Influenza v
17	851	76.7	1765	14	FLAHALR	J02132 Influenza v
18	843	75.9	1738	14	FLAHAL	J02090 Influenza A
19	833.4	75.1	1765	6	AX350190	AX350190 Sequence
20	832	75.0	1764	6	AX350204	AX350204 Sequence
21	831.8	74.9	1768	14	OR1N12	V01086 Hemagglutin
22	830.2	74.8	1765	14	FLAN2HAC	M73774 Influenza v
23	830.2	74.8	1768	14	OR1N1	V01098 Influenza v
24	827.6	74.6	1765	14	FLADORNHA	M54895 Influenza A
25	814.8	73.4	1744	14	IA007146	U07146 Influenza v
26	814.2	73.4	1653	14	FLAHM3DKC	M16739 Influenza v
27	811.6	73.1	1762	6	ORA77HA	X05907 Influenza A
28	808.4	72.8	1653	14	FLAHM3DKG	E01133 CDNA encodl
29	807.8	72.8	1653	14	FLAHM3DKF	M16743 Influenza v
30	806.2	72.6	1653	14	FLAHM3DKA	M16737 Influenza v
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32	803	72.3	1685	14	IYU08858	U08858 Influenza A
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36	795	71.6	1765	14	FLAHM3DKB	M16738 Influenza v
37	791.8	71.3	1653	14	FLAHAPB	M19057 Influenza A
38	791.2	71.3	1647	14	FLAHAPB	M19056 Influenza A
39	788	71.0	1647	14	FLAHAPB	J02092 Influenza A
40	787	70.9	1653	14	FLAHM3DKD	D00929 Influenza A
41	785.4	70.8	1653	14	FLAHM3DKD	M16740 Influenza v
42	783.8	70.6	1653	14	FLAHM3DKD	AJ252129 Influenza
43	782.2	70.5	1759	14	IY1252129	AJ252131 Influenza
44	782.2	70.5	1759	14	IY1252131	D00930 Influenza A
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ALIGNMENTS

RESULT 1
LOCUS AR181971 1110 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 57 from patent US 6337070.
ACCESSION AR181971
VERSION AR181971.1 GI:20224887
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1110)
AUTHORS Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.
TITLE Polypeptides for use in generating anti-human Influenza virus
antibodies
JOURNAL Patent: US 6337070-A 57 08-JAN-2002;

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FEATURES
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Query Match      100.0%; Score 1110; DB 6; Length 1110;
Best Local Similarity 100.0%; Pred. No. 4.2e-295;
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGAGCAAGCAGGCGATATTTCTATTATCATGAGACCATATTCGTTGAGCTAC 60
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Db 1 CTAGAGCAAGCAGGCGATATTTCTATTATCATGAGACCATATTCGTTGAGCTAC 60

QY 61 ATTTCTGTGCTGCTCGGCCAAGACCTTCCAGGAATGACAAGCAGCAGCAGCTG 120
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Db 181 ATTAAGTGAATAGCTACTAGAGTACTGAGCTCTCTCAACGGGAAATATGCAAC 240

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QY 361 ACCGTGAAGTGGACACAGGAGATGGGCAATGACCAAGAAACAAACATAGAGCCTATTC 420
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Db 361 ACCGTGAAGTGGACACAGGAGATGGGCAATGACCAAGAAACAAACATAGAGCCTATTC 420

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QY 601 CATCAATTCGAAAGAAATTCCTCAGAAATAGAGGAGAAATTCAGAGCCTCGAGAAATAC 660
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Db 601 CATCAATTCGAAAGAAATTCCTCAGAAATAGAGGAGAAATTCAGAGCCTCGAGAAATAC 660

QY 661 GTTAAAGACACTAAATATGATCTCTGCTTTCACATGCGGAGCTTCTGTGCTGAG 720
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Db 661 GTTAAAGACACTAAATATGATCTCTGCTTTCACATGCGGAGCTTCTGTGCTGAG 720

QY 721 AATCAACATACATTTGACCTGACTGACTCGGAATGAAACAGCTGTTGAAAAAACAAG 780
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Db 721 AATCAACATACATTTGACCTGACTGACTCGGAATGAAACAGCTGTTGAAAAAACAAG 780

QY 781 AGGCACTGAGGAGAAATGCTGAGAGATGGCAATGCTTCAAAATATACACAAA 840
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RESULT 2
E08994
LOCUS      E08994      1110 bp      DNA      linear      PAT 29-SEP-1997
DEFINITION DNA encoding an immunogenic peptide derived from human influenza A
            virus haemagglutinin that doesn't have globular region.
ACCESSION  E08994.1 GI:22024632
VERSION    E08994.1
KEYWORDS   JP 1995089992-A/4.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 1110)
            Okuno, Y., Isekawa, Y., Sasao, F. and Ueda, S.
            IMMUNOGENIC ARTIFICIAL POLYPEPTIDE
            Patent: JP 1995089992-A 4 04-APR-1995;
            TAKARA SHUZO CO LTD
COMMENT    OS None
            OC Artificial sequences.
            PN JP 1995089992-A/4
            PD 04-APR-1995
            PE 16-MAR-1994 JP 1994070194
            PF 20-APR-1993 JP 93P 115216
            PI OKUNO YOSHINOBU, ISEKAWA YUJI, SASAO FUYOKO, UEDA SHIGEHARU PC
            C07K7/08,A61K39/145,C12N15/44,C12P21/02//C12N15/06,C12P21/08, PC
            (C12P21/02,
            PC C12R1:91),(C12P21/08,C12R1:91),C07K9:00;
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            FH topology: linear;
            FE key
            FT source
            FT 34.1077 /product='immunogenic peptide' FT CDS
            FT sig_peptide 34..81.
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    Location/Qualifiers
      1..1110
      /organism="unidentified"
      /mol_type="genomic DNA"
      /db_xref="taxon:32644"
BASE COUNT      374 a      216 c      258 g      262 t
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Query Match      100.0%; Score 1110; DB 6; Length 1110;
Best Local Similarity 100.0%; Pred. No. 4.2e-295;
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGAGCAAGCAGGCGATATTTCTATTATCATGAGACCATATTCGTTGAGCTAC 60
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Db 1 CTAGAGCAAGCAGGCGATATTTCTATTATCATGAGACCATATTCGTTGAGCTAC 60

QY 61 ATTTCTGTGCTGCTCGGCCAAGACCTTCCAGGAATGACAAGCAGCAGCAGCTG 120
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QY 121 TGCCGTGGACATCATCGCGTGCACAAACGGAACACTAGTAAACATCAGATGATCAG 180
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Db 121 TGCCGTGGACATCATCGCGTGCACAAACGGAACACTAGTAAACATCAGATGATCAG 180

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QY 181 ATTGAAGTACTAATCTACTGAGCTAGTTCAGAGCTCCTCAACGGGGAAATATGCAAC 240
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 Db 241 AATATTGATCTGTATTTCTGAATGCATCACTCCAAATGAAGCATTTCCCAATGACAG 300
 QY 301 CCCCTTCAAAACGTAACAGATACATATGAGCATGCCCAAGTATGTTAAGCAAAAC 360
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 Db 301 CCCCTTCAAAACGTAACAGATACATATGAGCATGCCCAAGTATGTTAAGCAAAAC 360
 QY 361 ACCCTGAAGTTGGCAACAGGATGCGGAATGTACAGAGAAACAAACTAGAGCCCTATTC 420
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 Db 361 ACCCTGAAGTTGGCAACAGGATGCGGAATGTACAGAGAAACAAACTAGAGCCCTATTC 420
 QY 421 GGGCGAATAGCAGGTTTCATAGAAAATGTTGGAGGGAATATAGAGCGTTGTACGCT 480
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 Db 421 GGGCGAATAGCAGGTTTCATAGAAAATGTTGGAGGGAATATAGAGCGTTGTACGCT 480
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 QY 781 AGGCAATGAGGGAATGCTGAAGAGATGGGCATGTTGCTTCAAAATATACCAAAA 840
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 Db 781 AGGCAATGAGGGAATGCTGAAGAGATGGGCATGTTGCTTCAAAATATACCAAAA 840
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 Db 841 TGTGACAAAGCTTGCATAGATCAATCAAGAAATGTAATGACATGATATACAGA 900
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 Db 961 GACTGATCTGTGGAATTCCTTTGCCATATCATGCTTTTTCCTTTGTGTTTGGCTG 1020
 QY 1021 GGGTTCATCATGTGGGCTGGCAGAGAGAGCAATTAGTGCACATTTGCATTGGAGTG 1080
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ORGANISM Unknown.
 REFERENCE Unclassified.
 1 (bases 1 to 1110)
 AUTHORS Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.
 TITLE Anti-human Influenza virus antibody
 JOURNAL Patent: US 5589174-A 57 31-DEC-1996;
 FEATURES Location/Qualifiers
 source 1..1110
 BASE COUNT 374 a 216 c 258 g 262 t.
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 Query Match 100.0%; Score 1110; DB 6; Length 1110;
 Best Local Similarity 100.0%; Pred. No. 4.2e-295;
 Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGAAGCAAGACAGGGGATTAATTCATTATCATGAGAGACCATCTGCTTGAGCTAC 60
 |||||
 Db 1 CTAGAAGCAAGACAGGGGATTAATTCATTATCATGAGAGACCATCTGCTTGAGCTAC 60
 QY 61 ATTTCTGTGCTGCTCTGGCCAGACCTTCAGAGAAATGACAAACGACAGCAACGCTG 120
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 QY 121 TGCCTGGACATCATGCGGTGCCAAACGAGACATAGTGAACAAATCAATCAGATGATCAG 180
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 Db 241 AATATTGATCTGTATTTCTGAATGCATCACTCCAAATGAAGCATTTCCCAATGACAG 300
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 Db 601 CATCAAAATCGAAAAGCAATCTCAGAGATGAGAAAGGAGAAATTCAGAGCTCGAGAAATTC 660
 QY 661 GTTGAAGACACTAAATATGATCTGTGTACAAATGCGAGACTTCTTGCTCTGGAG 720
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 Db 661 GTTGAAGACACTAAATATGATCTGTGTACAAATGCGAGACTTCTTGCTCTGGAG 720
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 Db 721 AATCAACATACAAATGACCTGACTGCTCGAAATGAACAAAGCTTTTGAAAAACAAG 780
 QY 781 AGGCAATGAGGGAATGCTGAAGAGATGGGCATGTTGCTTCAAAATATACCAAAA 840
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RESULT 3
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 ACCESSION I32536
 VERSION I32536.1 GI:1823327
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 SOURCE Unknown.

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ACCESSION 143481
VERSION 143481.1 GI:2468725
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1110)
AUTHORS Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.
TITLE Anti-human influenza virus antibody
JOURNAL Patent: US 5631350-A 57 20-MAY-1997;
FEATURES
Source 1..1110
Location/Qualifiers
BASE COUNT 374 a 216 c 258 g 262 t
Origin
Query Match 100.0%; Score 1110; DB 6; Length 1110;
Best Local Similarity 100.0%; Pred. No. 4.2e-25;
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTAGAACCAAGCAGGGGATTAATCTTATTAATCATGAAGACCATTTGTTGAGCTAC 60
Db 1 CTAGAACCAAGCAGGGGATTAATCTTATTAATCATGAAGACCATTTGTTGAGCTAC 60
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QY 301 CCCTTCAAAAACGTAACAGATACATATGAGACATGCCCCAAGTATGTTAAGCAAAAC 360
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QY 421 GCGCAATATACAGGTTTCATAGAAATGTTGGAGAGGAATGATGAGCGTTGTACGCT 480

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AR181968 1777 bp DNA linear PAT 20-APR-2002
LOCUS AR181968
DEFINITION Sequence 54 from patent US 6337070.
ACCESSION AR181968
VERSION AR181968.1 GI:20224884
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1777)
AUTHORS Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.
TITLE Polypeptides for use in generating anti-human influenza virus
JOURNAL Patent: US 6337070-A 54 08-JUN-2002;
FEATURES
Source 1..1777
Location/Qualifiers
BASE COUNT 565 a 363 c 421 g 428 t
Origin
Query Match 78.2%; Score 868; DB 6; Length 1777;
Best Local Similarity 100.0%; Pred. No. 2.7e-228;
Matches 868; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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RESULT 7
LOCUS      143478
DEFINITION Sequence 54 from patent US 5631350.
ACCESSION  143478
VERSION    143478.1 GI:2468722
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 1777)
AUTHORS   Okuno, Y., Isegawa, Y., Sasao, F. and Ueda, S.
TITLE     Anti-human influenza virus antibody
JOURNAL   Patent: US 5631350-A 54 20-MAY-1997;
FEATURES   Location/Qualifiers
           source          1..1777
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BASE COUNT      565 a      363 c      421 g      428 t
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Query Match      78.2%; Score 868; DB 6; Length 1777;
Best Local Similarity 100.0%; Pred. No. 2.7e-228;
Matches 868; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      1023 CCTGAAGTTGGACAGAGGATCGGAATGTACCAAGAAACAACTAGAGGCTTATTCGG 1082
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OY      1083 CGCATAGAGGTTTCATGAAATGCTGGAGGAGAAATGATGACGTTGGTACGTTT 1142
DB      483 CAGGATCAAAATTTCTGAGGCGACAGACAGACAGATCTTAAAGCAGCTCAACGAC 542
OY      1143 CAGGATCAAAATTTCTGAGGCGACAGACAGACAGATCTTAAAGCAGCTCAACGAC 1202
DB      543 CATGACCAATTCATTTGGGAAATTTGAACAGGCTAATCGAAGAGACGAGAAATTTCA 602
OY      1203 CATGACCAATTCATTTGGGAAATTTGAACAGGCTAATCGAAGAGACGAGAAATTTCA 1262
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DB      663 TGAAGACACTAAATAGATCTCTGCTTTCATATCGAGAGCTTCTTGGCTCTGGAGAA 722
OY      1323 TGAAGACACTAAATAGATCTCTGCTTTCATATCGAGAGCTTCTTGGCTCTGGAGAA 1382
DB      723 TCAACATTCATTTGACCTGACTGACTCGGAAATGAAACAAGCTGTTGAAAAACAAGAG 782
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OY      1083 TTAGTAATTTAAACACCCCTGTTCTG 1110
DB      1743 TTAGTAATTTAAACACCCCTGTTCTG 1770

RESULT 8
LOCUS      1765 bp RNA linear VRL 08-MAR-2000
DEFINITION Hemagglutinin gene of Influenza virus strain A/Alchi/2/68.
ACCESSION  V01085
VERSION    V01085.1 GI:60752
KEYWORDS   haemagglutinin.
SOURCE     Influenza A virus
ORGANISM   Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza
REFERENCE  1 (bases 1 to 1765)
AUTHORS   Verhoeven, M., Fang, R., Jou, W.M., Devos, R., Huylebroeck, D., Saman, E.
           and Fiers, W.
TITLE     Antigenic drift between the haemagglutinin of the Hong Kong
           Influenza strains A/Alchi/2/68 and A/Victoria/3/75
JOURNAL   Nature 286 (5775), 771-776 (1980)
MEDLINE   80254693
PUBMED    7402351
FEATURES   Location/Qualifiers
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BASE COUNT      563 a      360 c      416 g      426 t
ORIGIN
Query Match      78.1%; Score 867; DB 14; Length 1765;
Best Local Similarity 100.0%; Pred. No. 5.1e-228;
Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      243 TATTGATACCTGATTTTCGATGCTACCTCCAAATGAGAGCATTCCCAATGACAAGCC 302
DB      896 TATTGATACCTGATTTTCGATGCTACCTCCAAATGAGAGCATTCCCAATGACAAGCC 955
OY      303 CTTTCAAAAGCTAAACAGATCAGATATGAGAGCAGCCCAATGATTTAGCAAAACAC 362
DB      956 CTTTCAAAAGCTAAACAGATCAGATATGAGAGCAGCCCAATGATTTAGCAAAACAC 1015
OY      363 COTGAAGTTGGCAACAGGATCGGAGATGTACCAAGAAACAACTAGAGGCTTATTCGG 422
DB      1016 COTGAAGTTGGCAACAGGATCGGAGATGTACCAAGAAACAACTAGAGGCTTATTCGG 1075
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QY	423	CGCAATAGCAGGTTTATAGAAAATGTTGGAGGAGATGATGACGGTTGTACGGTTT	482
Db	1076	CGCAATAGCAGGTTTATAGAAAATGTTGGAGGAGATGATGACGGTTGTACGGTTT	1135
QY	483	CAGGATCAAAATTCGAGGGCAGACAGACAGATCTTAAAAAGCATCAAGCAGC	542
Db	1136	CAGGATCAAAATTCGAGGGCAGACAGACAGATCTTAAAAAGCATCAAGCAGC	1195
QY	543	CATCGACCAATCAATGGGAAATGTAAGGGGTATCGAAGACAGACAGAAATTCGA	602
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QY	663	TGAAGACACTAAATTCATCTCTGGTCTTCAATGCGGAGCTTCTTGCTCGAGAA	722
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Db	1376	TCAACATACATGATCTGACTCGGAAATGAACAAGCTGTTGAAAAACAAGGAG	1435
QY	783	GCAACTGAGGAGAAAATGCTGAAGAGATGGGCAATGGTCTTCAAAATATACCAAAATG	842
Db	1436	GCAACTGAGGAGAAAATGCTGAAGAGATGGGCAATGGTCTTCAAAATATACCAAAATG	1495
QY	843	TGACAAAGCTTGATGATGATCAATCGAAATGCTACTTATGACCATGATGATACAGAG	902
Db	1496	TGACAAAGCTTGATGATGATCAATCGAAATGCTACTTATGACCATGATGATACAGAG	1555
QY	903	CGAAGCATTAACAAACGGTTTCAGATCAAGGTTGTAAGTGAAGTCTGGATACAAAGA	962
Db	1556	CGAAGCATTAACAAACGGTTTCAGATCAAGGTTGTAAGTGAAGTCTGGATACAAAGA	1615
QY	963	CTGGATCTCTGGATTCCTTTGGCATATCATGCTTTTGTGTTGTTTGTCTGGG	1022
Db	1616	CTGGATCTCTGGATTCCTTTGGCATATCATGCTTTTGTGTTGTTTGTCTGGG	1675
QY	1023	GTTTCATCATGTGGCCCTGGCAGAGAGGCAACATTTAGGTGCAACATTTGATGAGTGA	1082
Db	1676	GTTTCATCATGTGGCCCTGGCAGAGAGGCAACATTTAGGTGCAACATTTGATGAGTGA	1735
QY	1083	TTAGTAATTAATAAACACCCCTGTTTCT	1109
Db	1736	TTAGTAATTAATAAACACCCCTGTTTCT	1762
RESULT 9	AF348176	1736 bp RNA linear VRL 07-JUN-2001	
LOCUS	AF348176	Influenza A virus (A/Hong Kong/1/68(H3N2))	
DEFINITION	complete cds.	hemagglutinin gene.	
ACCESSION	AF348176		
VERSION	AF348176.1	GI:14009691	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
AUTHORS			
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JOURNAL			

FEATURES	University of Ottawa, 451 Smyth Rd, Ottawa, Ont K1H 8M5, Canada				
source	Location/Qualifiers				
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ORIGIN					
Query Match	77.7% Score 862.2; DB 14; Length 1736;				
Best Local Similarity	99.7%; Pred. No. 1.1e-226;				
Matches	864; Conservative	0; Mismatches	3; Indels	0; Gaps	0;
QY	243	TATGTATACCTGTATTTCTG	AATGATC	ATCCTCCAAATGGAAGCATGCCAATGACAGCC	302
Db	867	TATGTATACCGTATTTCTG	AATGATC	ATCCTCCAAATGGAAGCATGCCAATGACAGCC	926
QY	303	CTTTCAAAGCTAAACAGAT	CACATATG	GAGCATGCCCAAGTATGTTAAGCAAAAC	362
Db	927	CTTTCAAAGCTAAACAGAT	CACATATG	GAGCATGCCCAAGTATGTTAAGCAAAAC	986
QY	363	CCTGAAGTTGGCAACAGG	ATGCGGATG	TATACCAAGAAACAATAGAGGCTATTCGG	422
Db	987	CCTGAAGTTGGCAACAGG	ATGCGGATG	TATACCAAGAAACAATAGAGGCTATTCGG	1046
QY	423	CGCAATAGCAGGTTTCTA	GAAAATG	CGTTGGAGAGGAATGATGACGGTTGTACG	482
Db	1047	CGCAATAGCAGGTTTCTA	GAAAATG	CGTTGGAGAGGAATGATGACGGTTGTACG	1106
QY	483	CAGGCATCAAAATTTCT	GAGGGCAG	CAAGCAGCATCTTAAAGCACTCAAGCAGC	542
Db	1107	CAGGCATCAAAATTTCT	GAGGGCAG	CAAGCAGCATCTTAAAGCACTCAAGCAGC	1166
QY	543	CATCGACCAATCAATG	GGAAATTT	GAGCAGGTTAATCGAAGAGCAGACAGAAATTC	602
Db	1167	CATCGACCAATCAATG	GGAAATTT	GAGCAGGTTAATCGAAGAGCAGACAGAAATTC	1226
QY	603	TCAAAATGGAAGAATTC	TACAGAAAT	GAGAGCAATTCAGGACCTCGAGAAATACGT	662
Db	1227	TCAAAATGGAAGAATTC	TACAGAAAT	GAGAGCAATTCAGGACCTCGAGAAATACGT	1286
QY	663	TGAAGACACTAAATTA	GATCTCTG	GTCTTCAATGCGGAGCTTCTTGCTCGCTG	722
Db	1287	TGAAGACACTAAATTA	GATCTCTG	GTCTTCAATGCGGAGCTTCTTGCTCGCTG	1346
QY	723	TCAACATACAAATGAC	TGACTGAC	TGCGGAAATGAACAAGCTGTTGAAAAACAAGAG	782
Db	1347	TCAACATACAAATGAC	TGACTGAC	TGCGGAAATGAACAAGCTGTTGAAAAACAAGAG	1406
QY	783	GCAACTAGGAGAAAAT	GCTGAAGAG	ATGGGCAATGGTCTTCAAAATATACCAAAATG	842
Db	1407	GCAACTAGGAGAAAAT	GCTGAAGAG	ATGGGCAATGGTCTTCAAAATATACCAAAATG	1466
QY	843	TGACAAAGCTTGATAG	TCAATCAG	AAATGGTACTTATGACCATGATGTATACAGAG	902

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RESULT 10
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LOCUS Influenza A virus (A/Hong Kong/1/68(H3N2)) isolate MA12
DEFINITION hemagglutinin gene, complete cds.
ACCESSION AF348177
VERSION AF348177.1 GI:14009693
KEYWORDS
SOURCE
ORGANISM
Influenza A virus (A/Hong Kong/1/68(H3N2))
Influenza A virus (A/Hong Kong/1/68(H3N2))
viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza
A viruses; Influenzavirus A; Influenza A virus; H3N2 subtype.
1 (bases 1 to 1736)
Brown, E.G., Liu, H., Kit, L.C., Baird, S. and Nesraliah, M.
Pattern of mutation in the genome of Influenza A virus on
adaptation to increased virulence in the mouse lung: identification
of functional themes
Proc. Natl. Acad. Sci. U.S.A. 98 (12), 6883-6888 (2001)

JOURNAL MEDLINE
PUBMED 11371620
2 (bases 1 to 1736)
Brown, E.G., Liu, H., Chang Kit, L., Baird, S. and Nesraliah, M.
Direct Submission
Submitted (12-FEB-2001) Biochemistry, Microbiology, and Immunology,
University of Ottawa, 451 Smyth Rd, Ottawa, Ont K1H 8M5, Canada
JOURNAL
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BASE COUNT 552 a 356 c 409 g 419 t

ORIGIN

Query Match 77.7%; Score 862.2; DB 14; Length 1736;
Best Local Similarity 99.7%; Pred. No. 1.le-226;

Matches 864; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 303 CTTTCAAAACGTAACAGATCATATGAGAGATGCCCAAGTATGTATGACAAAAC 362

Db 927 CTTTCAAAACGTAACAGATCATATGAGAGATGCCCAAGTATGTATGACAAAAC 986

QY 363 CCTGAAGTTGGCAGAGGATGCGAATGTACAGAGAAACAACTAGAGCCTATTGG 422

Db 987 CCTGAAGTTGGCAGAGGATGCGAATGTACAGAGAAACAACTAGAGCCTATTGG 1046

QY 423 CGCATATACAGGTTTCTATGAAATGCTTGGAGAGGAAATGTATAGAGTTGATCGGTT 482

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Db 1167 CATGACCAATATCAATGGGAATTTGACAGAGGCTATGACAGAGCAAGCAATTTCCA 1226

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Db 1227 TCAATTCGAAAGGAATTTCTGAGAGTGAAGGAGGAATTCAGAGCTCGAAGATTCGT 1286

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Db 1527 CGAAGCATTTAAACACCGGTTTCAGATCAAAAGGTGTTGAACGATGATGTATACAGCA 1586

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Db 1587 CTGATCCTGTGGATTTCTGTCATATCATGCTTTTGTGTTGTTTGTGCTGG 1646

QY 1023 GTTCATCATGTGGGCTTCGACAGAGGACACATTGAGTCAACATTGATTTGAGTGA 1082

Db 1647 GTTCATCATGTGGGCTTCGACAGAGGACACATTGAGTCAACATTGATTTGAGTGA 1706

QY 1083 TTAGTAATTTAAACACCGCTTGTCT 1109

Db 1707 TTAGTAATTTAAACACCGCTTGTCT 1733

RESULT 11

ORIN6

LOCUS ORIN6 1765 bp RNA linear VRL 15-FEB-1999

DEFINITION Influenza virus genes for the two haemagglutinins.

ACCESSION V01103 J02135

VERSION V01103.1 GI:60800

KEYWORDS haemagglutinin.

SOURCE Influenza A virus

ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza

Db	Accession	Source	Length	Strain	Isolate	Subtype	Reference
Db	1256	TCMAATGGAAGAATTTCCAGAGATGAGAAGGAGAAATTCAGGACCTCGAGAAATTCGT	1313				
QY	663	TGAAGACACTMAATAGATCTCTGGCTTTCACATGCGAGCTCTTGCTCGTGAGAA	722				
Db	1316	TGAAGACACTMAATAGATCTCTGGCTTTCACATGCGAGCTCTTGCTCGTGAGAA	1375				
QY	723	TCMACTATCAAAATGACCTGACTGCTCGGAAATGACAACTGTTTGAATAAACAGAG	782				
Db	1376	TCMACTATCAAAATGACCTGACTGCTCGGAAATGACAACTGTTTGAATAAACAGAG	1435				
QY	783	GCAACTGAGGAAATCTGTAAGAGATGGGCAATGTTGCTTCAAAATATACCAATG	842				
Db	1436	GCAACTGAGGAAATCTGTAAGAGATGGGCAATGTTGCTTCAAAATATACCAATG	1495				
QY	843	TGACAAACGCTTGCATAGATGTCATCAGAAATGCTACTTATGACCATGATGTATACAGAGA	902				
Db	1496	TGACAAACGCTTGCATAGATGTCATCAGAAATGCTACTTATGACCATGATGTATACAGAGA	1555				
QY	903	CGAAGCATTAACACACCGGTTTCAGATCAAAAGGTGTGAACCTGAAGTCTGGATACAAAGA	962				
Db	1556	CGAAGCATTAACACACCGGTTTCAGATCAAAAGGTGTGAACCTGAAGTCTGGATACAAAGA	1615				
QY	963	CTGATATCTGCGATTTCTTTGTCACATATGCTTTTCTGTTGTTGTTGCTGGG	1022				
Db	1616	CTGATATCTGCGATTTCTTTGTCACATATGCTTTTCTGTTGTTGTTGCTGGG	1675				
QY	1023	GTTTCATCATGTTGGGCTTCGCGAGAGGCAACATTAGGTGCAACATTTGCATTTGAGTGTA	1082				
Db	1676	GTTTCATCATGTTGGGCTTCGCGAGAGGCAACATTAGGTGCAACATTTGCAATTTGAGTGTA	1735				
QY	1083	TTAGTAATTTAAAAACACCCCTTTGTTCT	1109				
Db	1736	TTAGTAATTTAAAAACACCCCTTTGTTCT	1762				
RESULT 12							
AF348178							
LOCUS	AF348178	1736 bp	RNA	linear	VRL 07-JUN-2001		
DEFINITION	Influenza A virus (A/Hong Kong/1/68(H3N2))	isolate MA20					
ACCESSION	hemagglutinin gene, complete cds.						
VERSION	AF348178						
KEYWORDS	AF348178.1	GI:14009695					
SOURCE	Influenza A virus (A/Hong Kong/1/68(H3N2))						
ORGANISM	Influenza A virus (A/Hong Kong/1/68(H3N2))						
REFERENCE	1. (bases 1 to 1736)						
AUTHORS	Brown,E.G., Liu,H., Kit,L.C., Baird,S. and Nesrallah,M.						
TITLE	Pattern of mutation in the genome of Influenza A virus on						
	adaptation to increased virulence in the mouse lung: identification						
	of functional themes						
	Proc. Natl. Acad. Sci. U.S.A. 98 (12), 6883-6888 (2001)						
JOURNAL	21287244						
MEDLINE	21287244						
PUBMED	11371620						
REFERENCE	2. (bases 1 to 1736)						
AUTHORS	Brown,E.G., Liu,H., Chang Kit,L., Baird,S. and Nesrallah,M.						
TITLE	Direct Submission						
JOURNAL	Submitted (12-FEB-2001)						
	University of Ottawa, 451 Smyth Rd, Ottawa, Ont K1H 8M5, Canada						
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Query Match      77.5%: Score 860.6; DB 14; Length 1736;
Best Local Similarity 99.5%: Pred. No. 3e-226;
Matches 863; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 303 CTTTCAAAACGTAACAGATCATATGAGACATGCCCAAGTATGTTAAGCAAAACAC 362
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DB 927 CTTTCAAAACGTAACAGATCATATGAGACATGCCCAAGTATGTTAAGCAAAACAC 986

QY 363 CCTGAAGTTGGCAACAGGATCGGAATGTACAGAGAAACAATAGAGGCTTATTCG 422
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DB 987 CCTGAAGTTGGCAACAGGATCGGAATGTACAGAGAAACAATAGAGGCTTATTCG 1046

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QY 483 CAGGATCAAAATTTCTGAGGCGACAGCAACACACAGATCTTAAAGCAGCTCAGACAC 542
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QY 543 CATGACCAAAATCATATGGGAAATTAACAGGGTATTCGAGAGCAAGCAAGAAATTC 602
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QY 1083 TTAGTAATTAACACACCTTGTCT 1109
DB 1707 TTAGTAATTAACACACCTTGTCT 1733

RESULT 13
AF348179
LOCUS
DEFINITION
AF348179 1736 bp. RNA linear. VRL 07-JUN-2001
hemagglutinin gene, complete cds.
AF348179
AF348179.1 GI:14009697
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Influenza A virus (A/Hong Kong/1/68(H3N2))
Influenza A virus (A/Hong Kong/1/68(H3N2))
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza
A viruses; Influenzavirus A; Influenza A virus; H3N2 subtype.
REFERENCE
1 (bases 1 to 1736)
Brown, E.G., Liu, H., Kit, L.C., Baird, S. and Nesrallah, M.
Pattern of mutation in the genome of Influenza A virus on
adaptation to increased virulence in the mouse lung: identification
of functional themes
Proc. Natl. Acad. Sci. U.S.A. 98 (12), 6883-6888 (2001)
2 (bases 1 to 1736)
Brown, E.G., M. Liu, H., Chang Kit, L., Baird, S. and Nesrallah, M.
Direct Submission
Submitted (12-FEB-2001) Biochemistry, Microbiology, and Immunology,
University of Ottawa, 451 Smyth Rd, Ottawa, Ont K1H 8M5, Canada
LOCATION/Qualifiers
1. 1736
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BASE COUNT      553 a      356 c      408 g      419 t
ORIGIN
Query Match      77.5%: Score 860.6; DB 14; Length 1736;
Best Local Similarity 99.5%: Pred. No. 3e-226;
Matches 863; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 243 TATTGATACCTGTATTTCTGAAATGATCATCTCCAATGAGACATTCCTCCATGACAGCC 302
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DB 867 TATTGATACCTGTATTTCTGAAATGATCATCTCCAATGAGACATTCCTCCATGACAGCC 926

QY 303 CTTTCAAAACGTAACAGATCATATGAGACATGCCCAAGTATGTTAAGCAAAACAC 362
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QY 363 CCTGAAGTTGGCAACAGGATCGGAATGTACAGAGAAACAATAGAGGCTTATTCG 422
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QY	483	CAGGATCAAAATTCGAGGGCAGAGACAGCAGATCTTTAAAGCACTCAACGACG	542
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QY	723	TCAACATCAATGACCTGCTGCTGAGAAATGACACGCTTGAAGAAACAGAGAG	782
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QY	783	GCAACTGAGGAGAAATGCTGAGAGATGAGGCAATGCTTCAAAATATACCAAAATG	842
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QY	843	TGACAAAGCTTGATGATGATCAATCAAGAAATGCTTATGACCATGATGATACAGAG	902
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Db	1707	TTAGTAATTAATAACATCCTTGTCTTCT	1733
RESULT 14			
FLAHAMA		1765 bp ss-RNA linear VRL 10-JUN-2002	
LOCUS		Influenza A virus (A/NT/60/68/29c(H3N2)) hemagglutinin	
DEFINITION		Prepropeptide gene complete cds.	
ACCESSION		J02135	
VERSION		J02135.1 GI:324156	
KEYWORDS		glycoprotein; haemagglutinin.	
SOURCE		Influenza A virus (A/NT/60/68/29c(H3N2))	
ORGANISM		Influenza A virus (A/NT/60/68/29c(H3N2))	
REFERENCE		1 (bases 1 to 1765)	
AUTHORS		Both, G.W. and Sleight, M.J.	
TITLE		Complete nucleotide sequence of the haemagglutinin gene from a human influenza virus of the Hong Kong subtype	
JOURNAL		Nucleic Acids Res. 8 (12), 2561-2575 (1980)	
MEDLINE		81053698	
PUBMED		6253883	
REFERENCE		2 (bases 79 to 1061)	
AUTHORS		Sleight, M.J., Both, G.W., Underwood, P.A. and Bender, V.J.	
TITLE		Antigenic drift in the hemagglutinin of the Hong Kong influenza subtype: correlation of amino acid changes with alterations in	

JOURNAL	Viral antigenicity	
MEDLINE	J. Virol. 37 (3), 845-853 (1981)	
PUBMED	81194918	
REFERENCE	3 (bases 78 to 1730)	
AUTHORS	Sleigh,M.J., Both,G.W., Underwood,P.A. and Bender,V.J.	
TITLE	Antigenic drift in the hemagglutinin of the Hong Kong influenza subtype: correlation of amino acid changes with alterations in viral antigenicity	
JOURNAL	J. Virol. 37 (3), 845-853 (1981)	
MEDLINE	81194918	
PUBMED	6164798	
COMMENT	A/NT/60/68/29c is a laboratory-isolated variant of A/NT/60/68. Hemagglutinin is cleaved after translation to yield HA1 & HA2. The putative assignments for signal, HA1 & HA2 are suggested by comparison to the protein sequence for A/mem/102/72 Ward,C.W. & Doppeide,T.A. (1980) Virology 103, 37-53). Sequence compared with NBRF data.	
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Query Match	77.5%; Score 860.6; DB 14; Length 1765;	
Best Local Similarity	99.5%; Pred. No. 3e-226;	
Matches	863; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
QY	243	TATGTACTCTGATTTTCGATGCTACCTCCAAATGGAAGCATTTCCCAATGACAGCC 302
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QY	303	CTTCAACAACGTAACAACATGCATATGAGAGATCCCAAGTATGTAAGCAAAAC 362
Db	956	CTTCAACAACGTAACAACATGCATATGAGAGATCCCAAGTATGTAAGCAAAAC 1015
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Db	1016	CCTGAAGTTGGCAACAGGATGGGAATGTACACAGAAACAACATAGAGGCTATTGG 1075
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Db	1076	CGCAATAGCAGGTTTATAGAAATGGTTGGAGGAGATGATGACGTTGGTACGCTTT 1135
QY	483	CAGGATCAAAATTCGAGGGCAGAGACAGCAGATCTTTAAAGCACTCAACGACG 542
Db	1136	CAGGATCAAAATTCGAGGGCAGAGACAGCAGATCTTTAAAGCACTCAACGACG 1195
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QY      903  CGAAGCATTAACAAACCGGTTTCAGATCAAAAGCTTGAAGTGAAGTGAAGTGAAG 962
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Db      1616  CTGATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1675
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RESULT 15
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DEFINITION Influenza A virus segment 4 gene for haemagglutinin, genomic RNA, strain clone 7a (H3N2).
ACCESSION AJ289703.1 GI:11595851
VERSION haemagglutinin; segment 4 gene.
KEYWORDS Influenza A virus (A/PR/8/34 (H1N1) x A/England/939/69 (H3N2))
SOURCE Influenza A virus (A/PR/8/34 (H1N1) x A/England/939/69 (H3N2))
ORGANISM Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses; Influenzavirus A; Influenza A virus.

REFERENCE
AUTHORS 1. Mobis, M.A., Morris, S.J., Smith, H. and Sweet, C.
TITLE Influenza virus-induced apoptosis: a dual role for viral neuraminidase
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1765)
AUTHORS Sweet, C.
TITLE Direct Submission
JOURNAL Submitted (05-JUN-2000) Sweet, C., School of Biosciences, University of Birmingham, Edgbaston, Birmingham, West Midlands, B15 2TT, UNITED KINGDOM

FEATURES
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BASE COUNT 564 a 30. 178 415 g 419 t

ORIGIN

Query Match 77.5%; Score 860.6; DB 14; Length 1765;
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Matches 872; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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QY      279  TGAAGCATTCACCAATGCAAGCCCTTCAAAACGTAACAGATCAATATGAGAGATG 338
Db      932  TGAAGCATTCACCAATGCAAGCCCTTCAAAACGTAACAGATCAATATGAGAGATG 991
QY      339  CCCCAGATGTATTAAGCAAAACACCTGTAAGTGGCAAGGATGGGAATGATACAGA 398
Db      992  CCCCAGATGTATTAAGCAAAACACCTGTAAGTGGCAAGGATGGGAATGATACAGA 1051
QY      399  GAAACAACTAGAGGCGCTATTCGGGCAATAGAGTTCATAGAAAATGTTGGGAGG 458
Db      1052  GAAACAACTAGAGGCGCTATTCGGGCAATAGAGTTCATAGAAAATGTTGGGAGG 1111
QY      459  AATGATAGACGTTGTGACGGTTTCAGGCATCAAAATTTGAGGGCAGACAGACAGC 518
Db      1112  AATGATAGACGTTGTGACGGTTTCAGGCATCAAAATTTGAGGGCAGACAGACAGC 1171
QY      519  AGATCTTAAAGCACTCAAGCAGCATTCGACCAATATATGGGAATTTGAACAGGTA 578
Db      1172  AGATCTTAAAGCACTCAAGCAGCATTCGACCAATATATGGGAATTTGAACAGGTA 1231
QY      579  CGAGAGAGCAAGCAAGAAATTCATCAAAATGGAAGAAATTCGACAGCTAGAGAG 638
Db      1232  CGAGAGAGCAAGCAAGAAATTCATCAAAATGGAAGAAATTCGACAGCTAGAGAG 1291
QY      639  AATTCAGACCTGAGAAATACGTTGAAGCACTAAATAGATCTGCTTACCAATGC 698
Db      1292  AATTCAGACCTGAGAAATACGTTGAAGCACTAAATAGATCTGCTTACCAATGC 1351
QY      699  GGAGCTTCTGCTGCTGAGAAATCAACATATGACACTGACAGCTAGAGAGAGAG 758
Db      1352  GGAGCTTCTGCTGCTGAGAAATCAACATATGACACTGACAGCTAGAGAGAGAG 1411
QY      759  CAAGCTGTTGAAAAACAGGAGCAACAGAGGAAATGCTGAAGAGATGGGCAATGG 818
Db      1412  CAAGCTGTTGAAAAACAGGAGCAACAGAGGAAATGCTGAAGAGATGGGCAATGG 1471
QY      819  TTGCTTCAAAATATACCAAAATGTCAGACGCTTGATAGATCAATCAAGAAATGGT 878
Db      1472  TTGCTTCAAAATATACCAAAATGTCAGACGCTTGATAGATCAATCAAGAAATGGG 1531
QY      879  TTATGACCATGATATATACAGAGAGCAAGCATTAACACCGGTTTCAGATCAAGGT 938
Db      1532  TTATGACCATGATATATACAGAGAGCAAGCATTAACACCGGTTTCAGATCAAGGT 1591

```

OY 939 TGAAGTGAAGTGGTACAAAGACTGATCCTGTGATTTGCTTGGCATATCATGCTT 998
 |||||
 Db 1592 TGAAGTGAAGTGGTACAAAGACTGATCCTGTGATTTGCTTGGCATATCATGCTT 1651
 OY 999 TTTGCTTTGTGTGTTTTCCTGGGGTTCATCATGTGGGCTGCAGAGAGGCAACATTAG 1058
 |||||
 Db 1652 TTTGCTTTGTGTGTTTTCCTGGGGTTCATCATGTGGGCTGCAGAGAGGCAACATTAG 1711
 OY 1059 GTGCAACATTTGCATTTGAGTGTATTAGTAATTAAACACCCCTGTTCT 1109
 |||||
 Db 1712 GTGCAACATTTGCATTTGAGTGTATTAGTAATTAAACACCCCTGTTCT 1762

Search completed: August 10, 2003, 09:14:30
 Job time : 2797.67 secs

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genCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2013, 18:20:24 ; Search time 213.016 Seconds
(without alignments)
14066.412 Million cell updates/sec

Title:	US-09-918-568-57
Perfect score:	1110
Sequence:	1 CTAGAGCAAAACAGGGGATTAAACACACCTTGTTCGTG 1110

scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length:	0
Maximum DB seq length:	2000000000

Maximum Match	100%
Listing first	45 summaries

Database : N_Geneseq_19Jun03:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1110	100.0	1110	15	AA072807	DNA encoding stem
2	866.4	78.1	1777	15	AA072855	Full length H3N2 i
3	833.4	75.1	1765	24	ABA93937	Influenza A/U03om/
4	832	75.0	1764	24	ABA93944	Influenza A/U03om/
5	808.4	72.8	1762	8	AA070642	Sequence encoding
6	787	70.9	1653	24	AA082723	Influenza A/Bangkok
7	774.8	69.8	1793	18	AA059212	Influenza A/Berlin
8	774.8	69.8	1793	20	AA007773	Influenza virus A/

9	774.8	69.8	1793	22	AAO05986	Influenza virus A/
10	768.8	69.3	6477	11	AAO203030	Plasmodium falciparum
11	756.6	68.2	1757	18	AAAT59216	Influenza A/Shandong
12	756.6	68.2	1757	20	AAO007177	Influenza virus A/
13	756.6	68.2	1757	22	AAO095900	Influenza virus A/
14	751.8	67.7	1757	18	AAAT59219	Influenza virus A/
15	751.8	67.7	1757	20	AAO00780	Influenza A/Johannesburg
16	751.8	67.7	1757	22	AAO09593	Influenza virus A/
17	745.4	67.2	1701	19	AAAY49298	Influenza virus A/
18	745.4	67.2	1701	21	AAAY49298	SV strain H3N2
19	645.2	58.1	666	14	AAO473558	Sequence encoding
20	645.2	58.1	666	15	AAO70204	Influenza haemaggl
21	642	57.8	666	14	AAO47359	Sequence encoding
22	642	57.8	666	15	AAO70205	Influenza haemaggl
23	641.4	57.8	918	14	AAO47361	Sequence encoding
24	641.4	57.8	918	15	AAO70190	Sequence encoding
25	631.8	56.9	918	15	AAO70208	Sequence encoding
26	630.2	56.8	670	15	AAO70207	Sequence encoding
27	605.2	54.5	1762	21	AAE50976	Cold-adapted equine
28	603.6	54.4	1762	13	AAO29111	ETV HA (A1/Fontaine
29	603.6	54.4	1762	13	AAO29112	ETV HA (A2/Suffolk
30	602	53.0	1762	21	AAE50975	Wild type equine
31	587.8	53.0	1797	11	AAO04597	Equine haemagglut
32	586	52.8	1788	8	AAAT1067	Sequence encoding
33	582.8	52.5	1698	20	AAAT30211	Sequence of the ha
34	582.8	52.5	1698	21	AAAT47007	Equine Influenza v
35	581.2	52.4	1698	19	AAAY49391	ETV Fontainebleau
36	578	52.1	1698	20	AAAT30213	Sequence of the ha
37	418.4	37.7	690	14	AAO47362	Sequence encoding
38	418.4	37.7	690	15	AAO70209	Sequence encoding
39	418.4	37.7	690	15	AAO70191	Sequence encoding
40	333.6	30.1	2005	21	AAAT5000	Nucleotide sequenc
41	333.6	30.1	4930	21	AAAT5000	Nucleotide sequenc
42	332.8	30.0	4610	21	AAAT5005	Nucleotide sequenc
43	329	29.6	329	15	AAO64661	A/Alachua/2/68 hu
44	329	29.6	329	15	AAO72840	HA gene fragment
45	321	28.9	1711	24	AAAT50113	Recombinant infect
46	320.2	28.8	6802	22	AAAT62468	Modified Influenza

ALIGNMENTS

RESULT 1
AAQ72807

AC AAQ72807;

DT	25-MAR-2003	(updated)
DT	22-JUN-1995	(first entry)

DE DNA encoding stem region of A2/Aichi/2/68 influenza virus.

KV Conserved peptide; stem region; hemagglutinin; HA; H1N1; H2N2;
KW subtype; human; influenza A virus; immunogenic artificial peptide

OS Human influ enza A virus.

EH	Key	Location/Qualifiers
FT		34.1077
FT	CDS	/*tag= a

PN EP621339-A2.

PD 26-OCT-1994 -
xy

PE 20-APR-1994; 94EP-0302819.

PR 20-APR-1993; 93JP-0115216.
PR 16-MAR-1994; 94JP-0070194.

PA (TAKI) TAKARA SHUZO CO LTD.

XX Isegawa Y, Okuno Y, Sasao F, Ueda S;
 XX MPI: 1994-325949/41.
 DR P-PSDB: AAR63591.
 XX
 PT Human influenza-A virus haemagglutinin polypeptide(s) - useful in
 XX Influenza-A vaccine composition
 PS
 XX Claim 17, Page 59: 68pp: English.
 CC This sequence encodes the stem region of the hemagglutinin (HA) molecule
 CC of the A2/Aichi/2/68 strain of human influenza A virus. This antigenic
 CC molecule contains the conserved peptides derived from the stem region
 CC of the H1N1 and H2N2 subtypes of human influenza A virus. Immunogenic
 CC polypeptides such as these are antigenically equivalent to the stem region
 CC of the HA molecule of influenza A virus. This artificial peptide may be
 CC used as a vaccine for prophylaxis of influenza A virus infection.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 1110 BP; 374 A; 216 C; 258 G; 262 T; 0 other;
 Query Match 100.0%; Score 1110; DB 15; Length 1110;
 Best Local Similarity 100.0%; Pred. No. 7.2e-310; Indels 0; Gaps 0;
 Matches 1110; Conservative 0; Mismatches 0;
 QY 1 CTGAGCAAGCAAGCAGGAGTAATCTATTAATCATGAACCATCTTGTGAGCTAC 60
 DB 1 CTGAGCAAGCAAGCAGGAGTAATCTATTAATCATGAACCATCTTGTGAGCTAC 60
 QY 61 ATTTTCTGTGGCTCTCGGCCAAGACCTTCCAGGAATGACACAGCAGCAACGCTG 120
 DB 61 ATTTTCTGTGGCTCTCGGCCAAGACCTTCCAGGAATGACACAGCAGCAACGCTG 120
 QY 121 TGCCGCGGACATCATGCGGTGCGCAAGCAACAGTACTGTAATCAATCATGATGTCAG 180
 DB 121 TGCCGCGGACATCATGCGGTGCGCAAGCAACAGTACTGTAATCAATCATGATGTCAG 180
 QY 181 ATTGAAGTGAATGCTACTGAGTCTAGTCTAGAGCTCCTCAACGGGAAATATGCAAC 240
 DB 181 ATTGAAGTGAATGCTACTGAGTCTAGTCTAGAGCTCCTCAACGGGAAATATGCAAC 240
 QY 241 AATATGATACCTGATTTTCTGATGATGATGATGATGATGATGATGATGATGATG 300
 DB 241 AATATGATACCTGATTTTCTGATGATGATGATGATGATGATGATGATGATGATG 300
 QY 301 CCCCTTCAAAACGCTAAACAGATCAATATGAGATGCGCCCAAGATGTTAAGCAAAAC 360
 DB 301 CCCCTTCAAAACGCTAAACAGATCAATATGAGATGCGCCCAAGATGTTAAGCAAAAC 360
 QY 361 ACCCTGAAGTGGCAACAGGATGCGAATGTCAGAGAAACAACTAGAGCGCTATTC 420
 DB 361 ACCCTGAAGTGGCAACAGGATGCGAATGTCAGAGAAACAACTAGAGCGCTATTC 420
 QY 421 GCGCGAATAGCAGGTTTCAATAGAAAATGTTGGGAGGATGATGACGTTGTACGCT 480
 DB 421 GCGCGAATAGCAGGTTTCAATAGAAAATGTTGGGAGGATGATGACGTTGTACGCT 480
 QY 481 TTCAGGCAATCAAAATTTCTGAGGCGACAGACAAGAGAGATCTTAAAGCACTCAAGA 540
 DB 481 TTCAGGCAATCAAAATTTCTGAGGCGACAGACAAGAGAGATCTTAAAGCACTCAAGA 540
 QY 541 GCCATCGACCAATCAATGAGAAATTTGAACAGGATTAATCGAAGAGCAAGAAATTC 600
 DB 541 GCCATCGACCAATCAATGAGAAATTTGAACAGGATTAATCGAAGAGCAAGAAATTC 600
 QY 601 CATCAAAATCGAAAAGAAATTCACAGAGAGAGAGAAATTCAGAGACTCGAAGAAATAC 660
 DB 601 CATCAAAATCGAAAAGAAATTCACAGAGAGAGAGAAATTCAGAGACTCGAAGAAATAC 660
 QY 661 GTTGAAGACATAAAATAGATCTCTGCTTCAATGCGGAGACTTCTGTGCTCTGGAG 720
 DB 661 GTTGAAGACATAAAATAGATCTCTGCTTCAATGCGGAGACTTCTGTGCTCTGGAG 720

QY 721 AATCAACATCAATGACCTGACTGCTGGAAATGAACAAGCTTTGAAAAACAAG 780
 DB 721 AATCAACATCAATGACCTGACTGCTGGAAATGAACAAGCTTTGAAAAACAAG 780
 QY 781 AGGCAACTGAGGAAATGCTGAGAGATGGGCAATGGTCTTCAAAATATACACAA 840
 DB 781 AGGCAACTGAGGAAATGCTGAGAGATGGGCAATGGTCTTCAAAATATACACAA 840
 QY 841 TGTGACACGCTTGCATGAGATCATGAGAAATGTAATTTGACCATGATGATACAGA 900
 DB 841 TGTGACACGCTTGCATGAGATCATGAGAAATGTAATTTGACCATGATGATACAGA 900
 QY 901 GAGCAAGCAATTAACAAACCGGTTTCAGATCAAGGTTGTAACGATGATACAAA 960
 DB 901 GAGCAAGCAATTAACAAACCGGTTTCAGATCAAGGTTGTAACGATGATACAAA 960
 QY 961 GACTGGATCTGTGATTTCTTTGCCATATCATGCTTTTGTGTTGTTTCTG 1020
 DB 961 GACTGGATCTGTGATTTCTTTGCCATATCATGCTTTTGTGTTGTTTCTG 1020
 QY 1021 GGGTCATCATGTCGCGCTGCGAGAGCAACATTAAGTCACATTTGATTTGAGTG 1080
 DB 1021 GGGTCATCATGTCGCGCTGCGAGAGCAACATTAAGTCACATTTGATTTGAGTG 1080
 QY 1081 TATTAGTAATTAACACCCCTTGTCTG 1110
 DB 1081 TATTAGTAATTAACACCCCTTGTCTG 1110
 RESULT 2
 ID AA072855 standard; cDNA; 1777 BP.
 XX
 AC AA072855;
 XX
 DT 25-MAR-2003 (updated)
 DT 23-JUN-1995 (first entry)
 XX
 DE Full length H3N2 influenza A virus, strain A2/Aichi/2/68 HA gene.
 XX
 KW Conserved peptide: stem region; hemagglutinin; HA; H1N1; H2N2; PCR;
 KW subtype; human; influenza A virus; immunogenic artificial peptide;
 KW antibody; vaccine; infection; polymerase chain reaction; primer;
 KW amplify; C179; region A; region B; ds.
 XX
 OS Influenza A virus.
 XX
 FH Key
 FT CDS
 FT 36..1737
 FT /*tag= a
 FT /product= Full length HA from H3N2 subtype
 FT sig_peptide
 FT 37..84
 FT /*tag= b
 FT /product= Stem region of N-terminal domain
 FT misc_feature
 FT 85..246
 FT /*tag= c
 FT /product= Stem region of C-terminal domain
 FT FT
 FT misc_feature
 FT 904..1734
 FT /*tag= e
 FT /product= Stem region of C-terminal domain
 PN EP621339-A2.
 XX
 PD 26-OCT-1994.
 XX
 PF 20-APR-1994; 94EP-0302819.
 XX
 PR 20-APR-1993; 93JP-0115216.
 PR 16-MAR-1994; 94JP-0070194.
 XX

PA (TAKI) TAKARA SHUZO CO LTD.
 XX
 PI Isegawa Y, Okuno Y, Saito F, Ueda S;
 XX
 DR WPI; 1994-325949/41.
 XX
 DR P-PSDB; AAR63590.
 XX
 PT Human Influenza-A virus haemagglutinin polypeptide(s) - useful in
 PT Influenza-A vaccine composition
 XX
 XX Example 2; Page 54-58; 6fpp; English.
 CC This sequence was amplified using the primer sequences given in
 CC AA07852-54 and represents a cDNA which encodes the full length
 CC hemagglutinin (HA) gene of the H3N2 subtype of human influenza A
 CC virus, strain A2/Alchi/2/68. The full length protein encoded by this
 CC amplified cDNA contains two conserved regions, the A' region, TGRN
 CC and the B region, QINGLR(L/V)IEK. These regions are close to
 CC each other in the stem of the HA molecule and they represent epitopes
 CC which are recognised by the antibody C179. C179 binds to the stem
 CC of the HA molecule and thus inhibits the membrane fusion action
 CC of the HA molecule and neutralises the virus. Polypeptide molecules
 CC which contain the conserved peptide regions, A and B, esp. HA molecules
 CC lacking the globular head region (see also AA072807), are antigenically
 CC equivalent to the stem region of the HA molecule of influenza A virus.
 CC These artificial peptides may be used as vaccines for prophylaxis of
 CC influenza A virus infection.
 CC (updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 XX Sequence 1777 BP; 565 A; 363 C; 420 G; 429 T; 0 other;
 SQ
 Query Match 78.1%; Score 866.4; DB 15; Length 1777;
 Best Local Similarity 99.5%; Pred. No. 1.8e-239;
 Matches 867; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 243 TATGTACCTGATTTCTGAATGATCACTCCAAATGGAAGCATTCCCAATGACAAGCC 302
 DB 903 TATGTACCTGATTTCTGAATGATCACTCCAAATGGAAGCATTCCCAATGACAAGCC 962
 QY 303 CTTTCAAAACGTAAACAAATGACATATGAGCATGCCCAAGTATGTTAAAGCAAAAC 362
 DB 963 CTTTCAAAACGTAAACAAATGACATATGAGCATGCCCAAGTATGTTAAAGCAAAAC 1022
 QY 363 CCTGAAGTTGGCAACATGGATGCGAATGTACAGAGAAACAACATAGAGGCTATTGCG 422
 DB 1023 CCTGAAGTTGGCAACATGGATGCGAATGTACAGAGAAACAACATAGAGGCTATTGCG 1082
 QY 423 CGCAATAGCAGGTTTCATAGAAATGTTGGAGGGAATGATAGACGTTGTTAGCGTTT 482
 DB 1083 CGCAATAGCAGGTTTCATAGAAATGTTGGAGGGAATGATAGACGTTGTTAGCGTTT 1142
 QY 483 CAGGCATCAAAATTCCTTACGGCAGCAGAGCAACAGATCTTAAAGCACTCAAGCAGC 542
 DB 1143 CAGGCATCAAAATTCCTTACGGCAGCAGAGCAACAGATCTTAAAGCACTCAAGCAGC 1202
 QY 543 CATCGACCAATCAATTCGGAATTTGAACAGGTAATCGAAGACAGACGAAATTCACA 602
 DB 1203 CATCGACCAATCAATTCGGAATTTGAACAGGTAATCGAAGACAGACGAAATTCACA 1262
 QY 603 TCAATTCGAAAGGAATTCAGAACTAGAGGAGAAATTCAGAGCCTCGAGAAATACGT 662
 DB 1263 TCAATTCGAAAGGAATTCAGAACTAGAGGAGAAATTCAGAGCCTCGAGAAATACGT 1322
 QY 663 TGAAGACATAAATTCATCTCTGCTTACAAATGCGGAGCTTCTGTGCTCTGGAGAA 722
 DB 1323 TGAAGACATAAATTCATCTCTGCTTACAAATGCGGAGCTTCTGTGCTCTGGAGAA 1382
 QY 723 TCAACATCAATTCAGCTGACTCGGAAATGAACAAGCTGTTGAAAAACAAGAG 782
 DB 1383 TCAACATCAATTCAGCTGACTCGGAAATGAACAAGCTGTTGAAAAACAAGAG 1442
 QY 783 GCAACTGAGGAGAAATTCGAAGAGATGGCAATGGTCTCTCAAAATATACCAAAATG 842
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 1443 GCAACTGAGGAGAAATTCGAAGAGATGGCAATGGTCTCTCAAAATATACCAAAATG 1502
 QY 843 TGACAACGCTTCATGATGATCAATCGAATGCTACTTATGACCATGATGATACAGACA 902
 DB 1503 TGACAACGCTTCATGATGATCAATCGAATGCTACTTATGACCATGATGATACAGACA 1562
 QY 903 CGAAGCATTAACAACACCGGTTTCAGATCAAGGTGTGAACGTGATGATACAAAGA 962
 DB 1563 CGAAGCATTAACAACACCGGTTTCAGATCAAGGTGTGAACGTGATGATACAAAGA 1622
 QY 963 CTGGATCTGTGGATTTCTTTGCCATATCATGCTTTTGTGTTGTTTGTCTGG 1022
 DB 1623 CTGGATCTGTGGATTTCTTTGCCATATCATGCTTTTGTGTTGTTTGTCTGG 1682
 QY 1023 GTTCATCATGTGGCGCTGCGACAGAGCAACATTAGCTCAACATTTGATTTGACTGTA 1082
 DB 1683 GTTCATCATGTGGCGCTGCGACAGAGCAACATTAGCTCAACATTTGATTTGACTGTA 1742
 QY 1083 TTAGTAATTAACAACACCGCTTGTCTG 1110
 DB 1743 TTAGTAATTAACAACACCGCTTGTCTG 1770
 RESULT 3
 ABA93937
 ID ABA93937 standard; DNA; 1765 BP.
 AC ABA93937;
 XX
 XX 07-MAY-2002 (first entry)
 XX
 DE Influenza A/Udorn/72 (H3N2) Strain HA encoding DNA SEQ ID NO:7.
 XX
 XX Influenza A/Udorn/72 (H3N2) strain; Influenzavirus A; diagnosis;
 KW Influenza A virus; genome; gene; ds.
 XX
 XX Influenzavirus A.
 FH
 FT Key Location/Qualifiers
 FT CDS 30..1730
 FT /tag= a
 PR /product= "HA protein"
 XX
 PN MO200200884-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 21-JUN-2001; 2001MO-US19826.
 XX
 PR 23-JUN-2000; 2000US-213650P.
 XX
 PA (AMCY) AMERICAN CYANAMID CO.
 XX
 PI Galarza JM, Latham TE;
 XX
 DR WPI; 2002-139923/18.
 XX
 DR P-PSDB; ABB05767.
 PT Polynucleotide encoding complete sequence of influenza A/Udorn/72 and
 PT polypeptide, useful in diagnosis and for generating new influenza A
 PT variant strains -
 XX
 PS Claim 1; Page 61-64; 103pp; English.
 CC The present invention describes an isolated polynucleotide (1) having
 CC the complete sequence of the Influenza A/Udorn/72 (H3N2) strain in
 CC positive strand, antigenomic message sense. ABA93934 to ABA93944 encode
 CC the Influenza A/Udorn/72 (H3N2) strain proteins given in ABB05764 to
 CC ABB05774 from the present invention. (1) is useful for designing
 CC polymerase chain reaction (PCR) primers for use in a PCR assay to detect
 CC the presence of the corresponding virus segment in a sample or for
 CC designing and selecting peptides for use in an enzyme linked
 CC immunosorbant assay to detect the presence of the corresponding protein

CC produced by that segment in a sample, hence is useful in diagnosis and
 CC may be modified by mutation to generate new influenza A variant strains.
 CC ABA94945 to ABA94039 represent Influenza A/udorn/72 (H3N2) strain
 CC sequencing primers, which are used in an example from the present
 CC invention.

XX Sequence 1765 BP; 568 A; 355 C; 414 G; 428 T; 0 other;

Query Match 75.1%; Score 833.4; DB 24; Length 1765;

Best Local Similarity 97.6%; Pred. No. 66-230;

Matches 846; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

243 TATTGATACCTGTTATTTCTGAATGATCATCTCCAAATGAGACATTTCCAAATGACAGCC 302
 DB TATTGACACCTCATTTCTTGATGATCATCTCCAAATGAGACATTTCCAAATGACAGCC 955
 303 CTTTCAAAACGTTAAACAGATCATATGAGACATGCCCCCAAGTATGTTAAGCAAAACAC 362
 DB CTTTCAAAACGTTAAACAGATCATATGAGACATGCCCCCAAGTATGTTAAGCAAAACAC 1015
 363 CTTGAAAGTTGGCAGCAGGATCGGAAATGATGACAGAGAAACAACAGTACAGGCTATTGG 422
 DB CTTGAAAGTTGGCAGCAGGATCGGAAATGATGACAGAGAAACAACAGTACAGGCTATTGG 1016
 423 CGCAATAGCAGGTTTCATAGAAATGTTGGAGGGAATGATAGACGTTGGTACGCTTT 482
 DB CGCAATAGCAGGTTTCATAGAAATGTTGGAGGGAATGATAGACGTTGGTACGCTTT 11076
 483 CAGGATCAAAATTTCTGAGGGCAGACAGCAACAGCAGATCTTTAAAGACATCAAGCAGC 542
 DB CAGGATCAAAATTTCTGAGGGCAGACAGCAACAGCAGATCTTTAAAGACATCAAGCAGC 11336
 543 CATCGACCAATCAATGGGAAATTTGAACAGGTAATCGAGAGCAAGCAAGAAATTCACA 602
 DB CATCGACCAATCAATGGGAAATTTGAACAGGTAATCGAGAGCAAGCAAGAAATTCACA 1196
 603 TCAATTCGAAAAGGAATTTCTGAGAGTAGAAGGGAATTTGAGACCTCGAGAAATACGT 662
 DB TCAATTCGAAAAGGAATTTCTGAGAGTAGAAGGGAATTTGAGACCTCGAGAAATACGT 1256
 663 TGAAGACACTAAATAGATCTGTGCTTACAAATCGGAGCTTCTTGCTCTGAGAGA 722
 DB TGAAGACACTAAATAGATCTGTGCTTACAAATCGGAGCTTCTTGCTCTGAGAGA 1316
 723 TCAACATCAATTTGACTGACTGACTCGGAATGAAACAAGCTGTTGAAAAACAAGAG 782
 DB TCAACATCAATTTGACTGACTGACTCGGAATGAAACAAGCTGTTGAAAAACAAGAG 1376
 783 GCAACTGAGGAAATGCTGAGAGATGGGCAATGCTTCAAAATATACCAAAATG 842
 DB GCAACTGAGGAAATGCTGAGAGATGGGCAATGCTTCAAAATATACCAAAATG 1436
 843 TGACAAGCTTGACATGAGTCAATGAGAAATGCTTATGACCTGATGATGATACAGAGA 902
 DB TGACAAGCTTGACATGAGTCAATGAGAAATGCTTATGACCTGATGATGATACAGAGA 1496
 903 CGAAGCATTAACAACCGGTTTCAGATCAAAAGTTTGAACAGAGTCTGATACAAAGA 962
 DB CGAAGCATTAACAACCGGTTTCAGATCAAAAGTTTGAACAGAGTCTGATACAAAGA 1556
 963 CTGATCTCTGATGATTTCTTTGCCATATCATGCTTTTGTCTTGTGTTCTCTGG 1022
 DB CTGATCTCTGATGATTTCTTTGCCATATCATGCTTTTGTCTTGTGTTCTCTGG 1616
 1023 GTTATCATGTTGGGCTCGCCAGAGAGCAACATTAGTGCAACATTTGATGAGTGA 1082
 DB GTTATCATGTTGGGCTCGCCAGAGAGCAACATTAGTGCAACATTTGATGAGTGA 1735
 1083 TTACTAATTAACAACCCCTGTTCT 1109
 DB TTACTAATTAACAACCCCTGTTCT 1736
 1736 TTACTAATTAACAACCCCTGTTCT 1762

RESULT 4
 ID ABA93944
 XX ABA93944 standard; DNA; 1764 BP.
 AC ABA93944;

DT 07-MAY-2002 (first entry)

DE Influenza A/udorn/72 (H3N2) Strain HA encoding DNA SEQ ID NO:21.

KW Influenza A/udorn/72 (H3N2) Strain; Influenzavirus A; diagnosis;

KW Influenza A virus; genome; gene; ds.

OS Influenzavirus A.

FH Key Location/Qualifiers

FT CDS 30..1730 /tag= a

FT /product= "HA protein"

PN MO200200884-A2.

PD 03-JAN-2002.

PF 21-JUN-2001; 2001WO-US19826.

PR 23-JUN-2000; 2000US-213650P.

PA (AMCY) AMERICAN CYANAMID CO.

PI Galarza JM, Latham TE;

PI MPI: 2002-139923/18.

DR P-PSDB; ABB05774.

PT Polynucleotide encoding complete sequence of influenza A/udorn/72 and

PT polypeptide, useful in diagnosis and for generating new influenza A

PT variant strains

PS Claim 1; Page 80-83; 103pp; English.

CC The present invention describes an isolated polynucleotide (I) having
 CC the complete sequence of the influenza A/udorn/72 (H3N2) strain in
 CC positive strand, antigenomic message sense. ABA93944 to ABA93944 encode
 CC the influenza A/udorn/72 (H3N2) strain proteins given in ABB05764 to
 CC ABB05774 from the present invention. (I) is useful for designing
 CC polymerase chain reaction (PCR) primers for use in a PCR assay to detect
 CC the presence of the corresponding virus segment in a sample or for
 CC designing and selecting peptides for use in an enzyme linked
 CC immunosorbent assay to detect the presence of the corresponding protein
 CC produced by that segment in a sample, hence is useful in diagnosis and
 CC may be modified by mutation to generate new influenza A variant strains.
 CC ABA94945 to ABA94039 represent Influenza A/udorn/72 (H3N2) strain
 CC sequencing primers, which are used in an example from the present
 CC invention.

CC Sequence 1764 BP; 568 A; 355 C; 414 G; 427 T; 0 other;

Query Match 75.0%; Score 832; DB 24; Length 1764;

Best Local Similarity 97.7%; Pred. No. 1.5e-229;

Matches 844; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

243 TATTGATACCTGTTATTTCTGAATGATCATCTCCAAATGAGACATTTCCAAATGACAGCC 302
 DB TATTGACACCTCATTTCTTGATGATCATCTCCAAATGAGACATTTCCAAATGACAGCC 955
 303 CTTTCAAAACGTTAAACAGATCATATGAGACATGCCCCCAAGTATGTTAAGCAAAACAC 362
 DB CTTTCAAAACGTTAAACAGATCATATGAGACATGCCCCCAAGTATGTTAAGCAAAACAC 1015
 956 CTTTCAAAACGTTAAACAGATCATATGAGACATGCCCCCAAGTATGTTAAGCAAAACAC 1015
 363 CTTGAAAGTTGGCAGCAGGATCGGAAATGATGACAGAGAAACAACAGTACAGGCTATTGG 422
 DB CTTGAAAGTTGGCAGCAGGATCGGAAATGATGACAGAGAAACAACAGTACAGGCTATTGG 1016
 1016 CTTGAAAGTTGGCAGCAGGATCGGAAATGATGACAGAGAAACAACAGTACAGGCTATTGG 1075

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QY 423 CGCAATAGAGGTTTATAGAAAATGGTTGGAGGGAATGATAGACGTTGTACGTTT 482
    |||||
Db 1076 CGCAATAGAGGTTTATAGAAAATGGTTGGAGGGAATGATAGACGTTGTACGTTT 1135
QY 483 CAGGCATCAAAATTCGAGGCAACAGACAGACAGATCTTTAAAGCACTCAAGCAC 542
    |||||
Db 1136 CAGGCATCAAAATTCGAGGCAACAGACAGACAGATCTTTAAAGCACTCAAGCAC 1195
QY 543 CATCGACCAATCAATGGGAAATTTGAACGGGTATCGAAGACAGACAGAAATTCGA 602
    |||||
Db 1196 CATCGACCAATCAATGGGAAATTTGAACGGGTATCGAAGACAGACAGAAATTCGA 1255
QY 603 TCAAAATCGAAAAGATTTCTCAGAAATAGAGGAGAAATTCAGACCTCGAGAAATACG 662
    |||||
Db 1256 TCAAAATCGAAAAGATTTCTCAGAAATAGAGGAGAAATTCAGACCTCGAGAAATACG 1315
QY 663 TGAAGACATTAATATGATCTCTGGTCTTACAATCGGAGCTTCTTGTGCTCTGGAGAA 722
    |||||
Db 1316 TGAAGACATTAATATGATCTCTGGTCTTACAATCGGAGCTTCTTGTGCTCTGGAGAA 1375
QY 723 TCAACATACAAATGACCTGACTCGGAAATGAACAAGCTGTTGAAAAACAAGAG 782
    |||||
Db 1376 CCAACATACAAATGATCTGACTCGGAAATGAACAAGCTGTTGAAAAACAAGAG 1435
QY 783 GCAACTGAGGAAAATBCTGAAGAGATGGGCAATGGTCTTCAAAATATACCAAAATG 842
    |||||
Db 1436 GCAACTGAGGAAAATBCTGAAGAGATGGGCAATGGTCTTCAAAATATACCAAAATG 1495
QY 843 TGACAAAGCTTGCATATGATCAATCAAGAAATGATCTTATGACCATGATGTATACAGACA 902
    |||||
Db 1496 TGACAAAGCTTGCATATGATCAATCAAGAAATGATCTTATGACCATGATGTATACAGACA 1555
QY 903 CGAAGCATTAACAACBGGTTTCAGATCAAGAGTGTGAATGAAGTGGATGATACAAAGA 962
    |||||
Db 1556 CGAAGCATTAACAACBGGTTTCAGATCAAGAGTGTGAATGAAGTGGATGATACAAAGA 1615
QY 963 CTGGAATCCTGTGGATTTCCTTGGCCATATCATGCTTTTGTGTTGTGCTGGG 1022
    |||||
Db 1616 CTGGAATCCTGTGGATTTCCTTGGCCATATCATGCTTTTGTGTTGTGCTGGG 1675
QY 1023 GTTCATCATAGTGGCCCGCCAGAGAGGCAACATTAAGTGCACATTTGATTTGAGTGA 1082
    |||||
Db 1676 GTTCATCATAGTGGCCCGCCAGAGAGGCAACATTAAGTGCACATTTGATTTGAGTGA 1735
QY 1083 TTAGTAATTAATAACACCTGTTT 1106
    |||||
Db 1736 TTAGTAATTAATAACACCTGTTT 1759

RESULT 5
AAN70642
ID AAN70642 standard: cDNA: 1762 BP.
XX
AC AAN70642:
XX
DT 25-MAR-2003 (updated)
DT 29-APR-1991 (first entry)
XX
DE Sequence encoding influenza HA protein.
XX
KW HA; vaccine: ds.
XX
OS Influenza/A/Nilgata 10218.
XX
PN JP62051992-A.
XX
PD 06-MAR-1987.
XX
PF 30-AUG-1985; 85JP-0192915.
XX
PR 30-AUG-1985; 85JP-0192915.
XX
```

```
PA (KAGA ) KAGAKU KASEI RYOHO KENKYUSHO.
XX
XX WPI; 1987-104909/15.
XX
PT Recombinant plasmid - combines influenza virus gene and
PT transformation enzyme and can be used for prepn. of influenza
PT virus protein
XX
PS Disclosure; Fig 3; 14pp; Japanese.
XX
CC Sequence may be inserted into a plasmid under the control of a
CC phosphatase promoter, and used to transfer an E.coli expression
CC system. The HA protein product may be used as vaccine against
CC influenza viral infection.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1762 BP; 579 A; 359 C; 404 G; 420 T; 0 other:

Query Match 72.8%; Score 808.4; DB 8; Length 1762;
Best Local Similarity 96.7%; Pred. No. 9,9e-223;
Matches 837; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

QY 244 ATTGATACCTGATTTTCTAATGATCATCTCCAAATGAGAGATTTCCCATGACAGCCC 303
    |||||
Db 897 ATTGGCACCCTGCAGTTCGAATGCATCACTCCAAATGAGAGATTTCCCATGACAGCCC 956
QY 304 TTTCAAAACGTAAACAGATCATATGAGAGATGCGCCCAAGATGTTAAGCAAAACACC 363
    |||||
Db 957 TTTCAAAACGTAAACAGATCATATGAGAGATGCGCCCAAGATGTTAAGCAAAACACT 1016
QY 364 CTGAAGTTGGCAACAGGATGCGGAATGTACAGAGAAAACAACTAGAGGCTATTTCGCC 423
    |||||
Db 1017 CTGAAGTTGGCAACAGGATGCGGAATGTACAGAGAAAACAACTAGAGGCTATTTCGCC 1076
QY 424 GCAATAGCAGGTTTTCATATAAAATGTTGGAGGAAATATAGAGGTTGTACGTTTC 483
    |||||
Db 1077 GCAATAGCAGGTTTTCATATAAAATGTTGGAGGAAATATAGAGGTTGTACGTTTC 1136
QY 484 AGGCATCAAAATTTGAGGGGACAGAGACAGAGCATCTTAAAGCACTCAAGCAGCC 543
    |||||
Db 1137 AGGCATCAAAATTTGAGGGGACAGAGACAGAGCATCTTAAAGCACTCAAGCAGCC 1196
QY 544 ATCGACCAAAATGAGGAAATTTGAACAGGATTAATGAGAGAGCAAGCAGAAATTCAT 603
    |||||
Db 1197 ATCGACCAAAATGAGGAAATTTGAACAGGATTAATGAGAGAGCAAGCAGAAATTCAT 1256
QY 604 CAAATCGAAAAGAAATTCACAGAAATGAGAGGAAATTCAGAGCTCGAGAAATACGTT 663
    |||||
Db 1257 CAAATCGAAAAGAAATTCACAGAAATGAGAGGAAATTCAGAGCTCGAGAAATACGTT 1316
QY 664 GAGACACTAAATATGATCTGTGCTTTCATATGGGAGCTTGTGCTGTGGAGAT 723
    |||||
Db 1317 GAGACACTAAATATGATCTGTGCTTTCATATGGGAGCTTGTGCTGTGGAGAT 1376
QY 724 CAACATACAAATGACCTGACTGACTCGGAAATGAACAAGCTTTGAAAAACAAGAGAG 783
    |||||
Db 1377 CAACATACAAATGACCTGACTGACTCGGAAATGAACAAGCTTTGAAAAACAAGAGAG 1436
QY 784 CAACTGAGGAAAATGCTGAGAGATGGGCAATGTTGCTTAAATATATACCAAAATGT 843
    |||||
Db 1437 CAACTGAGGAAAATGCTGAGAGATGGGCAATGTTGCTTAAATATATACCAAAATGT 1496
QY 844 GACAAGCGCTTGATGAGTCAATCGAATGATGTTATGACATGATGATATACAGAGAC 903
    |||||
Db 1497 GACAAGCGCTTGATGAGTCAATCGAATGATGTTATGACATGATGATATACAGAGAC 1556
QY 904 GAAGCATTAACAACCGGTTTCAGATCAAAAGCTTTGAACAGTCTGATGATCAACAAGAC 963
    |||||
Db 1557 GAAGCATTAACAACCGGTTTCAGATCAAAAGCTTTGAACAGTCTGATGATCAACAAGAC 1616
QY 964 TGGATCCTGTGATTTCTTGGCCATATACGCTTTTGTGTTGTGTTGCTGGGG 1023
    |||||
Db 1617 TGGATCCTGTGATTTCTTGGCCATATACGCTTTTGTGTTGTGTTGCTGGGG 1676
```

OY 1024 TTCAATCATGTGGCCCTGCAGAGCAACATTAGTGCATTTGAGTAT 1083
 |||||||
 Db 1677 TTCAATCATGTGGCCCTGCAGAGCAACATTAGTGCATTTGAGTAT 1736
 |||||||
 OY 1084 TAGTAATTAATAAACACCCCTTTGTTCT 1109
 |||||||
 Db 1737 --TAATTAATAAACACCCCTGTTCT 1759
 |||||||
 RESULT 6
 ABQ82723
 ID ABQ82723 standard; cDNA; 1653 BP.
 XX
 AC ABQ82723;
 XX
 DT 07-JAN-2003 (first entry)
 XX
 DE Influenza A/Bangkok/1/79(H3N2), haemagglutinin encoding cDNA.
 XX
 KW Influenza: Influenza A virus; pathogenicity: RNA viral disease;
 KM viral infection; selenium; vaccine; virulence; anti-HIV; gene; ss.
 XX
 OS Influenza A virus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1653
 FT /tag= a
 FT /partial
 FT /product= "haemagglutinin protein"
 FT mat_peptide 1..984
 FT /tag= b
 FT /product= "ha1 chain"
 FT mat_peptide 984..1650
 FT /tag= c
 FT /product= "ha2 chain"
 FT
 PN WO200278717-A2.
 PD 10-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-EP03025.
 XX
 PR 28-MAR-2001; 2001US-0819387.
 XX
 PA (NEST) SOC PROD NESTLE SA.
 PA (UNNC-) UNIV NORTH CAROLINA.
 XX
 PI Beck M, German B, Levander O, Van Dael P;
 XX
 DR WPI: 2002-759948/82.
 DR P-PSDB; ABP53894.
 XX
 PT Treatment of influenza or reducing the risk of contracting influenza
 PT involves administering selenium to an individual
 XX
 PS Example 1; Page -: 31pp: English.
 XX
 CC The present invention describes a method for treating influenza or
 CC reducing the risk of contracting influenza, which involves administering
 CC selenium to an individual. Also described is a method for enhancing the
 CC efficacy of a viral vaccine by administering an antioxidant, preferably
 CC selenium, to an individual receiving the viral vaccine. The method can
 CC be used for treating influenza, for reducing the risk of contracting
 CC influenza, and for enhancing the efficacy of viral vaccine (preferably
 CC influenza vaccine) in an infant, elderly, a patient or a pet. It can
 CC also be used for treating virus such as coxsackie and HIV virus. The
 CC method provides an improved treatment for viral infection, by reducing
 CC in vivo mutations of the RNA virus. The method also improves a vaccine
 CC used to prevent transmission of an RNA viral disease. The present
 CC sequence encodes the haemagglutinin protein from influenza A/Bangkok/1/79
 CC (H3N2).
 CC N.B. The present sequence is not given in the specification, but is taken

CC from the Genbank accession number J02092, as specified on page 7.
 XX
 SQ Sequence 1653 BP; 540 A; 330 C; 389 G; 386 T; 8 other:
 Query Match 70.9%; Score 787; DB 24; Length 1653;
 Best Local Similarity 96.0%; Pred. No. 1.4e-216;
 Matches 802; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
 OY 243 TATTGATACCTGCTATTCTGATGATCATCTCCAAATGAGCAATTCCTCAATGACAGCC 302
 |||||
 Db 819 TATTGGACCTGCACTGCTGATGATCATCTCCAAATGAGCAATTCCTCAATGACAGCC 878
 |||||
 OY 303 CTTTCAAAACGTAACAGATCACATATGATGAGCCGCCCAAGATGTATTAAGCAAAACAC 362
 |||||
 Db 879 CTNTCAAAACGTAACAGATCACATATGATGAGCCGATGTCCTCAAGTATGTTAAGCAAAACAC 938
 |||||
 OY 363 CCTGAAGTTGGCAGACAGGATGCCGAATGTACAGAGAAACAGCTAGAGCCCTATTCCG 422
 |||||
 Db 939 TCTGAAGTTGGCAGACAGGATGCCGAATGTACAGAGAAACAGCTAGAGCCATATTCGG 998
 |||||
 OY 423 CGCAATACAGGTTTCATAGAAATGCTGGGAGGGAATGATAGACGGTTGTCAGGTTT 482
 |||||
 Db 999 CGCAATACAGGTTTCATAGAAATGCTGGGAGGGAATGATAGACGGTTGTCAGGTTT 1058
 |||||
 OY 483 CAGGCATCAAAATTCCTGAGGCGACAGCAAGCAGCATCTTAAAGCAGCTCAAGCAGC 542
 |||||
 Db 1059 CAGGCATCAAAATTCCTGAGGCGACAGCAAGCAGCATCTTAAAGCAGCTCAAGCAGC 1118
 |||||
 OY 543 CATCGACCAAAATCAATGGGAAATTTGAACAGGGTATCGAGAGAGCAAGCAAGCAAAATCCA 602
 |||||
 Db 1119 AATCGACCAAAATCAATGGGAAATTTGAATAGGTTATCGAGAGAGCAAGCAAGCAAAATCCA 1178
 |||||
 OY 603 TCAATGCAAAAGGATCTCAGAAAGTGAAGGAGGAATTCAGACCTCGAGAAATACGT 662
 |||||
 Db 1179 TCAATGCAAAAGGATCTCAGAAAGTGAAGGAGGAATTCAGACCTCGAGAAATACGT 1238
 |||||
 OY 663 TGAAGACACTAAATAGATCTCTGCTCTTACAAATGCGAGCTTCTGCTCGTGAGAA 722
 |||||
 Db 1239 TGAAGACACTAAATAGATCTCTGCTCTTACAAAGCGGAGCTTCTGCTCGTGAGAA 1298
 |||||
 OY 723 TCAATATCAATTTGACTGACTGACTCGGAATATCAACAGCTGTTTAAAAAACAGAG 782
 |||||
 Db 1299 CCAACATCAATTTGACTGACTGACTCGGAATATCAACAGCTGTTTAAAAAACAGAG 1358
 |||||
 OY 783 GCAACTGAGGGAATGCTGGAAGATGGGCAATGTTGCTCAAAATATACCACAATG 842
 |||||
 Db 1359 GCAACTGAGGGAATGCTGGAAGATGGGCAATGTTGCTCAAAATATACCACAATG 1418
 |||||
 OY 843 TGACAACGCTTGCAATAGATCAATCAGAAATGTTACTTATGACCATGATATATACAGAGA 902
 |||||
 Db 1419 TGACAATGCTTGCAATAGATCAATCAGAAATGTTACTTATGACCATGATATATACAGAGA 1478
 |||||
 OY 903 CGAAGCATTAATAACACCGGTTTCAGATCAAAAGTGTGAACCTGAGTCTGAGATCAAAAGA 962
 |||||
 Db 1479 CGAAGCATTAATAACACCGGTTTCAGATCAAAAGTGTGAACCTGAGTCTGAGATCAAAAGA 1538
 |||||
 OY 963 CTGATCTCTGCAATTCCTGCTTGCAATATGATGTTTCTGTTGCTGTTGCTGCGG 1022
 |||||
 Db 1539 CTGATCTCTGCAATTCCTGCTTGCAATATGATGTTTCTGTTGCTGTTGCTGCGG 1598
 |||||
 OY 1023 GTTCATCATGTGGCCCTGCAGAGCAACATTAGTGCATTTGAGTAT 1077
 |||||
 Db 1599 GTTCATCATGTNNCCCTGCCAAAGGCAACATTAGTGCATTTGAGTAT 1653
 |||||
 RESULT 7
 AAT59212
 ID AAT59212 standard; DNA; 1793 BP.
 XX
 AC AAT59212;
 XX
 DT 25-MAR-2003 (updated)
 DT 19-AUG-1997 (first entry)

DE	Influenza A/Beijing/32/92	recombinant haemagglutinin gene.
XX		
KM	primer: PCR; polymerase chain reaction; universal; amplify: HA;	
KM	haemagglutinin; recombinant production; baculovirus expression system;	
KW	vaccine; insect cell culture; ss.	
XX		
OS	Synthetic.	
XX		
EH	Key	Location/Qualifiers
FT	misc_signal	1..18
FT		/*tag= a
FT		/note= "polyhedrin mRNA leader (partial)"
FT	CDS	19..1731
FT		/*tag= b
FT	sig_peptide	19..72
FT		/*tag= c
FT		/note= "AcNPV 61k protein signal peptide"
FT	mat_peptide	73..1728
FT		/*tag= d
FT		/note= "Coding region for mature rHA"
FT	misc_signal	1783..1793
FT		/*tag= e
FT		/note= "universal translation termination signal"
XX		
PN	WO9637624-A1.	
XX		
PD	28-NOV-1996.	
XX		
PF	26-MAY-1995;	95WO-US06750.
XX		
PR	26-MAY-1995;	95WO-US06750.
XX		
PA	(MICR-) MICROGENESYS INC.	
PA	(MGPM-) MG-PMC LLC.	
XX		
PI	Smith GE, Volovitz F, Wilkinson BE, Voznesensky AI, Hackett CS;	
XX		
DR	WPI: 1997-021228/02.	
DR	P-PSDB; AAM01669.	
XX		
PT	Recombinant influenza haemagglutinin produced in baculovirus system	
PT	- avoids problems of growing virus in eggs and produces stable,	
PT	un-cleaved protein useful in vaccines	
XX		
PS	Example 3; Page 68-69; 1(77pp; English.	
XX		
CC	Recombinant influenza haemagglutinin (HA) expressed in a	
CC	baculovirus expression system in cultured insect cells, allows vaccine	
CC	production without the need to grow virus in eggs. A purer, less	
CC	allergenic product is obtained and antigen drift caused by passages	
CC	through eggs is avoided. There is no need for viral inactivation or	
CC	organic solvent extr. of viral membrane components and vaccines can be	
CC	prepd. rapidly and cost effectively from primary sources of infection.	
CC	Recombinant HA is more stable (esp. for B strains) than HA1/HA2 complexes	
CC	and maintain correct folding during purification and storage. The present	
CC	sequence encodes the 5' end sequence of the HA gene for influenza	
CC	A/Beijing/32/93 (sequence range 1-481). The 61k signal peptide for	
CC	baculovirus expression and the polyhedrin promoter are included in the	
CC	vector.	
XX	(Updated on 25-MAR-2003 to correct PI field.)	
XX		
SQ	Sequence 1793 BP; 593 A; 359 C; 408 G; 433 T; 0 other;	
XX		
Query Match	69.8%; Score 774.8; DB 18; Length 1793;	
Best Local Similarity	94.8%; Pred. No. 5e-213;	
Matches	816; Conservative	0; Mismatches 47; Indels 3; Gaps 1
QY	244 ATGTACACTCTATTTCTGATGCACTCACTCCAAATGAGACATCCCAATGACAAGCCC	303
Db	898 ATGTGACACCTGACATCTGATGCACTCACTCCAAATGAGACATTCCTCCATGACAACCT	957
QY	304 TTTCAAAACGTAAACAGATCAATATGAGAGACAGCCCAAGTATGTTAAGCAAAAACAC	363

[illegible]

FT mat.peptide 73..1728 /tag= /product= "Influenza virus A/Beijing/32/92 mature
FT HA protein 1783..1713 /tag= /note= "Universal translation termination signal"
FT misc_signal 1783..1713 /tag= /note= "Universal translation termination signal"
FT FT
XX US6245532-B1.
XX 12-JUN-2001.
XX 09-OCT-1998; 9805-0169427.
XX 30-MAY-1995; 9505-045348.
XX 13-SEP-1993; 9305-0120407.
XX (PROT-) PROTEIN SCI CORP.
XX Smith GE, Volovitz F, Wilkinson BE, Voznesensky AI, Hackett CS;
XX WPI: 2001-407272/43.
XX P-PSDB: AAE04951.
XX
XX Expressing a protein e.g. recombinant influenza virus haemagglutinin
XX PT comprising a vector encoding a polypeptide comprising a
XX baculovirus signal peptide and a baculovirus expression system is
XX PT useful as a multivalent influenza vaccine -
XX
XX Claim 5; Column 35-38; 51bp; English.
XX
XX The present invention relates to a method for expressing an exogenous
XX protein in a baculovirus expression system which comprises using a vector
XX encoding a polypeptide comprising a baculovirus signal peptide operably
XX linked to a heterologous amino acid sequence. The method is especially
XX useful for preparing a protein which may be used to make a multivalent
XX influenza vaccine based on a mixture of recombinant haemagglutinin
XX (HA) antigens cloned from influenza viruses having epidemic potential.
XX CC The recombinant haemagglutinin proteins are full length,
XX CC uncleaved (HA0) glycoproteins including both the HA1 and HA2 subunits
XX CC (HA0) purified under non-denaturing conditions. The use of recombinant
XX CC DNA (rDNA) technology to produce influenza vaccine offers several
XX CC advantages, e.g., a recombinant DNA influenza vaccine can be produced
XX CC under safer and more stringently controlled conditions; propagation with
XX CC infectious influenza in eggs is not required; recombinant haemagglutinin
XX CC (rHA) protein can be more highly purified; purification procedures for
XX CC rHA do not have to include virus inactivation or organic extraction of
XX CC viral membrane components; production of HA via rDNA technology provides
XX CC an opportunity to avoid the genetic heterogeneity which occurs during
XX CC the adaptation and passage through eggs, which should make it possible to
XX CC better match vaccine strains with influenza epidemic strains, resulting in
XX CC improved efficacy. The present sequence is recombinant haemagglutinin
XX CC (rHA) DNA comprising Autographa californica Nuclear Polyhedrosis Virus
XX CC (AcNPV) 61k gene partial polyhedrin promoter and signal sequence linked
XX CC to Influenza virus A/Beijing/32/92 mature HA coding region.
XX
XX SO Sequence 1793 BP; 593 A; 359 C; 408 G; 433 T; 0 other:
XX
XX Query Match 69.8%; Score 774.8; DB 22; Length 1793;
XX Best Local Similarity 94.2%; Pred. No. 5e-213;
XX Matches 816; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

QY 424 GCATAGCAGGTTTCATAGAAAATGGTTGGAGGAGATGATGACGGTTGTCAGGTTTC 483
DB 1078 GCATCGCAGGTTTCATAGAAAATGGTTGGAGGAGATGATGACGGTTGTCAGGTTTC 1137
QY 484 AGGCATCAAAATTCGTAGGGGACAGGACAGCAGCAGATCTTAAAGCAGCTCAAGCAGCC 543
DB 1138 AGGCATCAAAATTCGTAGGGGACAGGACAGCAGCAGATCTTAAAGCAGCTCAAGCAGCA 1197
QY 544 ATGACCAAAATTCATGAGGAAATGAAACAGGATATGAGAGAGCAGAAACAGAAATTCAT 603
DB 1198 ATGACCAAAATTCATGAGGAAATGAAACAGGATATGAGAGAGCAGAAACAGAAATTCAT 1257
QY 604 CAATCGAAAAGCAATTCAGAGAGATGAGAGAGATTCAGAGCCTCGAATATTCGT 663
DB 1258 CAATCGAAAAGCAATTCAGAGAGATGAGAGAGATTCAGAGCCTCGAATATTCGT 1317
QY 664 GAAGACATTAATATAGATCTCTGCTTACAAATGCGAGCTTCTGCTCGAGAAAT 723
DB 1318 GAAGACATTAATATAGATCTCTGCTTACAAATGCGAGCTTCTGCTCGAGAAAT 1377
QY 724 CAACATACAAATTCATGCTGACTGCTCGAATATGAAAGCTGTTGAAAAACAGAGAG 783
DB 1378 CAACATACAAATTCATGCTGACTGCTCGAATATGAAAGCTGTTGAAAAACAGAGAG 1437
QY 784 CAACATGAGGAAAATGCTGAGAGATGGGCAATGTTGCTTCAAAATATCCCAAAATGT 843
DB 1438 CAACATGAGGAAAATGCTGAGAGATGGGCAATGTTGCTTCAAAATATCCCAAAATGT 1497
QY 844 GACAAAGCTTGCATAGATCAATCAGAAATGATGACTTATGACCATGATATACAGAGAC 903
DB 1498 GACAAAGCTTGCATAGATCAATCAGAAATGATGACTTATGACCATGATATACAGAGAC 1557
QY 904 GAAGCATTAACACAGCGTTTCATGATCAAAAGCTTGAAGTCTGATCAAAAGAC 963
DB 1558 GAAGCATTAACACAGCGTTTCATGATCAAAAGCTTGAAGTCTGATCAAAAGAC 1617
QY 964 TGATCTGCTGATGATTCCTTGCATATATGCTTTTGTGTTGTTGCTGGGG 1023
DB 1618 TGATCTGCTGATGATTCCTTGCATATATGCTTTTGTGTTGTTGCTGGGG 1677
QY 1024 TTGATCATGTGGGCTGCCAGAGAGCAACATTAGTGCACATTTGATGAGTAT 1083
DB 1678 TTGATCATGTGGGCTGCCAGAGAGCAACATTAGTGCACATTTGATGAGTAT 1737
QY 1084 TAGTATTTAAACACCCCTTGTTC 1109
DB 1738 --TAATTTAAACACCCCTTGTTC 1760
RESULT 10
AA002030
ID AA002030 standard; DNA: 6477 BP.
XX
XX AA002030;
XX
XX DT 09-JAN-2003 (updated)
XX DT 18-JUL-1989 (first entry)
XX
XX DE Plasmid pinf 4-49.
XX
XX XX
XX KM Fusion proteins; gram negative outer membrane protein A; vaccines;
XX KW Influenza; foot and mouth disease; ss.
XX
XX OS Synthetic.
XX
XX XX
XX key Location/Qualifiers
XX FH 392..2314
XX FT CDS /tag= a
XX FT /label=gram -ve outer membrane protein A
XX FT -10-signal 42..48
XX FT /tag= b
XX FT /label=lac promoter

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FT -35_signal 20..25
FT /label= c
FT /label= lac promoter
FT misc_feature 945..962
FT /tag= d
FT /label= polylinker
XX EP355737-A.
XX 28-FEB-1990.
XX 18-AUG-1989; 89EP-0115263.
XX 24-AUG-1988; 88DE-3828666.
XX (BEHW ) BEHRINGWERKE AG.
XX Hobom G, Pistor S, Arnold N;
XX WPI; 1990-060498/09.
XX
XX Fusion proteins contg. Gram negative outer membrane protein A and immuno-
XX genetic component, useful as vaccines, and cells expressing them, useful as
XX live vaccines.
XX
XX Disclosure; page 11-15; 21pp; German.
XX
XX This plasmid is constructed by inserting a hybrid gram -ve outer membrane
XX protein A (comp A) gene into plasmid pBK236 forming pHS 56. This has a
XX fragment replaced by an 18bp polylinker resulting in plasmids pHS 64 and
XX pHS 164, the only difference being the presence of an improved promoter/
XX operator region from pBK 509 in latter. A cDNA sequence encoding human
XX Influenza H3 haemagglutinin (IHA) can be inserted in polylinker region
XX forming plasmids pIntf 4-6 or pIntf 4-39 respectively. The replacement of
XX IHA region of pIntf 4-39 with an oligonucleotide linker results in this
XX expression plasmid (pIntf 4-49) into which eg the alpha toxin gene from S.
XX aureus can be inserted and eg E.coli cells transformed.
XX The resulting expressed alpha toxin is produced as a fusion protein.
XX Such fusion proteins are useful as vaccines and the transformed bacteria
XX are useful as live (oral) vaccines eg against Influenza and foot and
XX mouth disease
XX (Updated on 09-JAN-2003 to add missing OS field.)
XX
XX Sequence 6477 BP; 1668 A; 1617 C; 1696 G; 1496 T; 0 other:
XX
XX Query Match 69.3%; Score 768.8; DB 11; Length 6477;
XX Best Local Similarity 90.8%; Pred. No. 4.8e-211;
XX Matches 843; Conservative 0; Mismatches 52; Indels 33; Gaps 1;
XX
XX 42 CATATTGCTTTGAGCTACATTTCTGTGCTCTCGGCCAAGACCTTCAGAAATGA 101
XX || || || || || || || || || || || || || || || || || || || ||
XX 769 CACCAAGCTCACAACAATGTGACAGTGAATCGATAGGCCAAGACCTTCAGAAATGA 828
XX
XX 102 CAACAGCAGACCAAGCGTGTGCGGACATCATCGGTGGCAAGCAACACTGTA 161
XX || || || || || || || || || || || || || || || || || || || ||
XX 829 CAACAGCAGACCAAGCGTGTGCGGACATCATCGGTGGCAAGCAACACTGTA 888
XX
XX 162 AACATCAGACATGATGATGAAAGTGAATGCTACTAGTACTAGTACTGCTC 221
XX || || || || || || || || || || || || || || || || || || || ||
XX 889 AACATCAGACATGATGATGAAAGTGAATGCTACTAGTACTAGTACTGCTC 944
XX
XX 222 AACGGGAAAAATATGACAATATGATACCTGATTTCTGAATGCATCACTCCAATGG 281
XX || || || || || || || || || || || || || || || || || || || ||
XX 945 -----CTAGAGTACTCAATATGATCACTCACTCCAATGG 975
XX
XX 282 AAGCATCCCAATGACAAGCCCTTTCAAAAGTAAACAAGATGACATGTGAGCATGCC 341
XX || || || || || || || || || || || || || || || || || || || ||
XX 976 AAGCATCCCAATGACAAGCCCTTTCAAAAGTAAACAAGATGACATGTGAGCATGCC 1035
XX
XX 342 CAAGTATGTTAAGCAAAACACCTGAAAGTGGCAACAGGAGTGGGATGTACAGAGAA 401
XX || || || || || || || || || || || || || || || || || || || ||
XX 1036 CAAGTATGTTAAGCAAAACACCTGAAAGTGGCAACAGGAGTGGGATGTACAGAGAA 1095

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QY 402 ACAACTAGAGCCCTATTTCGGGCAATAGCAGGTTTCATAGAAAATGGTTGGAGGAAT 461
DB || || || || || || || || || || || || || || || || || || || ||
DB 1096 ACAAACTAGAGCCCTATTTCGGGCAATAGCAGGTTTCATAGAAAATGGTTGGAGGAAT 1155
QY 462 GATAGACGTTGTCACGTTTCAGGCATCAAAATTTGAGGGCGACAGACAGCAGACA 521
DB || || || || || || || || || || || || || || || || || || || ||
DB 1156 GATAGACGTTGTCACGTTTCAGGCATCAAAATTTGAGGGCGACAGACAGCAGACA 1215
QY 522 TCTTAAAGCACTCAAGCAGCATGACCAATCAATGGAATTTGAACAGGGTTAATCA 581
DB || || || || || || || || || || || || || || || || || || || ||
DB 1216 TCTTAAAGCACTCAAGCAGCATGACCAATCAATGGAATTTGAACAGGGTTAATCA 1275
QY 582 GAAGACGAGCAAGAAATTCATCAAAATGAAAGGAATTTCTAGACAGTGAAGGAGAA 641
DB || || || || || || || || || || || || || || || || || || || ||
DB 1276 GAAGACGAGCAAGAAATTCATCAAAATGAAAGGAATTTCTAGACAGTGAAGGAGAA 1335
QY 642 TCAGACCTCGAAGAAATACGTTGAAGACACTTAATATAGATCTGCTTCAATGCGGA 701
DB || || || || || || || || || || || || || || || || || || || ||
DB 1336 CCAGATCTCGAAGAAATACGTTGAAGACACTTAATATAGATCTGCTTCAATGCGGA 1395
QY 702 GCTTCTGCTCGTGGAGAAATCAACATGACCTGACCTGACCGGAAATGACAA 761
DB || || || || || || || || || || || || || || || || || || || ||
DB 1396 GCTTCTGCTCGTGGAGAAATCAACATGACCTGACCTGACCGGAAATGACAA 1455
QY 762 GCTGTTGAAAAACAGAGGCAACTGAGGAAAAATGCTGAGAGATGGGCAATGGTTG 821
DB || || || || || || || || || || || || || || || || || || || ||
DB 1456 GCTGTTGAAAAACAGAGGCAACTGAGGAAAAATGCTGAGAGATGGGCAATGGTTG 1515
QY 822 CTTCAAAATATACCAAAATGTCACACGCTTGATGACATCAATGTAATGTTACTTA 881
DB || || || || || || || || || || || || || || || || || || || ||
DB 1516 CTTCAAAATATACCAAAATGTCACACGCTTGATGACATCAATGTAATGTTACTTA 1575
QY 882 TGACCATGATGATATACAGAGCAAGCAATTAACACCGGTTTCAGATCAAAAGGTGTA 941
DB || || || || || || || || || || || || || || || || || || || ||
DB 1576 TGACCATGATGATATACAGAGCAAGCAATTAACACCGGTTTCAGATCAAAAGGTGTA 1635
QY 942 ACTGAAGTCTGGATACAAAGACTGATC 969
DB || || || || || || || || || || || || || || || || || || || ||
DB 1636 ACTGAAGTCTGGATACAAAGACTGATC 1663

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RESULT 11
AAT59216
ID AAT59216 standard; DNA; 1757 BP.
XX
XX AAT59216;
AC 25-MAR-2003 (updated)
XX 19-AUG-1997 (first entry)
DT
DT 19-AUG-1997 (first entry)
XX
XX Influenza A/Shandong/9/93 recombinant haemagglutinin gene.
DE
DE primer: PCR; polymerase chain reaction; universal; amplify: HA;
KW haemagglutinin; recombinant production; baculovirus expression system;
KW vaccine; insect cell culture; ss.
XX
XX Synthetic.
OS
OS key
FH key
FH misc_signal 1..18
FT location/qualifiers
FT /tag= a
FT /note= "polyhedrin mRNA leader (partial)"
FT CDS 19..1734
FT /tag= b
FT sig_peptide 19..72
FT /tag= c
FT /note= "AcNPV 61k protein signal peptide"
FT mat_peptide 73..1728
FT /tag= d
FT /note= "coding region for mature rHA"
FT misc_signal 1747..1757
FT /tag= e
FT /note= "universal translation termination signal"

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XX XX WO637624-A1.
XX PN
XX PD 28-NOV-1996.
XX PF 26-MAY-1995; 95WO-US06750.
XX PR 26-MAY-1995; 95WO-US06750.
XX PA (MICR-) MICROGENESYS INC.
XX PA (MGPM-) MG-PMC LLC.
XX PI Smith GE, Volovitz F, Wilkinson BE, Voznesensky AI, Hackett CS;
XX DR MPI: 1997-021228/02.
XX DR P-PSDB; AAM01673.
XX PT Recombinant influenza haemagglutinin produced in baculovirus system
XX PT - avoids problems of growing virus in eggs and produces stable,
XX PT un-cleaved protein useful in vaccines
XX PS Example 12; Page 80-81; 107pp; English.
XX CC Recombinant influenza haemagglutinin (HA) expressed in a
XX CC baculovirus expression system in cultured insect cells, allows vaccine
XX CC production without the need to grow virus in eggs. A purer, less
XX CC allergenic product is obtained and antigen drift caused by passages
XX CC through eggs is avoided. There is no need for viral inactivation or
XX CC organic solvent extn. of viral membrane components and vaccines can be
XX CC prepared, rapidly and cost effectively from primary sources of infection.
XX CC Recombinant HA is more stable (esp. for B strains) than HA1/HA2 complexes
XX CC and maintain correct folding during purification and storage. The present
XX CC sequence encodes the 5' end sequence of the HA gene for influenza
XX CC A/Shandong/9/93. The 61k signal peptide for baculovirus expression
XX CC and the polyhedrin promoter are included in the vector. It was used
XX CC in a study to compare the 1994-1995 formulation of the trivalent rHA
XX CC influenza vaccine with a licensed purified virus surface antigen
XX CC vaccine, Fluvirin (an attenuated influenza viral vaccine produced by
XX CC culturing in eggs).
XX CC (Updated on 25-MAR-2003 to correct PI field.)
XX SQ Sequence 1757 BP; 582 A; 352 C; 403 G; 420 T; 0 other;

Query Match 68.2%; Score 756.6; DB 18; Length 1757;
Best local similarity 94.1%; Pred. No. 8.8e-208;
Matches 786; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

OY 244 ATTGATACCTGTATTTTTGATGATGCATCACTCCAAATGGAAGCATTCCCAATGACAAGCCC 303
DB 901 ATTGCACTGCAGTTTGTGAATGCATCACTCCAAATGGAAGCATTCCCAATGACAAGCCT 960
OY 304 TTTCAAACGTTAAACAGATCAGATGAGAGATGCCCAAGTATGTTAAGCAAAACACC 363
DB 961 TTTCAAATGTTAAACATCATCATATGAGGCTCCCAAGTATGTTAAGCAAAACACT 1020
OY 364 CTGAGTTGGCAACAGCGATGCGGAATGTACAGAGAAACAACATAGAGGCTTATTGGC 423
DB 1021 CTGAAATTGGCAACAGCGATGCGGAATGTACAGAGAAACAACATAGAGGCTTATTGGC 1080
OY 424 GCAATGAGAGGTTTCACTAGAAATGTTGGAGGGAATGATAGAGCGTTGTACGCTTTC 483
DB 1081 GCAATGCGAGGTTTCACTAGAAATGTTGGAGGGAATGATAGAGCGTTGTACGCTTTC 1140
OY 484 AGGCATCAAAATTTCTGAGGCGACAGACAGACAGATCTTTAAAGCACTCAACAGCC 543
DB 1141 AGGCATCAAAATTTCTGAGGCGACAGACAGACAGATCTTTAAAGCACTCAACAGCA 1200
OY 544 ATGCACCAATCAATGCGAATTTGAACAGAGGTAAATCGAGAAAGACAGAGAAATTCAT 603
DB 1201 ATGCACCAATCAATGCGAATTTGAATGTTAATCGAGAAAGACAGAGAAATTCAT 1260
OY 604 CAAATCGAAAAGCAATCTCAGAACTAGAGAGGAGAAATTCAGACCTCGAGAAATACGTT 663

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DB 1261 CAAATCGAAAAGCAATTTCTCAGAACTAGAGAGGAGAAATTCAGACCTCGAGAAATATGTT 1320
OY 664 GAAGACACTAAATATGATCTGTCTTACAAATGGGAGACTCTGTGCTCGTGAGAT 723
DB 1321 GAAGACACTAAATATGATCTGTCTTACAAATGGGAGACTCTGTGCTCGTGAGAT 1380
OY 724 CAACATACAAATGACCTGACTGCTCGAATATGACAACAGCTGTTGAAAACAGAGAG 783
DB 1381 CAACATACAAATGATCTAATCTAGCTAGCAATATGACAAACCTGTTGAAAACAGAG 1440
OY 784 CAAGTACAGGAAATCTCAGAGATGGGCAATGTTGCTTCAAAATATACCAAAATCT 843
DB 1441 CAAGTACAGGAAATCTCAGAGATGGGCAATGTTGCTTCAAAATATACCAAAATCT 1500
OY 844 GACACGCTTGATAGATCATCATCAATATGTTGTTACTTATGACCATGATATATACAGAC 903
DB 1501 GACAAATGCTGATAGGCTCAATGAAATGGAACCTATGACCATGATATATACAGAC 1560
OY 904 GAAGCATTTAAACACCGGTTTCAGATCAAGGTTGGAAGCTGAGTCAAGTCAAGAC 963
DB 1561 GAAGCATTTAAACACCGGTTTCAGATCAAGGTTGGAAGCTGAGTCAAGTCAAGAC 1620
OY 964 TGATCTGCTGATTTTCCTTTGCAATATCATCTTTTTCCTTTGCTGCTGCGG 1023
DB 1621 TGATCTGCTGATTTTCCTTTGCAATATCATCTTTTTCCTTTGCTGCTGCGG 1680
OY 1024 TTATCATATGTTGGCTGCGGAGAGGCAACATTAGTGAACATTTGCTGCTGAG 1078
DB 1681 TTATCATATGTTGGCTGCGGAGAGGCAACATTAGTGAACATTTGCTGCTGAG 1735

RESULT 12
AAX00777
ID AAX00777 standard; DNA; 1757 BP.
XX AC AAX00777;
XX AC AAX00777;
XX DT 13-APR-1999 (first entry)
XX DE Influenza virus A/Shandong/9/93 recombinant HA gene.
XX KW Recombinant; glycosylation; influenza virus; haemagglutinin; baculovirus;
XX KW fusion protein; expression system; insect cell; immunogen; vaccine;
XX KW immune response; primer; PCR; amplification; reverse transcription;
XX KW human; bird; ss.
XX OS Synthetic.
XX OS Influenza virus.
XX FH Key Location/Qualifiers
XX FH 5'UTR 1..18
XX FT /*tag= a
XX FT /note= "polyhedrin mRNA leader sequence"
XX FT CDS 19..1731
XX FT /*tag= b
XX FT sig_peptide 19..72
XX FT /*tag= c
XX FT mat_peptide 73..1728
XX FT /note= "AcNPV 61k signal peptide"
XX FT FT /*tag= d
XX FT terminator 1747..1757
XX FT /*tag= e
XX PN US5858368-A.
XX PD 12-JAN-1999.
XX PF 30-MAY-1995; 95US-0453848.
XX PF 30-MAY-1995; 95US-0453848.
XX PR 13-SEP-1993; 93US-0120607.
XX

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8810
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 1110 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
ORIGINAL SOURCE:
ORGANISM: A2/Aichi/2/48
US-08-630-918-57

Query Match      100.0%; Score 1110; DB 1; Length 1110;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGAAGCAAAAGCAGGCGATTAATTCATATGATGAAGACCATCATGCTTTGAGCTAC 60
DB 1 CTAGAAGCAAAAGCAGGCGATTAATTCATATGATGAAGACCATCATGCTTTGAGCTAC 60
QY 61 ATTTCTGTCTGGCTCTGGGCCAAGACCTCCAGAAATGACACAGCAGCAACGCTG 120
DB 61 ATTTCTGTCTGGCTCTGGGCCAAGACCTCCAGAAATGACACAGCAGCAACGCTG 120
QY 121 TGCCTGGGACATCATGCGTGGCCAAAGGACACTAGTGAAGAAACATCAGATGATGAG 180
DB 121 TGCCTGGGACATCATGCGTGGCCAAAGGACACTAGTGAAGAAACATCAGATGATGAG 180
QY 181 ATTGAAGTACTAATGTTACTAGAGTCTCTCAACGGGGGAAAAATATGCAAC 240
DB 181 ATTGAAGTACTAATGTTACTAGAGTCTCTCAACGGGGGAAAAATATGCAAC 240
QY 241 AATATTGATCTGTATTTTCTAATGCATCACTCCAAATGGAAGCATCCCATGACAG 300
DB 241 AATATTGATCTGTATTTTCTAATGCATCACTCCAAATGGAAGCATCCCATGACAG 300
QY 301 CCCCTTCAAAAAGCTAAACAGATCAGATGAGGAGCGCCCAAGTATGTTAAGCAAAAC 360
DB 301 CCCCTTCAAAAAGCTAAACAGATCAGATGAGGAGCGCCCAAGTATGTTAAGCAAAAC 360
QY 361 ACCCTGAAGTTGGCAATAGGGATGGGGAATGTACCAAGAAACAACTAGAGCGCTATT 420
DB 361 ACCCTGAAGTTGGCAATAGGGATGGGGAATGTACCAAGAAACAACTAGAGCGCTATT 420
QY 421 GCGCGAATAGCAGGTTTCATAGAAAATGGTTGGAGGAGATATAGCGTTGTACGGT 480
DB 421 GCGCGAATAGCAGGTTTCATAGAAAATGGTTGGAGGAGATATAGCGTTGTACGGT 480
QY 481 TTCAGGCAATCAAAATTTGAGGGGACAGGACAGCAGATCTTAAAGCACTCAAGCA 540
DB 481 TTCAGGCAATCAAAATTTGAGGGGACAGGACAGCAGATCTTAAAGCACTCAAGCA 540
QY 541 GCCATCGACCAATCAATGGGAAATTTGAACAGGGTAATCGAAGACGACAGCAAGAAAT 600
DB 541 GCCATCGACCAATCAATGGGAAATTTGAACAGGGTAATCGAAGACGACAGCAAGAAAT 600
QY 601 CATCAAAATCGAAAAGGATTTCTCAGAGTGAAGGAGCAATTCAGAGCTCGAGAAATAC 660
DB 601 CATCAAAATCGAAAAGGATTTCTCAGAGTGAAGGAGCAATTCAGAGCTCGAGAAATAC 660
QY 661 GTTGAAGACACTAAATAGATCTGTGCTTTACATGCGGAGCTCTTGCGCTGTGGAG 720
DB 661 GTTGAAGACACTAAATAGATCTGTGCTTTACATGCGGAGCTCTTGCGCTGTGGAG 720
QY 721 AATCAACATACAAATGATCTGACTGACTCGAAGAAATGAACAAGCTTTTGAACAAAG 780
DB 721 AATCAACATACAAATGATCTGACTGACTCGAAGAAATGAACAAGCTTTTGAACAAAG 780
QY 781 AGGCAACGTGAGGAAATTCCTGAAGATGGGCATGTGTTCTTAAATATACCAAAA 840
DB 781 AGGCAACGTGAGGAAATTCCTGAAGATGGGCATGTGTTCTTAAATATACCAAAA 840
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DB 781 AGGCAACGTGAGGAAATTCCTGAAGATGGGCATGTGTTCTTAAATATACCAAAA 840
QY 841 TGTGCAACAGCTTGCATAGAGTCAATCAGAAATGATCTTATGACCATGATGATACAGA 900
DB 841 TGTGCAACAGCTTGCATAGAGTCAATCAGAAATGATCTTATGACCATGATGATACAGA 900
QY 901 GACGAAGCATTTAAACACCGGTTTCAGATCAAAAGGTGTTGAACGTGAAGTCTGGATCAAA 960
DB 901 GACGAAGCATTTAAACACCGGTTTCAGATCAAAAGGTGTTGAACGTGAAGTCTGGATCAAA 960
QY 961 GACTGATCTCTGATGATTTCTTTCCTTGCATATCATGCTTTTGTGTTGTTGCTG 1020
DB 961 GACTGATCTCTGATGATTTCTTTCCTTGCATATCATGCTTTTGTGTTGTTGCTG 1020
QY 1021 GGGTTCATCATGTGGGCGCTGCCAGAGAGCAACATAGGTGCAACATTTGATTTGAGTG 1080
DB 1021 GGGTTCATCATGTGGGCGCTGCCAGAGAGCAACATAGGTGCAACATTTGATTTGAGTG 1080
QY 1081 TATTAGTAATTAACAAACACCTTGTCTG 1110
DB 1081 TATTAGTAATTAACAAACACCTTGTCTG 1110

RESULT 3
US-09-004-422-57
Sequence 57, Application US/09004422
Patent No. 6337070
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,422
FILING DATE: January 8, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 1110 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL:
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ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: AZ/Alchi1/2/68
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-09-004-422-57

Query Match 100.0%; Score 1110; DB 4; Length 1110;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGAGCAAGCAGGGGATATCTTATTAATCATGAAGACCATTCCTTTGAGCTAC 60
DB 1 CTAGAGCAAGCAGGGGATATCTTATTAATCATGAAGACCATTCCTTTGAGCTAC 60
QY 61 ATTTTGTCTGGCTCTCGGCCAAGACCTTCCAGGAATGACACAGCAGCAACGCTG 120
DB 61 ATTTTGTCTGGCTCTCGGCCAAGACCTTCCAGGAATGACACAGCAGCAACGCTG 120
QY 121 TGCCTGGACATCATGGGCTGCCAAGGAGACACTAGTGAAGAAACATCAGATGATCAG 180
DB 121 TGCCTGGACATCATGGGCTGCCAAGGAGACACTAGTGAAGAAACATCAGATGATCAG 180
QY 181 ATTGAAGTACTAATGCTACTAGCTAGCTTCAAGAGCTCTCAACGGGGAAAAATATGCAAC 240
DB 181 ATTGAAGTACTAATGCTACTAGCTAGCTTCAAGAGCTCTCTCAACGGGGAAAAATATGCAAC 240
QY 241 AATATGTATACCTGTATTTTGCATGCTCACTCCAAATGGAAGATCCCAATGACAG 300
DB 241 AATATGTATACCTGTATTTTGCATGCTCACTCCAAATGGAAGATCCCAATGACAG 300
QY 301 CCCTTTGAAAAAGTAACAGATCATATGAGAGATCCCAAGTATGTTAAGCAAAAC 360
DB 301 CCCTTTGAAAAAGTAACAGATCATATGAGAGATCCCAAGTATGTTAAGCAAAAC 360
QY 361 ACCCTGAAGTTGGCAACAGGATCGGAATGTACAGAGAAACAACATGAGAGGCTATTTC 420
DB 361 ACCCTGAAGTTGGCAACAGGATCGGAATGTACAGAGAAACAACATGAGAGGCTATTTC 420
QY 421 GGGGCATACAGGTTTCATAGAAAATGTTGGGAGGAAATGATGAGCGTTGATCGGT 480
DB 421 GGGGCATACAGGTTTCATAGAAAATGTTGGGAGGAAATGATGAGCGTTGATCGGT 480

QY 481 TTCAGGATCAAAATTTCTGAGGGGACAGAGACAGCAGATCTTAAAGCACTCAAGCA 540
DB 481 TTCAGGATCAAAATTTCTGAGGGGACAGAGACAGCAGATCTTAAAGCACTCAAGCA 540
QY 541 GCCATCGACCAATCAATGGAATTTGAACAGGGATATCGAAGAGCAAGCAAGAAATTC 600
DB 541 GCCATCGACCAATCAATGGAATTTGAACAGGGATATCGAAGAGCAAGCAAGAAATTC 600
QY 601 CATCAATTCGAAAAGGAATTTCTCAGAGTACAGAGGAGATTCAGGACCTCGAGAAATAC 660
DB 601 CATCAATTCGAAAAGGAATTTCTCAGAGTACAGAGGAGAAATTCAGGACCTCGAGAAATAC 660
QY 661 GTTGAAGACACTAAATATGATCTGCTTACATGCGAGGACTCTTTCGCGCTCGAG 720
DB 661 GTTGAAGACACTAAATATGATCTGCTTACATGCGAGGACTCTTTCGCGCTCGAG 720
QY 721 AATCAACATACAAATTTGACCTGACCTCGAAGTGAACAAAGCTTTGAAAAACAAG 780
DB 721 AATCAACATACAAATTTGACCTGACCTCGAAGTGAACAAAGCTTTGAAAAACAAG 780
QY 781 AGGCACTGAGGGAATGCTGAAGAGATGGGCAATGCTTCAAAATATACCAAA 840
DB 781 AGGCACTGAGGGAATGCTGAAGAGATGGGCAATGCTTCAAAATATACCAAA 840
QY 841 TGTGACACGGCTTGATAGTCAATCGAAGTGTACTATGACATGATATACAGA 900
DB 841 TGTGACACGGCTTGATAGTCAATCGAAGTGTACTATGACATGATATACAGA 900
QY 901 GACGAGCATTAACAAACCGGTTTCAGATCAAGAGTGTGAAGTGTGATGATACAA 960
DB 901 GACGAGCATTAACAAACCGGTTTCAGATCAAGAGTGTGAAGTGTGATGATACAA 960
QY 961 GACTGATCTGTGATTTCTTTGCCATATCATGCTTTTGTCTTGTGTTTCTG 1020
DB 961 GACTGATCTGTGATTTCTTTGCCATATCATGCTTTTGTCTTGTGTTTCTG 1020
QY 1021 GGGTTCATCATGTGGGCTGCGCAGAGGCAACATTAAGTGCACATTTGATTTGAGT 1080
DB 1021 GGGTTCATCATGTGGGCTGCGCAGAGGCAACATTAAGTGCACATTTGATTTGAGT 1080
QY 1081 TATTAGTAAATTAACACCCCTTGTCTG 1110
DB 1081 TATTAGTAAATTAACACCCCTTGTCTG 1110

RESULT 4
US-08-229-781-54
Sequence 54, Application US/08229781
Patent No. 5589174
GENERAL INFORMATION:
APPLICANT: yoshinobu OKUNO et al.
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Menderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,781
FILING DATE: April 19, 1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993

Query Match	Best Local Similarity	Matches	868: Conservative	78.2%: Score 868; DB 1; Length 1777; 100.0%: Pired. No. 2,1e-277;	0: Mismatches	0: Indels	0: Gaps	0:
243	TATGATACCGGTAT	TTCTGAATGCATCATCCAAATGGAGCAATTCCTCAATGACAAAGCC	302					
903	TATGATACCTGTAT	TTCTGAATGCATCATCCAAATGGAGCAATTCCTCAATGACAAAGCC	962					
303	CTTTCAAACGTAAA	TAGATCACATATGAGCATGCCCAAGATGTTAAGCAAAACAC	362					
963	CTTTCAAACGTAAA	TAGATCACATATGAGCATGCCCAAGATGTTAAGCAAAACAC	1022					
363	CCTAAGTTGGCAAC	AGGATGCCGATGTACCCAGACAAACTAGAGGCTTATTCGG	422					
1023	CCTAAGTTGGCAAC	AGGATGCCGATGTACCCAGACAAACTAGAGGCTTATTCGG	1082					
423	CGCAATAGCAGGTTT	TATAGAAATGGTTGGAGGGAATGATACAGGTTGTACGGTTT	482					
1083	CGCAATAGCAGGTTT	TATAGAAATGGTTGGAGGGAATGATACAGGTTGTACGGTTT	1142					

```

OY      483 CAGCGATCAAAATTTCTGAGGCGACAGACGACAGCATCTTTAAAACACTCAAGCAGC 542
Db      1143 CAGCGATCAAAATTTCTGAGGCGACAGACGACAGCATCTTTAAAACACTCAAGCAGC 1202
OY      543 CATCGACCAATTCATGAGGAAATTTGAACAGGGATTAATCGAGAAGACGAACGAGAAATTTCCA 602
Db      1203 CATCGACCAATTCATGAGGAAATTTGAACAGGGATTAATCGAGAAGACGAACGAGAAATTTCCA 1262
OY      603 TCAATTCGAAAAGGAATTTCTAGAAGTATGAAGGGAGAAATTAGAGACTCGAGAAATACCT 662
Db      1263 TCAATTCGAAAAGGAATTTCTAGAAGTATGAAGGGAGAAATTTAGAGACTCGAGAAATACCT 1322
OY      663 TGAAGACACTTAAATATAGATCTCTGATCTTCAATATGCGGAGCTTCTGTCGCTCGAGAA 722
Db      1323 TGAAGACACTTAAATATAGATCTCTGATCTTCAATATGCGGAGCTTCTGTCGCTCGAGAA 1382
OY      723 TCAACATTCAAATTAAGCTGACTGACTGACTCGGAATTAACAAAGCTGTTTGAAGAAAACAGAG 782
Db      1383 TCAACATTCAAATTAAGCTGACTGACTGACTCGGAATTAACAAAGCTGTTTGAAGAAAACAGAG 1442
OY      783 GCACATGAGGGGAAAATGCTGAAAGAGATGGGCAATGTTGCTTCAAAATATACCAATG 842
Db      1443 GCAACTGAGGGGAAAATGCTGAAAGAGATGGGCAATGTTGCTTCAAAATATACCAATG 1502
OY      843 TGACAACGCTTGCATAGAGTCAATACAGAAATGTAATATGACCATGATGATACAGAGA 902
Db      1503 TGACAACGCTTGCATAGAGTCAATACAGAAATGTAATATGACCATGATGATACAGAGA 1562
OY      903 CGAAGCATTTAACAACCGGTTTCAGATCAAAAGGTGTTGAACGTGAGTACCAAGA 962
Db      1563 CGAAGCATTTAACAACCGGTTTCAGATCAAAAGGTGTTGAACGTGAGTACCAAGA 1622
OY      963 CTGATCTCTGAGATTCCTTGGCATATCATGCTTTTGGTTGTGTTGCTTGGCTGCGG 1022
Db      1623 CTGATCTCTGAGATTCCTTGGCATATCATGCTTTTGGTTGTGTTGCTTGGCTGCGG 1682
OY      1023 GTTATCATCTGAGGCGCTGCGACAGAGAGCAACATTAGGTGCAACATTTGCATTGAGTGA 1082
Db      1683 GTTATCATCTGAGGCGCTGCGACAGAGAGCAACATTAGGTGCAACATTTGCATTGAGTGA 1742
OY      1083 TTAGTAATTTAAAAACACCCCTGTTTCTG 1110
Db      1743 TTAGTAATTTAAAAACACCCCTGTTTCTG 1170

RESULT 5
US-08-630-918-54
/ Sequence 54, Application US/08630918
/ Patent No. 5631350
/ GENERAL INFORMATION:
/ APPLICANT: yoshinobu OKUNO et al.
/ TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
/ NUMBER OF SEQUENCES: 58
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Wenderoth, Lind & Ponack
/ STREET: 805 Fifteenth Street, N.W., #700
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: Wordperfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/630.918
/ FILING DATE: April 5, 1996
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/229,781
/ FILING DATE: April 19, 1994

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ. ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
ORIGINAL SOURCE:
ORGANISM: A2/Alchl/2/68
US-08-630-918-54

Query Match 78.2% Score 868: DB 1: Length 1777:

Best Local Similarity 100.0%: Pred. No. 2,1e-277:

Matches 868: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

243 TATGTATACCTGATTTCTGATGATCATCTCAATGGAAGCATCCCATGACAAAGCC 302
1023 CTTGTAAGTTGGCAACAGGATCGGGAATGTACCGAGAAACAACTAGAGCCCTATTCCG 422
1083 CGCAATAGCAGGTTTCATAGAAATGTGGGAGGGAATGATGAGCGTTGTACGGTTT 482
423 CGCAATAGCAGGTTTCATAGAAATGTGGGAGGGAATGATGAGCGTTGTACGGTTT 482
1083 CGCAATAGCAGGTTTCATAGAAATGTGGGAGGGAATGATGAGCGTTGTACGGTTT 1142
483 CAGGATCAAAATTTCTGAGGCGACAGGACAGCAGATCTTAAAGCACTCAAGCAGC 542
1143 CAGGATCAAAATTTCTGAGGCGACAGGACAGCAGATCTTAAAGCACTCAAGCAGC 1202
543 CATGACCAAAATCAATGGGAATTTGAAACGGGTAATCGAGAGCAAGAGAAATTTCA 602
1203 CATGACCAAAATCAATGGGAATTTGAAACGGGTAATCGAGAGCAAGAGAAATTTCA 1262
603 TCAATTCGAAAAGGAATTTCTCAGAGTAGAAGGGAATTCAGAGACCTCGAGAAATAGCT 662
1263 TCAATTCGAAAAGGAATTTCTCAGAGTAGAAGGGAATTCAGAGACCTCGAGAAATAGCT 1322
663 TGAAGACACTAAATAGATCTCTGCTTTACATGCGGAGCTTCTTGCTGCTCGAGAA 722
1323 TGAAGACACTAAATAGATCTCTGCTTTACATGCGGAGCTTCTTGCTGCTCGAGAA 1382
723 TCAACATCAAAATTTGACCTGACTGACTCGGAATGGAACAAGCTGTTGAAAAACAAGGAG 1442
1383 TCAACATCAAAATTTGACCTGACTGACTCGGAATGGAACAAGCTGTTGAAAAACAAGGAG 1442
783 GCAACTGAGGGAATTCGTAAGAGATGGGCAATGTTGCTTCAAAATATACCAAAAG 842
1443 GCAACTGAGGGAATTCGTAAGAGATGGGCAATGTTGCTTCAAAATATACCAAAAG 1502
843 TGACAACGCTTGACATAGAGTCAATGAGAAATGTAAGCAATGATGTATAGAGAGA 902
1503 TGACAACGCTTGACATAGAGTCAATGAGAAATGTAAGCAATGATGTATAGAGAGA 1562
903 CGAAGCATTTAAACAACCGGTTTCAATCAAAAGGTTTGAAGTCTGATATACAAAGA 962
1563 CGAAGCATTTAAACAACCGGTTTCAATCAAAAGGTTTGAAGTCTGATATACAAAGA 1622

963 CTGATCCGTGTGATTTCTTCCATATCATGCTTTGCTTGAGTTGTTGCTGGG 1022
1623 CTGATCCGTGTGATTTCTTCCATATCATGCTTTGCTTGAGTTGTTGCTGGG 1682
1023 GTTCATCATGTGGGCTGCGAGAGAGCAACATTTAGTGCAACATTTGATGAGTGA 1082
1683 GTTCATCATGTGGGCTGCGAGAGAGCAACATTTAGTGCAACATTTGATGAGTGA 1742
1083 TTGATTAATTAACAACCTTGTCTG 1110
1743 TTGATTAATTAACAACCTTGTCTG 1770

RESULT 6

US-09-004-422-54
Sequence 54, Application US/09004422
Patent No. 6337070
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,422
FILING DATE: January 8, 1998
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ. ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: A2/Alchl/2/68
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:

```
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-09-004-422-54

Query Match      78.2%; Score 868; DB 4; Length 1777;
Best Local Similarity 100.0%; Pred. No. 2.1e-277;
Matches 868; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 TATTGATACCTGATTTCTGAATGATCATCTCCAAATGAGACATTCCTCAATACAGCC 302
    |||||||
DB 903 TATTGATACCTGATTTCTGAATGATCATCTCCAAATGAGACATTCCTCAATACAGCC 962
QY 303 CTTTCAAAACGTAAACAGATCATATGAGAGCATGCCCAAGATATGTTAAGCAAAACAC 362
    |||||||
DB 963 CTTTCAAAACGTAAACAGATCATATGAGAGCATGCCCAAGATATGTTAAGCAAAACAC 1022
QY 363 CCTGAAGTTGGCAACAGATGTCGGAATGTACCAAGAAACAACTAGAGGCTTATTCGG 422
    |||||||
DB 1023 CCTGAAGTTGGCAACAGATGTCGGAATGTACCAAGAAACAACTAGAGGCTTATTCGG 1082
QY 423 CGCAATAGCAGGTTCTTAGAAATGTTGGAGGAATGATGAGCGTTGGTACGTTT 482
    |||||||
DB 1083 CGCAATAGCAGGTTCTTAGAAATGTTGGAGGAATGATGAGCGTTGGTACGTTT 1142
QY 483 CAGCATCAAAATTTCTGAGGACAGAGACAGAGATCTTAAAGCACTCAACGAGC 542
    |||||||
DB 1143 CAGCATCAAAATTTCTGAGGACAGAGACAGAGATCTTAAAGCACTCAACGAGC 1202
QY 543 CATGACCAAAATCAATGGAATTTGAACAGGTAATCGAAGACGACGAGAAATTCGA 602
    |||||||
DB 1203 CATGACCAAAATCAATGGAATTTGAACAGGTAATCGAAGACGACGAGAAATTCGA 1262
QY 603 TCAATCGAAAGGAATTTCTCAGAAATTAAGGGAATTCAGAGCTCGAGAAATACGT 662
    |||||||
DB 1263 TCAATCGAAAGGAATTTCTCAGAAATTAAGGGAATTCAGAGCTCGAGAAATACGT 1322
QY 663 TGAAGACACTAAATAGTCTCTGCTTTACAAATGGGAGCTTCTGTGCTTGAGAGA 722
    |||||||
DB 1323 TGAAGACACTAAATAGTCTCTGCTTTACAAATGGGAGCTTCTGTGCTTGAGAGA 1382
QY 723 TCAACATACAAATTGACCTACTGACTCGGAATGAACAAGCTGTTGAAAAACAAGAG 782
    |||||||
DB 1383 TCAACATACAAATTGACCTACTGACTCGGAATGAACAAGCTGTTGAAAAACAAGAG 1442
QY 783 GCAACTGAGGAGAAATGCTGGAAGAGATGGGCAATGGTCTTCAAAATATACCAAAATG 842
    |||||||
DB 1443 GCAACTGAGGAGAAATGCTGGAAGAGATGGGCAATGGTCTTCAAAATATACCAAAATG 1502
```

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QY 843 TGACAACGCTTGATGAGTCAATCAAGAAATGCTACTTATGACCATGATATACAGAGA 902
    |||||||
DB 1503 TGACAACGCTTGATGAGTCAATCAAGAAATGCTACTTATGACCATGATATACAGAGA 1562
QY 903 CGAAGCATTTAAACACCGGTTTCAGATCAAAAGTGTGAACGTAAGTCTGGATACAAAGA 962
    |||||||
DB 1563 CGAAGCATTTAAACACCGGTTTCAGATCAAAAGTGTGAACGTAAGTCTGGATACAAAGA 1622
QY 963 CTGATTCCTGATGATTTCTTCCATATCATGCTTTTCTGCTTGTGCTGGG 1022
    |||||||
DB 1623 CTGATTCCTGATGATTTCTTCCATATCATGCTTTTCTGCTTGTGCTGGG 1682
QY 1023 GTTCATCATGTGGGCTGCGAGAGAGCAACATTAGTGCACATTTGATTTGAGTGA 1082
    |||||||
DB 1683 GTTCATCATGTGGGCTGCGAGAGAGCAACATTAGTGCACATTTGATTTGAGTGA 1742
QY 1083 TTAGTAATTTAAACACCTTGTTCG 1110
    |||||||
DB 1743 TTAGTAATTTAAACACCTTGTTCG 1770
```

```
RESULT 7
US-08-453-848-6
; Sequence 6, Application US/08453848
; Patent No. 5858368
; GENERAL INFORMATION:
; APPLICANT: Smith, Gale Eugene
; APPLICANT: Voikovitz, Franklin
; APPLICANT: Wilkinson, Bethanie Eident
; APPLICANT: Voznesensky, Andrei I.
; APPLICANT: Hackett, Craig Stanway
; TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA
; TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,848
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/120,607
; FILING DATE: 13-SEPT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MGS101CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1793 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Influenza virus
```

```

: INDIVIDUAL ISOLATE: A/Beijing/32/92 rHA
: FEATURE:
: NAME/KEY: polyhedrin mRNA leader (partial)
: LOCATION: 1 to 18
: FEATURE:
: NAME/KEY: coding region for AcNPV 61k protein signal
: LOCATION: 19 to 72
: FEATURE:
: NAME/KEY: SmaI restriction site
: LOCATION: 76 to 81
: FEATURE:
: NAME/KEY: coding region for mature rHA
: LOCATION: 73 to 1728
: FEATURE:
: NAME/KEY: KpnI restriction site
: LOCATION: 1771 to 1777
: FEATURE:
: NAME/KEY: BglII restriction site
: LOCATION: 1776 to 1782
: FEATURE:
: NAME/KEY: universal translation termination signal
: LOCATION: 1783 to 1793
: US-08-453-848-6

```

```

Query Match      69.8%; Score 774.8; DB 2; Length 1793;
Best Local Similarity 94.2%; Pred. No. 1.7e-246;
Matches 816; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

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OY 244 ATTGATACCTGATTTTCGATATGATGATCTCCAAATGAGACATTTCCCAATGACAGACCC 303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 898 ATTGGACCTGGAGTCTGTAATGATGATCTCCAAATGAGACATTTCCCAATGACAGACCC 957
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 304 TTTCAAACGTAACAGATACATATGAGATGCGCCCAAGATGTTTGAAGCAAAACACC 363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 958 TTTCAAATGTAACAGATACATATGAGATGCGCCCAAGATGTTTGAAGCAAAACACC 1017
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 364 CTGAGTTGGCAACAGGATGCGGAATGTACAGAGAAACAACTGAGAGCCCTATTTCGGC 423
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1018 CTGAATTTGGCAACAGGATGCGGAATGTACAGAGAAACAACTGAGAGCCCTATTTCGGC 1077
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 424 GCAATAGAGAGTTTATAGAAAATGTTGGAGAGGAAATGATAGACGCTTGTAACGTTTC 483
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1078 GCAATAGAGAGTTTATAGAAAATGTTGGAGAGGAAATGATAGACGCTTGTAACGTTTC 1137
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 484 AGGATCAAAATTTGAGGGCAGACAGACAGATCTTAAAGCACTCAAGCAGCC 543
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1138 AGGATCAAAATTTGAGGGCAGACAGACAGATCTTAAAGCACTCAAGCAGCC 1197
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 544 ATGACCAAAATCAATGGAAATTTGAACAGGTAATCGAAGAGCAAGCAAGAAATTCAT 603
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1198 ATGACCAAAATCAATGGAAATTTGAACAGGTAATCGAAGAGCAAGCAAGAAATTCAT 1257
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 604 CAAATCGAAAAGATTTCTCAGAAATAGAAAGGAGAAATTCAGAGCTCGAGAAATTCGTT 663
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1258 CAAATCGAAAAGATTTCTCAGAAATAGAAAGGAGAAATTCAGAGCTCGAGAAATTCGTT 1317
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 664 GAAGACACTAAATATGATCTCTGCTTACAAATGCGGAGCTCTTGTCTGCGAGCAT 723
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1318 GAAGACACTAAATATGATCTCTGCTTACAAATGCGGAGCTCTTGTCTGCGAGCAT 1377
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 724 CAACATACAAATTTGACCTGACTGCTGGAATGAACAACCTGTTGAAAAAACAAGAGG 783
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1378 CAACATACAAATTTGACCTGACTGCTGGAATGAACAACCTGTTGAAAAAACAAGAGG 1437
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 784 CAACATGAGGAAAAATGCTGGAAGAGATGGCAATGGTTGTTAAATATACCAAAATGT 843
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1438 CAACATGAGGAAAAATGCTGGAAGAGATGGCAATGGTTGTTAAATATACCAAAATGT 1497
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 844 GACAACGGCTCATATGAGTCAATCAGAAATGTTACTTATGACCATGATGTATACAGAGAC 903
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1498 GACAATGCTCATATGAGTCAATCAGAAATGTTACTTATGACCATGATGTATACAGAGAC 1557
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

OY 904 GAACATTAACACACCGGTTTCAGATCAAAAGGTGTGATGATGATGATACAAAGAC 963
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1558 GAACATTAACACACCGGTTTCAGATCAAAAGGTGTGATGATGATGATACAAAGAC 1617
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 964 TGCATCTGTCGATTTCTTTGCAATATCATCTTTTGTGTTGTTGTTGCTGGGG 1023
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1618 TGCATCTGTCGATTTCTTTGCAATATCATCTTTTGTGTTGTTGTTGCTGGGG 1677
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1024 TTATCATATGAGGCTTCCAGAGAGGCAACATTTAGTGCATTTGATTTGATTTAT 1083
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1678 TTATCATATGAGGCTTCCAGAGAGGCAACATTTAGTGCATTTGATTTGATTTAT 1737
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1084 TACTAATTAACACACCTTTGTTCT 1109
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1738 --TAATTAACACACCTTTGTTCT 1760
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

RESULT 8
US-09-169-027-6
: Sequence 6, Application US/09169027
: Patent No. 6245532
: GENERAL INFORMATION:
: APPLICANT: Smith, Gale Eugene
: APPLICANT: Volkovitz, Franklin
: APPLICANT: Wilkinson, Bethanie Eident
: APPLICANT: Voznesensky, Andrei I.
: APPLICANT: Hackett, Craig Stanway
: TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Patrea L. Pabst
: STREET: 2800 One Atlantic Center
: STREET: 1201 West Peachtree Street
: CITY: Atlanta
: STATE: GA
: COUNTRY: USA
: ZIP: 30309-3450
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/169,027
: FILING DATE:
: CLASSIFICATION:
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US/08/453,848
: FILING DATE: 30-MAY-1995
: APPLICATION NUMBER: 08/120,607
: FILING DATE: 13-SEPT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Pabst, Patrea L.
: REGISTRATION NUMBER: 31,284
: REFERENCE/DOCKET NUMBER: MGS101CIP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (404)-873-8794
: TELEFAX: (404)-873-8795
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1793 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Influenza virus
: INDIVIDUAL ISOLATE: A/Beijing/32/92 rHA
: FEATURE:
: NAME/KEY: polyhedrin mRNA leader (partial)

```

```

? LOCATION: 1 to 18
? FEATURE:
? NAME/KEY: coding region for AcNPV 61k protein signal
? NAME/KEY: sequence
? LOCATION: 19 to 72
? FEATURE:
? NAME/KEY: SmaI restriction site
? LOCATION: 76 to 81
? FEATURE:
? NAME/KEY: coding region for mature rHA
? LOCATION: 73 to 1728
? FEATURE:
? NAME/KEY: KpnI restriction site
? LOCATION: 1771 to 1777
? FEATURE:
? NAME/KEY: BglII restriction site
? LOCATION: 1776 to 1782
? FEATURE:
? NAME/KEY: universal translation termination signal
? LOCATION: 1783 to 1793
? US-09-169-027-6

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Query Match          69.8%; Score 774.8; DB 3; Length 1793;
Best Local Similarity 94.2%; Pred. No. 1,76-246;
Matches 816; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

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? 244 ATTGATACCTGTATTTTGTGAATGCATCATCTCCAAATGGAAGATGCCCAATGACAAGCCC 303
? 898 ATTGGCACCCTGCAGTTTGTGAATGCATCATCTCCAAATGGAAGATGCCCAATGACAAGCCC 957
? 304 TTTCAAAACGTAACAGATCATCATATGAGAGCATGCCCAATGATTTAAGCAAAAACACC 363
? 958 TTTCAAAATGTAAACAGATCATCATATGAGAGCATGCCCAATGATTTAAGCAAAAACACT 1017
? 364 CTGAAGTTGGCAGACAGATGATGCGGATGTACCAAGAAAACACTAGAGGCTATTGCGC 423
? 1018 CTGAATTTGGCAACAGATGATGCGGATGTACCAAGAAAACACTAGAGGCTATTGCGC 1077
? 424 GCAATAGCAGGTTTCAAGAAAATGTTGGAGGGAATGATGAGGTTGGTACGGTTTC 483
? 1078 GCAATCGCAGGTTTCAAGAAAATGTTGGAGGGAATGATGAGGTTGGTACGGTTTC 1137
? 484 AGGCATCAAAATTTCTG/GGGCAGACAGACAGAGATCTTAAAGCACTCAAGCAGCC 543
? 1138 AGGCATCAAAATTTCTG/GGGCAGACAGACAGAGATCTTAAAGCACTCAAGCAGCA 1197
? 544 ATCGACCAAAATTCAGAAATTTGAACAGGGTAAATCGAGACAGACAGAAATTCAT 603
? 1198 ATCGACCAAAATTCAGAAATTTGAACAGGGTAAATCGAGACAGACAGAAATTCAT 1257
? 604 CAAATCGAAAAGGAATTTCTCAGAGTAGAAGGAGAGATTCAGAGCTCGAGAAATACGTT 663
? 1258 CAAATCGAAAAGGAATTTCTCAGAGTAGAAGGAGAGATTCAGAGCTCGAGAAATACGTT 1317
? 664 GAAGACACTAAATAGATCTCTGCTTACAAATGCGAGCTTCTTGCGCTCTGAGAAAT 723
? 1318 GAAGACACTAAATAGATCTCTGCTTACAAATGCGAGCTTCTTGCGCTCTGAGAAAT 1377
? 724 CAACATACAAATGAGCTTACTGACTCGGAAATGAACAGCTTTTGAAAAACAAGGAG 783
? 1378 CAACATACAAATGAGCTTACTGACTCGGAAATGAACAGCTTTTGAAAAACAAGGAG 1437
? 784 CAACATGAGGAAAATGCTGAGAGATGGGCAATGGTGGTCAAAATATACCAAAATGT 843
? 1438 CAACATGAGGAAAATGCTGAGAGATGGGCAATGGTGGTCAAAATATACCAAAATGT 1497
? 844 GACAACGCTTGCAATGATTCATTCAGAAATGCTTACTATGACCATGATGATATACAGAGC 903
? 1498 GACAATGCTTGCAATGATTCATTCAGAAATGCTTACTATGACCATGATGATATACAGAGC 1557
? 904 GAAGCATTAACACCGCTTTTACATCAAAAGTGTGGAATGAGTCTGAGATACAAAGAC 963
? 1558 GAAGCATTAACACCGCTTTTACATCAAAAGTGTGGAATGAGTCTGAGATACAAAGAT 1617

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? 964 TGAATCTGTGATTTCTTTGCAATATCATGCTTTTGTGTTGTTGCTGGG 1023
? 1618 TGAATCTGTGATTTCTTTGCAATATCATGCTTTTGTGTTGTTGCTGGG 1677
? 1024 TTTCATCATGTGGGCTGCGCAGAGAGCAACATTAGGTGCAACATTTGATGATGTAT 1083
? 1678 TTTCATCATGTGGGCTGCGCAGAGAGCAACATTAGGTGCAACATTTGATGATGTAT 1737
? 1084 TAGTATTTAAACACCTTGTTCT 1109
? 1738 ---TAATTAACACCTTGTTCT 1760

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RESULT 9

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US-08-453-848-14
? Sequence 14, Application US/08453848
? Patent No. 5858368
? GENERAL INFORMATION:
? APPLICANT: Smith, Gale Eugene
? APPLICANT: Volkovitz, Franklin
? APPLICANT: Wilkinson, Bethanie Eident
? APPLICANT: Voznesensky, Andrei I.
? TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA
? TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES
? NUMBER OF SEQUENCES: 31
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Patrea L. Pabst
? STREET: 2800 One Atlanta Center
? STREET: 1201 West Peachtree Street
? CITY: Atlanta
? STATE: GA
? COUNTRY: USA
? ZIP: 30309-3450
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/453,848
? FILING DATE: 30-MAY-1995
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/120,607
? FILING DATE: 13-SEPT-1993
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Pabst, Patrea L.
? REGISTRATION NUMBER: 31,284
? REFERENCE/DOCKET NUMBER: MGS101CIP
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (404)-873-8794
? TELEFAX: (404)-873-8795
? INFORMATION FOR SEQ ID NO: 14:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1757 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Influenza virus
? INDIVIDUAL ISOLATE: A/Shandong/9/93 rHA
? NAME/KEY: polyhedrin mRNA leader (partial)
? LOCATION: 1 to 18
? FEATURE:
? NAME/KEY: coding region for AcNPV 61k protein signal
? NAME/KEY: sequence

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; NAME/KEY: coding region for mature rRNA
; LOCATION: 73 to 1728

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US-08-453-848-20
: Sequence 20, Application US/08453848
: Patent No. 5858368
:
: GENERAL INFORMATION:
: APPLICANT: Smith, Gale Eugene
: APPLICANT: Volvovitz, Franklin
: APPLICANT: Wilkinson, Bethanie Elident
: APPLICANT: Voznesensky, Andrei I.
: APPLICANT: Hackett, Craig Stanway
: TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA
: TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES
: NUMBER OF SEQUENCES: 31
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Patrea L. pabst
: STREET: 2800 One Atlantic Center
: STREET: 1201 West Peachtree Street
: CITY: Atlanta
: STATE: GA
: COUNTRY: USA
: ZIP: 30309-3450
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/453,848
: FILING DATE: 30-MAY-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/120,607
: FILING DATE: 13-SEPT-1993
:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Pabst, Patrea L.
: REGISTRATION NUMBER: 31,284
: REFERENCE/DOCKET NUMBER: MGS101C1P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (404)-873-8794
: TELEFAX: (404)-873-8795
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1757 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
:
: ORIGINAL SOURCE:
: ORGANISM: Influenza virus
: INDIVIDUAL ISOLATE: A/Johannesburg/33/94 rHA
:
: FEATURE:
: NAME/KEY: polyhedrin mRNA leader (partial)
: LOCATION: 1 to 18
:
: FEATURE:
: NAME/KEY: coding region for ACPVY 61K protein signal
: NAME/KEY: peptide
: LOCATION: 19 to 72
:
: FEATURE:
: NAME/KEY: SmaI restriction site
: LOCATION: 76 to 81
:
: FEATURE:
: NAME/KEY: coding region for mature rHA
: LOCATION: 73 to 1731
:
: FEATURE:
: NAME/KEY: KpnI restriction site
: LOCATION: 1735 to 1740
:
: FEATURE:
: NAME/KEY: BglII restriction site
: LOCATION: 1741 to 1747
:
: FEATURE:
: NAME/KEY: universal translation termination signal

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LOCATION: 1747 to 1757
US-08-453-848-20

Query Match 67.7%; Score 751.8; DB 2; Length 1757;
Best Local Similarity 93.8%; Pred. No. 7.2e-239;
Matches 783; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

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OY 244 ATTGATACCTGTATTTCTGAATGCATCACTCCAAATGGAAGCATTCCTCAATGACAAAGCCC 303
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DB 901 ATTGGCAACTGCAGTTCTGAATGCATCACTCCAAATGGAAGCATTCCTCAATGACAAAGCCC 960
OY 304 TTTCAAAACGTAACACAGATACATATGAGCATGCCCAAGATATGTTAAGCAAAACACC 363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 961 TTTCAAAATGTAACAGCATACATATGAGCATGCCCAAGATATGTTAAGCAAAACACT 1020
OY 364 CTGAAGTTGGCAACAGGATGGGATGTACAGCAAAACAACTAGAGCCCTATTCGGC 423
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DB 1021 CTGAATTTGGCAACAGGATGGGATGTACAGCAAAACAACTAGAGCCATATTCGGC 1080
OY 424 GCAATAGCAGTTTTCATAGAAAATGGTTGGAGGAATGATAGACGGTTGTGTCAGGTTTC 483
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DB 1081 GCAATCGCAGTTTTCATAGAAAATGGTTGGAGGAATGATAGACGGTTGTGTCAGGTTTC 1140
OY 484 AGGCATCAAAATTTCTGAGGGCAGACAGCAAGCATCTTTAAAGCACTCAAGCAGCC 543
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DB 1141 AGGCATCAAAATTTCTGAGGGCAGACAGCAAGCATCTTTAAAGCACTCAAGCAGCA 1200
OY 544 ATCGACCAAAATCAATGGAATTTGAACAGGATTAATGAGCAAGCAAGCAAGCAATTCAT 603
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DB 1201 ATCGACCAAAATCAATGGAATTTGAACAGGATTAATGAGCAAGCAAGCAAGCAATTCAT 1260
OY 604 CAAATCGAAAAGAAATTTCTCAGAACTAGAGAGGAGAAATTCAGACCTCGAGAAATACGTT 663
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DB 1261 CAAATCGAAAAGAAATTTCTCAGAACTAGAGAGGAGAAATTCAGACCTCGAGAAATACGTT 1320
OY 664 GAAGCACTAAATATGATCTCTGCTTCAATGCGGAGCTTTCTGCTCGAGAAAT 723
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DB 1321 GAAGCACTAAATATGATCTCTGCTTCAATGCGGAGCTTTCTGCTCGAGAAAT 1380
OY 724 CAACATACAAATGACCTGACATCGGAAATGAACACCTGTTTAAAAAACAAGAGAG 783
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DB 1381 CAACATACAAATGATCTACTACTGACATGAATGAACAAACTGTTTAAAAAACAAGAGAG 1440
OY 784 CAACATGAGGAAATGCTGTAAGAGATGGCAATGGTTGCTTCAAAATATACCAAAATGT 843
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DB 1441 CAACATGAGGAAATGCTGTAAGAGATGGCAATGGTTGCTTCAAAATATACCAAAATGT 1500
OY 844 GACAACGGCTGCATGAGATCAATCAGAATGGTACTTATGACCATGATATATACAGAGC 903
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DB 1501 GACAATGGCTGCATGAGATCAATCAGAATGGTACTTATGACCATGATATATACAGAGC 1560
OY 904 GAAGCATTAACACACCGGTTTCAGATCAAAAGGTGTTGAAGTCAAGTCTGATACAAAGAC 963
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DB 1561 GAAGCATTAACACACCGGTTTCAGATCAAAAGGTGTTGAAGTCAAGTCTGATACAAAGAT 1620
OY 964 TGGATCTGTGATATTTCTTTGCCATATATGCTTTTCTTTGTTGTTTGTTCGGGG 1023
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DB 1621 TGGATCTGTGATATTTCTTTGCCATATATGCTTTTCTTTGTTGTTTGTTCGGGG 1680
OY 1024 TTCATCATGTGGGCTGCGCAGAGAGCAACATTAGTGCACATTTGCAATTTGAG 1078
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DB 1681 TTCATCATGTGGGCTGCGCAGAGAGCAACATTAGTGCACATTTGCAATTTGAG 1735

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RESULT 12

US-09-169-027-20

Sequence 20 Application US/09169027
Patent No. 6245352

GENERAL INFORMATION:

APPLICANT: Smith, Gale Eugene
APPLICANT: Volkovitz, Franklin
APPLICANT: Wilkenson, Bethanie Elident
APPLICANT: Voznesensky, Andrei I.

```

APPLICANT: Hackett, Craig Stanway
TITLE OF INVENTION: A METHOD FOR PRODUCING INFLUENZA
TITLE OF INVENTION: HEMAGGLUTININ MULTIVALENT VACCINES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESS: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/169,027
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/453,848
FILING DATE: 30-MAY-1995
APPLICATION NUMBER: 08/120,607
FILING DATE: 13-SEPT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MGS101CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8795
TELEFAX: (404)-873-8795
INFORMATION FOR SEO ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1757 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Influenza virus
INDIVIDUAL ISOLATE: A/Johannesburg/33/94 rHA
FEATURE:
NAME/KEY: polyhedrin mRNA leader (partial)
LOCATION: 1 to 18
FEATURE:
NAME/KEY: coding region for AcNPV 61K protein signal
peptide
LOCATION: 19 to 72
FEATURE:
NAME/KEY: SmaI restriction site
LOCATION: 76 to 81
FEATURE:
NAME/KEY: coding region for mature rHA
LOCATION: 73 to 1731
FEATURE:
NAME/KEY: KpnI restriction site
LOCATION: 1735 to 1740
FEATURE:
NAME/KEY: BglII restriction site
LOCATION: 1741 to 1747
FEATURE:
NAME/KEY: universal translation termination signal
LOCATION: 1747 to 1757

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US-09-169-027-20

Query Match 67.7%; Score 751.8; DB 3; Length 1757;
Best Local Similarity 93.8%; Pred. No. 7.2e-239;
Matches 783; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 666 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..663
PCT-US94-01149-1

Query Match 58.1%; Score 645.2; DB 5; Length 666;
Best Local Similarity 98.0%; Pred. No. 8.8e-204;
Matches 653; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY	412	GGCCTATTGGCGCATATGAGGTTTCATAGAAAATGTTGGAGGGAATGATGACGGT	471
Db	1	GGCATATTGCGCGCATATGAGGTTTCATAGAAAATGTTGGAGGGAATGATGACGGT	60
QY	472	TGGTAGGGTTTCAGGCAATTCAGAGGCGACAGACAGCAGCATCTTAAAGC	531
Db	61	TGGTAGGGTTTCAGGCAATTCAGAGGCGACAGACAGCAGCATCTTAAAGC	120
QY	532	ACTCAGCAGCATCGCAATTCAGAGGGAATTTGAACAGGTAATCGAAGACGAAC	591
Db	121	ACTCAGCAGCATCGCAATTCAGAGGGAATTTGAACAGGTAATCGAAGACGAAC	180
QY	592	GAGAAATTCATCAATTCGAAAAGGAATTCAGAGTACAGAGGAGAAATTCAGACCTC	651
Db	181	GAGAAATTCATCAATTCGAAAAGGAATTCAGAGTACAGAGGAGAAATTCAGACCTC	240
QY	652	GAGAAATACGTTGAGACACTAAATATGATCTGTCCTTACATGCGGAGCTTCTGTC	711
Db	241	GAGAAATACGTTGAGACACTAAATATGATCTGTCCTTACATGCGGAGCTTCTGTC	300
QY	712	GCTCTGAGAAATCAACATTAATGACCTGACTCGGAAATGAACAAGCTGTTGAA	771
Db	301	GCTCTGAGAAATCAACATTAATGATGATCTGTCCTTACATGCGGAGCTTCTGTC	360
QY	772	AAAAACAAGGAGGCACTGAGGGAATGCTGAGAGATGGCAATGCTGCTTCAAAATA	831
Db	361	AAAAACAAGGAGGCAACGAGGGAATGCTGAGAGATGGCAATGCTGCTTCAAAATA	420
QY	832	TACCACAAATGTGCAACGCTGATAGAGTCATCAGAAATGCTACTTATGACCATGAT	891
Db	421	TACCACAAATGTGCAATGCTGATAGAGTCATCAGAAATGCTACTTATGACCATGAT	480
QY	892	GTATACAGAGCAGAGATTAAACAACCGTTTCAGATCAAAAGGTGTTGAAGTGAAGTCT	951
Db	481	GTATACAGAGCAGAGATTAAACAACCGTTTCAGATCAAAAGGTGTTGAAGTGAAGTCA	540
QY	952	GGATACAAAGACTGGAATCTGTGATTTCTTTGCAATATCATGCTTTTGCTTGTGT	1011
Db	541	GGATACAAAGACTGGAATCTGTGATTTCTTTGCAATATCATGCTTTTGCTTGTGT	600
QY	1012	GTTTGTGGGGTTTCATAGTGGGCTCGCAGAGAGCAACATTTAGTGCACATTTGC	1071
Db	601	GTTTGTGGGGTTTCATAGTGGGCTCGCAGAGAGCAACATTTAGTGCACATTTGC	660
QY	1072	ATTGGA 1077	
Db	661	ATTGGA 666	

Search completed: August 10, 2003, 16:15:41
Job time : 59.4921 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 19:23:49 ; Search time 56.4921 Seconds
(Without alignments)
8672.640 Million cell updates/sec

Title: US-09-918-568-57

Perfect score: 1110

Sequence: 1 CTGAGAGCAAAACAGGGGAT.....TAAACACCCCTGTTCTG 1110

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/pdata/2/ina/6A_COMB.seq : *
4: /cgn2_6/pdata/2/ina/6B_COMB.seq : *
5: /cgn2_6/pdata/2/ina/PCOTUS_COMB.seq : *
6: /cgn2_6/pdata/2/ina/backfiles1.seq : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1110	100.0	1110	US-08-229-781-57	Sequence 57, Appl
2	1110	100.0	1110	US-08-630-918-57	Sequence 57, Appl
3	1110	100.0	1110	US-09-004-422-57	Sequence 57, Appl
4	868	78.2	1777	US-08-229-781-54	Sequence 54, Appl
5	868	78.2	1777	US-08-630-918-54	Sequence 54, Appl
6	868	78.2	1777	US-09-004-422-54	Sequence 54, Appl
7	774.8	69.8	1793	US-08-453-848-6	Sequence 6, Appl
8	774.8	69.8	1793	US-09-169-027-6	Sequence 6, Appl
9	756.6	68.2	1757	US-08-453-848-14	Sequence 14, Appl
10	756.6	68.2	1757	US-09-169-027-14	Sequence 14, Appl
11	751.8	67.7	1757	US-08-453-848-20	Sequence 20, Appl
12	751.8	67.7	1757	US-09-169-027-20	Sequence 20, Appl
13	745.4	67.2	1701	US-09-232-468A-21	Sequence 21, Appl
14	745.4	67.2	1701	US-09-784-984B-17	Sequence 17, Appl
15	645.2	58.1	666	PCT-US94-01149-1	Sequence 1, Appl
16	642	57.8	666	PCT-US94-01149-3	Sequence 3, Appl
17	641.4	57.8	918	PCT-US94-01149-9	Sequence 9, Appl
18	631.8	56.9	670	PCT-US94-01149-58	Sequence 58, Appl
19	630.2	56.8	670	US-09-506-286B-10	Sequence 10, Appl
20	605.2	54.5	1762	US-09-762-861B-10	Sequence 10, Appl
21	605.2	54.5	1762	US-08-105-483-284	Sequence 284, App
22	603.6	54.4	1762	US-08-105-483-300	Sequence 300, App
23	603.6	54.4	1762	US-08-709-209-284	Sequence 284, App
24	603.6	54.4	1762	US-08-709-209-300	Sequence 300, App
25	603.6	54.4	1762	US-08-458-101-284	Sequence 284, App
26	603.6	54.4	1762	US-08-458-101-300	Sequence 300, App
27	603.6	54.4	1762	US-08-458-101-300	Sequence 300, App

28	602	54.2	1762	4	US-09-506-286B-7	Sequence 7, Appl
29	602	54.2	1762	4	US-09-762-861B-7	Sequence 7, Appl
30	581.2	52.4	1698	3	US-09-232-478-15	Sequence 15, Appl
31	581.2	52.4	1698	4	US-09-785-055-15	Sequence 15, Appl
32	579.8	52.2	1695	4	US-09-506-286B-12	Sequence 12, Appl
33	579.8	52.2	1695	4	US-09-762-861B-12	Sequence 12, Appl
34	576.6	51.9	1695	4	US-09-506-286B-9	Sequence 9, Appl
35	576.6	51.9	1695	4	US-09-762-861B-9	Sequence 9, Appl
36	418.4	37.7	690	5	PCT-US94-01149-11	Sequence 11, Appl
37	418.4	37.7	690	5	PCT-US94-01149-71	Sequence 71, Appl
38	329	29.6	329	1	US-08-229-781-37	Sequence 37, Appl
39	329	29.6	329	1	US-08-630-918-37	Sequence 37, Appl
40	329	29.6	329	4	US-09-004-422-37	Sequence 37, Appl
41	320.2	28.8	6802	4	US-08-809-513A-6	Sequence 6, Appl
42	311.6	28.1	334	1	US-08-229-781-38	Sequence 38, Appl
43	311.6	28.1	334	1	US-08-630-918-38	Sequence 38, Appl
44	311.6	28.1	334	4	US-09-004-422-38	Sequence 38, Appl
45	306.2	27.6	1759	1	US-08-105-483-279	Sequence 279, App

ALIGNMENTS

RESULT 1
US-08-229-781-57
Sequence 57, Application US/08229781
Patent No. 5589174
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSES: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08229,781
FILING DATE: April 19, 1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 1110 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: A2/Alchl/2/68
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:

HAPLOTYPE:
TISSUE TYPE:
CELL LINE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-229-781-57

Query Match
Best Local Similarity 100.0%; Score 1110; DB 1; Length 1110;
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTAGAAGCAAGCAGGCGATATTTATTTATCATGAGACCATCATTTGCTTTGAGCTAC 60
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QY 121 TGCCCTGGACATCATGCGGTCGCCAAGCAACACTAGTGAAGCAATCATCAGATGATCAG 180
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QY 241 AATATGTACTCTGATTTCTGAATGATCATCTCCAAATGGAAGATTCCCAATGACAG 300
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DB 301 CCCTTTCAAAAGCTAATGATGAGATGAGAGATGCCCAAGTATGTTAAGCAAAAC 360
QY 361 ACCCTGAAGTTGGCAGACAGGATGCGGAATGACAGAGAAACAACTAGAGGCTATTG 420
DB 361 ACCCTGAAGTTGGCAGACAGGATGCGGAATGACAGAGAAACAACTAGAGGCTATTG 420
QY 421 GGGCAATAGCAGGTTTATGAAATGTTGGGAGGGAATGATGAGGCTGTTAGCGT 480
DB 421 GGGCAATAGCAGGTTTATGAAATGTTGGGAGGGAATGATGAGGCTGTTAGCGT 480
QY 481 TTTCAGGATCAAAATTTCTGAGGACACAGACAGAGATCTTAAAGACACTAAGCA 540
DB 481 TTTCAGGATCAAAATTTCTGAGGACACAGACAGAGATCTTAAAGACACTAAGCA 540
QY 541 GCCATCGACCAATCAATGAGAAATTTGAACAGGATTAATGAGAGCAAGCAAGAAATTC 600
DB 541 GCCATCGACCAATCAATGAGAAATTTGAACAGGATTAATGAGAGCAAGCAAGAAATTC 600

DB 541 GCCATCGACCAATCAATGAGAAATTTGAACAGGATTAATGAGAGCAAGCAAGAAATTC 600
QY 601 CATCAATTCGAAAGAAATTTCTCAGAAATTAAGAGGAAATTTCCAGACCTGAGAAATTC 660
DB 601 CATCAATTCGAAAGAAATTTCTCAGAAATTAAGAGGAAATTTCCAGACCTGAGAAATTC 660
QY 661 GTTGAAGACACTAAATATGATCTGCTCTTACAAATGCGGAGCTCTGCTGCTGAG 720
DB 661 GTTGAAGACACTAAATATGATCTGCTCTTACAAATGCGGAGCTCTGCTGCTGAG 720
QY 721 AATCAACATCAATTAATGACCTGACTGAGTGGAAATGAACAGCTGTTGAAAAACAAG 780
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DB 781 AGGCAACTGAGGAAATGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
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DB 901 GACGAGCATTAACACACCGGTTTCAATCAAGAGTGTGAACAGTCTGATACAAA 960
QY 961 GACTGAGCTCTGATTTCTTCCCTTGCATATCATGCTTTGCTTGTGTTTCTG 1020
DB 961 GACTGAGCTCTGATTTCTTCCCTTGCATATCATGCTTTGCTTGTGTTTCTG 1020
QY 1021 GGTTTCATCATGAGGCGCTGCGAGAGAGCAACATTTAGGTGCAACATTTGATGAGT 1080
DB 1021 GGTTTCATCATGAGGCGCTGCGAGAGAGCAACATTTAGGTGCAACATTTGATGAGT 1080
QY 1081 TATTAGTAAATTAACACACCTTTGTTCTG 1110
DB 1081 TATTAGTAAATTAACACACCTTTGTTCTG 1110

RESULT 2.

US-08-630-918-57
Sequence 57, Application US/08630918
Patent No. 5631350
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESS: Wenderoth, Lind & Penack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,918
FILING DATE: April 5, 1996
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993.
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 18:20:24 ; Search time 178.294 Seconds
(without alignments)
12843.535 Million cell updates/sec

Title: US-09-918-568 57

Perfect score: 1110

Sequence: 1 CTGAGAGCAAAACGAGGAGAT.....TAAACACCCCTGTTCTG 1110

Scoring table: IDENTITY_NUC

Gapop 10.0, (gapext 1.0)

Searched: 1439767 seqs, 1031500376 residues 2879534

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	LB	ID	Description
1	1110	100.0	1110	9	US-09-918-568-57	Sequence 57, Appl
2	868	78.2	1777	9	US-09-918-568-54	Sequence 54, Appl
3	329	29.6	329	9	US-09-918-568-37	Sequence 37, Appl
4	321	28.9	1711	13	US-10-099-619-1	Sequence 1, Appl
5	311.6	28.1	334	9	US-09-918-568-38	Sequence 38, Appl
6	305.2	27.5	334	9	US-09-918-568-40	Sequence 40, Appl
7	301.8	27.2	329	9	US-09-918-568-39	Sequence 39, Appl
8	295.4	26.6	329	9	US-09-918-568-41	Sequence 41, Appl
9	254.2	22.9	1754	9	US-09-918-568-27	Sequence 27, Appl
10	252.6	22.8	1135	9	US-09-918-568-49	Sequence 49, Appl
11	248.2	22.7	1783	9	US-09-918-568-46	Sequence 46, Appl
12	248.2	22.4	1728	9	US-09-918-568-28	Sequence 28, Appl
13	160.4	14.5	429	9	US-09-918-568-32	Sequence 32, Appl
14	157.4	14.2	424	9	US-09-918-568-31	Sequence 31, Appl
15	157	14.1	442	9	US-09-918-568-29	Sequence 29, Appl
16	152.6	13.7	424	9	US-09-918-568-30	Sequence 30, Appl

17	137.2	12.4	409	9	US-09-918-568-34	Sequence 34, Appl
18	134.6	12.1	394	9	US-09-918-568-36	Sequence 36, Appl
19	134.6	12.1	400	9	US-09-918-568-33	Sequence 33, Appl
20	134.6	12.1	410	9	US-09-918-568-35	Sequence 35, Appl
21	42	3.8	2981	14	US-10-242-056-56	Sequence 56, Appl
22	39.6	3.6	440	11	US-09-918-993-15008	Sequence 15008, A
23	39.6	3.6	1059	10	US-09-911-345-3	Sequence 3, Appl
24	38.6	3.5	10906	9	US-09-956-004-63	Sequence 63, Appl
25	38	3.4	414	14	US-10-123-155-418	Sequence 418, Appl
26	38	3.4	414	15	US-10-146-731-418	Sequence 418, Appl
27	37.4	3.4	592	13	US-10-027-632-215470	Sequence 215470, A
28	37.4	3.4	671	14	US-10-184-644-346	Sequence 346, Appl
29	37.4	3.4	1049	10	US-10-184-634-346	Sequence 346, Appl
30	37.4	3.4	1049	10	US-09-833-381-855	Sequence 855, Appl
31	37.4	3.4	1052	11	US-09-764-891-7527	Sequence 7527, Ap
32	37.4	3.4	1052	11	US-09-764-881-191	Sequence 191, Appl
33	37.4	3.4	1077	11	US-09-764-881-1210	Sequence 1210, Ap
34	37.4	3.4	1077	11	US-09-764-881-1210	Sequence 70, Appl
35	36.8	3.3	592	13	US-10-027-632-298985	Sequence 84403, A
36	36.8	3.3	2100	10	US-09-834-975-862	Sequence 862, Appl
37	36.8	3.3	2100	10	US-09-834-975-957	Sequence 957, Appl
38	36.8	3.3	2100	10	US-09-834-975-964	Sequence 964, Appl
39	36.8	3.3	2100	10	US-09-834-975-1008	Sequence 1008, Ap
40	36.8	3.3	15714	9	US-09-764-869-2355	Sequence 2355, Ap
41	36.8	3.3	15714	14	US-10-091-504-2355	Sequence 2355, Ap
42	36.8	3.3	696	9	US-09-770-149-281	Sequence 281, Appl
43	36.6	3.3	1160	14	US-10-123-155-234	Sequence 234, Appl
44	36.2	3.3	1160	15	US-10-146-731-234	Sequence 234, Appl
45	36.2	3.3	1160	15	US-10-146-731-234	Sequence 234, Appl

ALIGNMENTS

RESULT 1
US-09-918-568-57
Sequence 57, Application US/09918568
Patent No. US20020054882A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 1110 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <unknown>
ANTI-SENSE: <unknown>
FRAGMENT TYPE: <unknown>
ORIGINAL SOURCE:
ORGANISM: A2/Aichi/2/68
STRAIN: <unknown>
INDIVIDUAL ISOLATE: <unknown>
DEVELOPMENTAL STAGE: <unknown>
HAPLOTYPE: <unknown>
TISSUE TYPE: <unknown>
CELL TYPE: <unknown>
ORGANELLE: <unknown>
IMMEDIATE SOURCE:
LIBRARY: <unknown>
CLONE: <unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <unknown>
MAP POSITION: <unknown>
UNITS: <unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-918-568-57

Query Match 100.0%; Score 1110; DB 9; Length 1110;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 CTAGAGCAAGCAGGGGATATCTATTAATCATGAGACCATTCCTTTGAGCTAC 60
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DB 541 GCCATGACCAAAATCAATGGAATTTGAACAGGTAATTCGAGAACAGCAGCAAAATTC 600
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601 CATCAATGCAAAAGGAATTCAGAGATGAGAGGAGAAATTCAGGACCTCGAGAAATAC 660
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661 GTTGAAGACATAAATAGATCTGCTCTTACAAATGCGAGCTTCTGCTGCTGAGAG 720
DB 661 GTTGAAGACATAAATAGATCTGCTCTTACAAATGCGAGCTTCTGCTGCTGAGAG 720
721 AATCAACATACAAATGACCTGACTGCTGGAATGAACAGCTGTTGAAAAAACAAG 780
721 AATCAACATACAAATGACCTGACTGCTGGAATGAACAGCTGTTGAAAAAACAAG 780
DB 721 AATCAACATACAAATGACCTGACTGCTGGAATGAACAGCTGTTGAAAAAACAAG 780
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DB 1081 TATTAGTAATTAATAAACACCTTGTCTG 1110

RESULT 2
US-09-918-568-54
Sequence 58, Application US/09918568
Patent No. US2002005482A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESS: Wenderoth, Lind & Ponack, L.L.P.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.

ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: us/09/918,568
FILING DATE: 02 Aug-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A2/Aichl/2/68.
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
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AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUE: IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-09-918-568-54

Query Match 78.2%; Score 868; DB 9; Length 1777;
Best Local Similarity 100.0%; Pred. No. 2.1e-252;
Matches 868; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	903	TATTGATACCTGTATTTCTGTAATGATCATCTCCAAATGGAAGATTTCCCAATGACAAGCC	962
QY	303	CTTTCAAAACGTAACACAGATTCACATATGAGCATGCCCCCAAGTATGTTAAGCAAAACAC	362
DB	963	CTTTCAAAACGTAACACAGATTCACATATGAGCATGCCCCCAAGTATGTTAAGCAAAACAC	1022
QY	363	CCGAAGTTGGCAACAGGATGGGGAATGACAGAGAAACAAACTAGAGGCTATTTCGG	422
DB	1023	CCGAAGTTGGCAACAGGATGGGGAATGACAGAGAAACAAACTAGAGGCTATTTCGG	1082
QY	423	CGCAATAGCAGGTTTATAGAAAATGTTGGAGGGAATGATGACGCTTGATCGGTTT	482
DB	1083	CGCAATAGCAGGTTTATAGAAAATGTTGGAGGGAATGATGACGCTTGATCGGTTT	1142
QY	483	CAGGCATCAAAATTTGAGGGCACAGACAGACAGATCTTAAAGCACTCAAGCAGC	542
DB	1143	CAGGCATCAAAATTTGAGGGCACAGACAGACAGATCTTAAAGCACTCAAGCAGC	1202
QY	543	CATGACCAATATCAATGGGAAATTTGAACAGGTAATGAGAAACAGCAAGCAAAATTC	602
DB	1203	CATGACCAATATCAATGGGAAATTTGAACAGGTAATGAGAAACAGCAAGCAAAATTC	1262
QY	603	TCAATCGAAAAGAAATTCAGAGATGAGAGGAGAAATTCAGACCTCGAAGAAATCGT	662
DB	1263	TCAATCGAAAAGAAATTCAGAGATGAGAGGAGAAATTCAGACCTCGAAGAAATCGT	1322
QY	663	TGAAGACACTAAATATGATCTGCTCTTAACAATGCCGACCTTCTGCTCGAGAA	722
DB	1323	TGAAGACACTAAATATGATCTGCTCTTAACAATGCCGACCTTCTGCTCGAGAA	1382
QY	723	TCAACATCAATGACCTGACCTGACCTCGGAAATGAAACAACTGTTGAAAAACAAGAG	782
DB	1383	TCAACATCAATGACCTGACCTGACCTCGGAAATGAAACAACTGTTGAAAAACAAGAG	1442
QY	783	GCAACTGAGGGAATGCTGTAAGAGATGGCAATGTTGCTTCAAAATATACCAAAATG	842
DB	1443	GCAACTGAGGGAATGCTGTAAGAGATGGCAATGTTGCTTCAAAATATACCAAAATG	1502
QY	843	TGACAAAGCTTGCATGAGTCAATCAGAAATGTTACTTATGACCATGATGTATACAGAG	902
DB	1503	TGACAAAGCTTGCATGAGTCAATCAGAAATGTTACTTATGACCATGATGTATACAGAG	1562
QY	903	CGAAGCATTAACAAACCGGTTTCAGATCAAAAGGTTGAGCAATGCTGATACAAAGA	962
DB	1563	CGAAGCATTAACAAACCGGTTTCAGATCAAAAGGTTGAGCAATGCTGATACAAAGA	1622
QY	963	CTGATCTCTGTGATTTCTTTGCCATATCATCTTTTCTGTTGTTGCTGGG	1022
DB	1623	CTGATCTCTGTGATTTCTTTGCCATATCATCTTTTCTGTTGTTGCTGGG	1682
QY	1023	GTTTCATCATGTGGGCTGCGCAGAGAGCAACATTAGTGCACATTTGCAATTTGAGTGA	1082
DB	1683	GTTTCATCATGTGGGCTGCGCAGAGAGCAACATTAGTGCACATTTGCAATTTGAGTGA	1742
QY	1083	TTAGTAATTAACAAACCCCTGTTTCTG 1110	
DB	1743	TTAGTAATTAACAAACCCCTGTTTCTG 1770	

RESULT 3
US-09-918-568-37
Sequence 37, Application us/09918568
Patent No. US20020054882A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING

ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)

NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/228,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993

ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A2/Aichi/2/68
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>

FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:

PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 37;
US-09-918-568-37

Query Match 29.6%; Score 329; DB 9; Length 329;
Best Local Similarity 100.0%; Pred. No. 2,5e-89;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 293 ATGACAGCCCTTTCAAAAGTAAACAGATACATATGAGACATGCCCAAGTATGTTA 352
|||||
DB 1 ATGACAGCCCTTTCAAAAGTAAACAGATACATATGAGACATGCCCAAGTATGTTA 60
|||||

QY 353 AGCAAAACACCTGAGTTGGCAACAGGGATCGGAATGTACAGAGAAGAACTAGAG 412
|||||
DB 61 AGCAAAACACCTGAGTTGGCAACAGGGATCGGAATGTACAGAGAAGAACTAGAG 120
|||||

QY 413 GCCTATGCGGCGCAATAGAGGTTTCATAGAAATGTTGGAGGAAATGATAGCGTT 472
|||||
DB 121 GCCTATGCGGCGCAATAGAGGTTTCATAGAAATGTTGGAGGAAATGATAGCGTT 180
|||||

QY 473 GGTACGTTTCAGGCATCAAAATCTGAGGCGACAGCAAGCAGACATCTTAAAGCA 532
|||||
DB 181 GGTACGTTTCAGGCATCAAAATCTGAGGCGACAGCAAGCAGACATCTTAAAGCA 240
|||||

QY 533 CTCACAGCAGCCATCGACCAATCAATGGGAATGGAAGGTAATCGAGAAGCAAGC 592
|||||
DB 241 CTCACAGCAGCCATCGACCAATCAATGGGAATGGAAGGTAATCGAGAAGCAAGC 300
|||||

QY 593 AGAAATTCATCAATCGAAAGGAATTC 621
|||||
DB 301 AGAAATTCATCAATCGAAAGGAATTC 329
|||||

RESULT 4

US-10-099-619-1
Sequence 1, Application US/10099619
Publication No. US20020168384A1
GENERAL INFORMATION:
APPLICANT: CLAESSENS, JOHANNES AJ
APPLICANT: WALTER, FUCHS
TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS VACCINE
FILE REFERENCE: 20010010US
CURRENT APPLICATION NUMBER: US/10/099,619
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: EP012009759
PRIOR FILING DATE: 2001-03-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1711
TYPE: DNA
ORGANISM: AVIAN INFLUENZA VIRUS
FEATURE:
NAME/KEY: CDS
LOCATION: (11)..(1705)
OTHER INFORMATION: ISOLATE A/ITALY/445/99 (H7/N1)
US-10-099-619-1

Query Match 28.9%; Score 321; DB 13; Length 1711;
Best Local Similarity 63.3%; Pred. No. 1,9e-86;
Matches 517; Conservative 0; Mismatches 285; Indels 15; Gaps 1;

QY 280 GAACGATTCACCAATGACAGCCCTTCAAAACGTAACAGATACATATGAGCATGC 339
|||||
DB 893 GGGACAAATATATAGTAATTTGCCCTTCAGAACATAATATAGCAGGCAATGGAATGTT 952
|||||

QY 340 CCCAAGTATGTTAAGCAAAACACCCCTGAAGTTGGCAACAGGAGTGCAGAAATGTACAGAG 399
|||||

Db 1 ATGACAAACCCCTTTCAAAATGTAACAGATCATATATGGGCGATGTCACGGTATGTTA 60
QY 353 ACACAAACACCCCTGAAGTTGGCAACAGGGATGCGGATGTACACAGAAACAACTAGAG 412
Db 61 ACACAAACACCTGTGAATTTGGCAACAGGGATGCGGATGTACACAGAAACAACTAGAG 120
QY 413 GCCTATTCGGCCCAATAGCAGGTTTTCATAGAAAATGTTGGAGGGAATGATAGCGTT 472
Db 121 GCATATTCGGCCCAATAGCAGGTTTTCATAGAAAATGTTGGAGGGAATGATAGCGTT 180
QY 473 GGTAGCGTTTCAGGCATCAAAATTCGAGGGCACAGACAGCAGATCTTAAAGCA 532
Db 181 GGTAGCGTTTCAGGCATCAAAATTCGAGGGCACAGACAGCAGATCTTAAAGCA 240
QY 533 CTCAGACAGCCATCGACCAATTCATGGAATTTGAACAGGCTAATCGAAGACGAGC 592
Db 241 CTCAGACAGCCATCGACCAATTCATGGAATTTGAACAGGCTAATCGAAGACGAGC 300
QY 593 AGAAATTCATCAATCGAAGAAAGGAATTCCTAGA 626
Db 301 AGAAATTCATCAATCGAAGAAAGGAATTCCTAGA 334

RESULT 6

US-09-918-568-40
Sequence 40, Application US/09918568
Patent No. US20020054882A1

GENERAL INFORMATION:

APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 Inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/228,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:
LENGTH: 334 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>

ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/ibarak1/90
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-09-918-568-40

Query Match

27.5%; Score 305.2; DB 9; Length 334;

Best Local Similarity 94.6%; Pred. No. 4.3e-82;

Matches 316; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 293 ATGACAAACCCCTTTCAAAATGTAACAGATCATATGAGCATGCCCAAGTATGTTA 352
Db 1 ATGACAAACCCCTTTCAAAATGTAACAGATCATATGAGCATGCCCAAGTATGTTA 60
QY 353 ACACAAACACCCCTGAAGTTGGCAACAGGGATGCGGATGTACACAGAAACAACTAGAG 412
Db 61 ACACAAACACCTGTGAATTTGGCAACAGGGATGCGGATGTACACAGAAACAACTAGAG 120
QY 413 GCCTATTCGGCCCAATAGCAGGTTTTCATAGAAAATGTTGGAGGGAATGATAGCGTT 472
Db 121 GCATATTCGGCCCAATAGCAGGTTTTCATAGAAAATGTTGGAGGGAATGATAGCGTT 180
QY 473 GGTAGCGTTTCAGGCATCAAAATTCGAGGGCACAGACAGCAGATCTTAAAGCA 532
Db 181 GGTAGCGTTTCAGGCATCAAAATTCGAGGGCACAGACAGCAGATCTTAAAGCA 240
QY 533 CTCAGACAGCCATCGACCAATTCATGGAATTTGAACAGGCTAATCGAAGACGAGC 592
Db 241 CTCAGACAGCCATCGACCAATTCATGGAATTTGAACAGGCTAATCGAAGACGAGC 300
QY 593 AGAAATTCATCAATCGAAGAAAGGAATTCCTAGA 626
Db 301 AGAAATTCATCAATCGAAGAAAGGAATTCCTAGA 334

RESULT 7

US-09-918-568-39

Sequence 39, Application US/09918568

Patent No. US20020054882A1

GENERAL INFORMATION:

FILED DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/Suita/1/90
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-918-568-41
Query Match 26.6% Score 295.4 DB 9 Length 329:
Best Local Similarity 93.6% Pred No. 4e-79 Indels 0 Gaps 0:
Matches 308: Conservative 0; Mismatches 21; Indels 0; Gaps 0:
QY 293 ATGACAGCCCTTCAAAAAGTAAACAAGATCATATGAGACATGCCCAAGTATGTTA 352
DB 1 ATGACAAACCTTTCAAAATGTAACAGATCACAATATGGGCGCATGTCCACATATGTTA 60
QY 353 AGCAAAACACCTTGAAGTTGGCAACAGGATGCGGAATGTACAGAGAAACAACCTAGAG 412
DB 61 AGCAAAACACCTTGAAGTTGGCAACAGGATGCGGAATGTACAGAGAAACAACCTAGAG 120
QY 413 GCGTATTCGGGCAATAGCAGGTTTCATAGAAATGTTGGAGGAGGATGATAGCGGTT 472
DB 121 GCATATTCGGGCAATCGCAGGTTTCATAGAAATGTTGGAGGAGGATGATAGCGGTT 180
QY 473 GGTACGGTTTCAGGCATCAAAATTCGTAGGCGACAGGACAGCAACGACAGATCTTAAGACA 532

DB 181 GGTACGGTTTCAGGCATCAAAACTGTAGGCGACAGGACAGCAACGACAGATCTTAAGACA 240
QY 533 CTCAGACAGCCATCGACCAATCATATGGAATTTACAGGTTATCGAGACGACG 592
DB 241 CTCAGACAGCCATCGACCAATCATATGGAATTTACAGGAGGAACTGAATGTTATCGAGACGACG 300
QY 593 AGAAATTCATCAATCGAAAGGAATTC 621
DB 301 AGAAATTCATCAATCGAAAGGAATTC 329
RESULT 9
US-09-918-568-27
Sequence 27: Application US/09918568
Patent No. US20020054882A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918-568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004-422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1754 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/Suita/1/89
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>


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? ORGANELLE: <Unknown>
? IMMEDIATE SOURCE:
? LIBRARY: <Unknown>
? CLONE: <Unknown>
? POSITION IN GENOME:
? CHROMOSOME/SEGMENT: <Unknown>
? MAP POSITION: <Unknown>
? UNITS: <Unknown>
? FEATURE:
? NAME/KEY:
? LOCATION:
? IDENTIFICATION METHOD:
? OTHER INFORMATION:
? PUBLICATION INFORMATION:
? AUTHORS:
? TITLE:
? JOURNAL:
? VOLUME:
? ISSUE:
? PAGES:
? DATE:
? DOCUMENT NUMBER:
? FILING DATE:
? PUBLICATION DATE:
? RELEVANT RESIDUES IN SEQ ID NO:
? SEQUENCE DESCRIPTION: SEQ ID NO: 27:
? US-09-918-568-27

Query Match 22.9% Score 254.2; DB 9; Length 1754;
Best Local Similarity 57.7% Pred. No. 3,5e-06;
Matches 454; Conservative 0; Mismatches 333; Indels 0; Gaps 0;

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	Query Match	22.9%	Score 254.2	DB 9	Length 1754	
	Best Local Similarity	57.7%	Pred. No. 3.5e-66			
	Matches 454	Conservative	0	Mismatches 333	Indels 0	Gaps 0
QY	244	ATTGATACCTGTTATTT	TTGAATGCATCATCTCCAAATGGAAAGCATTTCCCAATGACAAAGCC	303		
Db	885	ATGGATGAAATGTGACG	TCGAAGTGTCAAAACACCACCGAGAGCTATTAACAGTAGTCTTCT	944		
QY	304	TTTCAAAAACGTAACA	AGATCACAATATGAGACATAGCCCAAGTAGTATTTAAGCAAAACAC	363		
Db	945	TTCCAGATGTACACC	AGTCCACATATGGAAGATGTCCAAAGTAGTACAGAGTACAAA	1004		
QY	364	CTGAAGTTGGCAACAG	CCATGCGGAATGTACAGAGAAACAAACATGAGGCTATTCCGC	423		
Db	1005	TTAAGATGTGTACAG	AGCTAAGGAAACATCCCATTCATTCATCCAGAGTTGTGTGGA	1064		
QY	424	GCATAGCAGGTTTCA	TGAAAATATGTTGGAGGGAATGATATAGCGTTGTTCACGTTTC	483		
Db	1065	GCCATTTCCTGGTTTCAT	TGGAAGGGGGGGGACTGGAAAGATAGATAGATGTATGTGTAT	1124		
QY	484	AGGCATCAAAATTTCTG	AGGCGACAGGACAAACAGACAGATCTTAAAGACATCAACAGCC	543		
Db	1125	CATCATCAGATGAAAC	AAGGATCTGCGCTATCTCTCGGATCAAAAAGACACACAAATATCC	1184		
QY	544	ATGCACCAATCAATG	CGAAATTGAACAGGTAATCGAAGAGACGAGAGAAATTCAT	603		
Db	1185	ATTACGGAATTAACAA	CCAGGTAATTTCTTAATCGAGAAATGAACATCAATTCACA	1244		
QY	604	CAATTCGAAAAGGAT	CTCGAGTGTGAAGGAGAAATTCAGGACCTCGAGAAATACGTT	663		
Db	1245	GCTGTGGGCAAGAAAT	CAACAAATTTGAAAGAAAGATGGAATCTTAATAAATAAAAGTT	1304		
QY	664	GAAACACATTAATAATAG	TCTCTGGTCTTACATCGGAGATCTTCTGTGCTCTGGAGAT	723		
Db	1305	GATGATGGAATTTGGG	CATTTTGACATATATATCGAAGATTTGTGGTTCTTACTGGAAAT	1364		
QY	724	CACATACAAATTGACC	GCATCGATCGGAATGAACAAGCTGTTTGAAAAACAAGAGG	783		
Db	1365	GAAAGGACTTTGGATT	TCATGAGCTCAAAATGTGAAGATCTGTATGAGAAAGTAAAGAGC	1424		
QY	784	CAACTGGAGGAAATGC	TGAAGAGATGGGCATGTTCTCTTCAAAATATTAACACAAATGT	843		
Db	1425	CAATTAAGAATATATGC	CAAGAATATAGATATACGGGTGTTTGAATTTCTACCAACAAGTGT	1484		
QY	844	GACACGCTTGCAATAG	GTCAATCAGAAATGTACTTATGACCATGATGTATACAGAGAC	903		

[illegible]

RESULT 10
 US-09-918-568-49
 Sequence 49, Application US/09918568
 Patent No. US20020054882A1
 GENERAL INFORMATION:
 APPLICANT: Yoshinobu OKUNO et al.
 TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
 ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
 STREET: 2033 K Street, N.W., #800
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20006
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/918,568
 FILING DATE: 02-Aug-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/004,422
 FILING DATE: January 8, 1998
 APPLICATION NUMBER: 08/443,862
 FILING DATE: May 22, 1995
 APPLICATION NUMBER: 08/229,781
 FILING DATE: April 19, 1994
 APPLICATION NUMBER: 08/054,016
 FILING DATE: April 29, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren M. Cheek, Jr.
 REGISTRATION NUMBER: 33,367
 REFERENCE/DOCKET NUMBER: <Unknown>
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-721-8200
 TELEFAX: 202-721-8250
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1135 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to genomic RNA
 HYPOTHETICAL: <Unknown>
 ANTI-SENSE: <Unknown>
 FRAGMENT TYPE: <Unknown>
 ORIGINAL SOURCE:
 ORGANISM: A/Okuda/57
 STRAIN: <Unknown>
 INDIVIDUAL ISOLATE: <Unknown>
 DEVELOPMENTAL STAGE: <Unknown>

HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-918-368-49

Query Match 22.8% Score 252.6; DB 9; Length 1135;
Best Local Similarity 56.6% Pred. No. 8.3e-66;
Matches 512; Conservative 0; Mismatches 384; Indels 9; Gaps 2;

QY 215 GCTCTCAACGGGAAATATGCAACAAATATGATACCTGTATTTCTGATGATCATGCTC 274
DB 227 GATCGGGATCATGTAAGAAAGAAACACTTGAGAACTGTGAGACCAATATGCCAAATCTC 286
QY 275 CAATGGAAGCTTTCCCATGACACCCCTTTCAAAAGCTAAACAGATACATATAGGAG 334
DB 287 CTTGGGAGCAATTAATACACATTACCTTTTCACAAATGTCACCCACAGCAATATAGTG 346
QY 335 CATGCCCAAGTATGTAAAGCAAAACACCTGAGTTGGCAACAGGATGCCGAATGTAC 394
DB 347 AGTGCCCAATATATTAATAATGGAGAGTTGTCTTACCAACAGGACTAAGGAATGTTC 406
QY 395 CAGAGAAACAATAGAGGCTTATTCGGGCAATAGCAGGTTTCATAGAAAATGTTGGG 454
DB 407 CCCAGATTGAATCAGAGGATGTTGGGGCAATAGCTGTTTATAGAAAGAGGATGGC 466
QY 455 AGGGAATGATAGAGGTTGTGAGGTTTCAGGCATCAAAATCTGAGGCAACAGCAAG 514
DB 467 AAGGAATGTTGACGGTTGTATGATACCATCAGCAATGACCAAGGATAGGGATAG 526
QY 515 CAGCAGATCTTAAAGACACTCAAGCAGCATGACCAATCAATGGGAATGGAACAGG 574
DB 527 CAGCAGACAAAGAAATCACTCAAAAGGCAATTTGATGAAATCCACAAAGAAATTCG 586
QY 575 TAAATGAGAGCAAGCAAGAAATTCATCAATGCAAAAGAAATTCAGAGTAGAG 634
DB 587 TGATTTGAAAGATTAACACCCCAATTTGAAGCTGTTGGAAAGAAATTCGTAATAGAGA 646
QY 635 GGAGATTCAGGAGCTCGAGAAATACGTTGAAGACACTAATATCTCTGCTTACA 694
DB 647 AAAGACTGGAACCTTGAACAAAAGATGGAAGAGGGTTCTAGATGTGTGACATACA 706
QY 695 ATGGGAGCTTCTGCTGAGAAATCAACATACATATGAGTACTGACTGCTGGAAA 754
DB 707 ATGCTGAGCTTTTACTTCTGATGAGAAATGAGAGACACTTCTTCAATGTTCTAATG 766
QY 755 TGAACAACTGTTTGAACAAAACAGAGGCAACTGAGGAAATCTCTGAGAGATGGCA 814

DB 767 TCAAGAACTGTATAGTAAGTACAGAAATGACACTGAGAGACAACTCAAGAACTAGGAA 826
QY 815 ATGCTGCTTCAAAATATATCCCAAAATGTGACAAAGCTTGCATAGAGTCAATCGAANTG 874
DB 827 ATGATGTTTAAATTTATATCACAATGTGATGATGATGATGATGATGATGATGATGATG 886
QY 875 GTACTATGACCATGATGATATACAGAGCAAGCAATTAACACCGCTTGCATGATCAAG 934
DB 887 GGCATATATATATATCCCAAGTATGAGAGAGCTTAAACTAATATGAAATATAATCAAG 946
QY 935 GTGTTGAACCTGAAGTGTGATCAAAAGACTGATCCCTGATTTCCCTTCCATATCAT 994
DB 947 GGGTAAATATGAGCAGCATGGGGTTTATCAAAATCCTTGCCATTTATGCTACATAGCAG 1006
QY 995 GCTTTTG---CTTTGTGTTGTTTGTGCTGGGTTATCATGTGGCTCCAGAGAGCA 1051
DB 1007 GTTCATATGCACTGCAATCATGATGCTGGGATCTTCTGCTGGGTGCTCCACCGCT 1066
QY 1052 ACATTAGTGCACAACTTGTGATTTGATGTA-----TTAGTAATTAACACACCTTGT 1105
DB 1067 CTCTGAGTGCAAGATCTGCATATATATATAGTATTTATTAATTAACACACCTTGT 1126
QY 1106 TTCTG 1110
DB 1127 TTCTG 1131

RESULT 11

US-09-918-568-46
Sequence 46, Application US/09918568
Patent No. US2002005482A1

GENERAL INFORMATION:

APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)

NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSER: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOHETICAL: <unknown>
ANTI-SENSE: <unknown>
FRAGMENT TYPE: <unknown>
ORIGINAL SOURCE:
STRAIN: A/Okuda/57
INDIVIDUAL ISOLATE: <unknown>
DEVELOPMENTAL STAGE: <unknown>
HAPLOTYPE: <unknown>
TISSUE TYPE: <unknown>
CELL LINE: <unknown>
ORGANELLE: <unknown>
IMMEDIATE SOURCE:
LIBRARY: <unknown>
CLONE: <unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <unknown>
MAP POSITION: <unknown>
UNITS: <unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 46;
US-09-918-568-46

Query Match 22.7% Score 252.4; DB 9; Length 1783;
Best Local Similarity 56.8%; Pred. No. 1.3e-65;
Matches 507; Conservative 0; Mismatches 376; Indels 9; Gaps 2;

QY 228 GAAATATGACAACTTTGATACCTGATTTCTGATGCATCCTCCAAATGGAGCAT 287
|||||
DB 885 GAAATGAGAGAACTTTGAGAACTGTGAGACCAATGCCAACTCTTTGGAGCAAT 944
|||||
QY 288 TCCCAATGACAGCCCTTCAAAAGCTAAACAGATCACATATGAGAGATGCCCAAGTA 347
|||||
DB 945 AAATCAACATCTTCTTCAATGTCACCCACTGACATATGATGAGTGCCTCAATA 1004
|||||
QY 348 TGTATGACAAACACCTTGAAGTTGGCAACAGGATGCGAATGTACACAGAAACAC 407
|||||
DB 1005 TGTAAATGCGAGAGTTGGTCTTACACAGAGCTAAGAAATGTTCCCAAGTGAATC 1064
|||||
QY 408 TAGAGCCATATCGGCACATAGAGGTTTCATAGAAATGTTGGAGGGAATGATAGA 467
|||||
DB 1065 AAGGAGATGTTGGGACATAGCTGTTTATAGAGAGAGATGCCAAGAAATGTTGA 1124
|||||
QY 468 CGGTGTAGCGTTTCAGCATCAAAATTTGAGGCGACAGACAGACAGATCTTAA 527
|||||
DB 1125 CGGTGTATGATATCATCATCAGACATGACAGGGATCAGGATATCCACAGACAAAGA 1184
|||||
QY 528 AAGCATCAGACGCCCTGACCAAAATCGGAATTTGAAACAGGTTATTCGAGAGAC 587
|||||
DB 1185 ATCCATCTAAAGGCAATTTATGGAATCACCACAGGTAATTTCTGTGATGAAAGAT 1244
|||||
QY 588 GAAAGAGAAATTCATTAATCGAAAGAAATTTCTGAGAGTGAAGGAGAAATTCAGA 647
|||||

DB 1245 AAACACCAATTTGAACCTTTGGGAAAGAAATTCGTAACCTTAGAGAAAGACTGAGAA 1304
|||||
QY 648 CCTGAGAAATACCTTGAAGACACTAAATATGATCTGTGCTTACATATGGGAGCTTCT 707
|||||
DB 1305 CTTGACAAAAGATGAGAGCGGTTCTTGAAGTGTGACATATGCTGAGCTTTT 1364
|||||
QY 708 TGTGCTGTGAGATCAACATCAATTTGACCTGACCTGACGGAATGAAACAGCTGT 767
|||||
DB 1365 AGTTCATGTAATGAGAGACACTTGCATTTTCATGATTTCTAATGTCAGAAATCTGTA 1424
|||||
QY 768 TGAATAAAGAGAGGACACTGAGGAAATGCTGAAGAGATGGCAATGTTCTTCAA 827
|||||
DB 1425 TAGTAAGTCAAGATGAGAGCTGAGAGACAGCTCAAGAACTAGAAATGATGTTTGA 1484
|||||
QY 828 AATATACCAATATGTACAACTGTCATAGATCAATCAGAAATGATATGACCA 887
|||||
DB 1485 ATTTATCACAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1544
|||||
QY 888 TGATGTATACAGAGAGAGCATTAACAAACCGTTTCAGATCAAGGTTGTGACAGAA 947
|||||
DB 1545 TCCCAAGTATGAGAGAGAGCTTAACATAATGAAATGAAATCAAGGGTAAATATGAG 1604
|||||
QY 948 GTCTGATACAAAGACTGATCTGTGATTTCTTGCATATATCATGCTTTTGG---CT 1004
|||||
DB 1605 CAGCATGGGGTTATCAAAATCCTTGCCATTTATGCTAGACATGACAGTTCATGCTACT 1664
|||||
QY 1005 TTGTGTTGTTTGTGCGGTTTCATGATGAGGCTGCGCAGAGAGCAACATATGAGTCAA 1064
|||||
DB 1665 GGCATATGATGATGCTGCTGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1724
|||||
QY 1065 CATTTGATTTGATGTA-----TTAGTATTAATAAACACCTTGTGTTG 1110
|||||
DB 1725 GATCTGCATGATTAATATGATGATTTATTAATAAAGACCTTGTGTTCTG 1776
|||||

RESULT 12
US-09-918-568-28
Sequence 28. Application US/09918568
Patent No. US20020054882A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918, 568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367

HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/Yamagata/120/86
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-918-568-31

Query Match 14.2% Score 157.4; DB 9; Length 424;
Best Local Similarity 60.8%; Pred. No. 3.5e-37;
Matches 257; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

DB 301 CCCCTTCAAAACGTAACAGATACATATGAGCATGCCCAAGTATGTTAAGCAAAAC 360
1 CTTTCCAGAAATGTACACCCAGTACAGATAGAGAGTGCACAAAGTATGTACAGAGTACA 60
361 ACCCTGAAGTTGGCAACAGGATGCGGATGTACACAGAGAACAACTAGAGGCTATTTC 420
61 AATTAAGGATGTTACAGAGTACAGATCCCATTCATTCATCCAGAGTTGTTT 120
421 GCGCAATAGCAGGTTTCATAGAAAATGGTTGGAGGAGTATACAGGTTGTCGGG 480
121 GGAGCATGGCCGTTTCATTGAAGGGGCTGACTGGAATGATAGATGATGTATGGT 180
481 TTCAGCATCAAAATTTCTGAGGCAAGAGCAAGACAGATCTTAAAGCACTCAAGCA 540
181 TATCATCATCAGATGACAGAGATCTGCTATGCTGCGATCAAAAAGACACAAAT 240
541 GCCATCGACCAATCAATGGGAAATTTGAACAGGTTATGACAGACGACGAATTC 600
241 GCCATTAAAGGATTAACAAGAGGAAATTTCTGATGAGAAATGAACACTCAATTC 300
601 CATCAATCGAAGAAATTTCTCAGAGTGAAGGAGAAATTCAGAGACTCGGAATAC 660
301 ACAGCTGTGGGCAAGAAATTCACAAATTAAGAAAGAGATGAAACTTAATAAATA 360
661 GTTGAAGACACTAAATAGATCTGTGTTTACAAATGCGAGCTTCTGCTCGTGAG 720
361 GTTGATGATGATTTCTGACATTGACATTAATGACGAATTTGTTGTTCTACTGAA 420
721 AAT 723

DB 421 AAT 423

RESULT 15
US-09-918-568-29
Sequence 29, Application US/09918568
Patent No. US20020054882A1
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/228,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/PR/8/34
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>

FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION SEQ ID NO: 29:
US-09-918-568-29

Query Match 14.8; Score 157; DB 9; Length 442;
Best Local Similarity 60.8; Pred. No. 4.7e-37;
Matches 262; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

QY 301 CCCTTCAAAACGTAACAGATCAGATGAGCATGCCCAAGTATGTTAAGCAAAAC 360
DB 1 CCTTCCAGATATTAACCCAGTCACAAATAGAGAGTCCCAAAATACGTACAGAGTCC 60
QY 361 ACCCTGAAGTTGGCAGAGGATCGGATGACAGAGAAACAACTAGAGGCTATTTC 420
DB 61 AAATTGAGATGGTTTCAGGACTAAGCAACATCCCGTCATCAATCCAGAGGCTATT 120
QY 421 GGGCAGATAGCAGTTTCATAGAAAATGTTGGAGGAGATGATAGCGGTGTACGGT 480
DB 121 GGAGCCATTCCCGTTTATTGAAAGGGGATGGACTGGAATGATGATGATGATGAT 180
QY 481 TTCAGGCATCAAAATCTGAGGGCAGACAGCAAGCAGATCTTAAAGCACTCAAGCA 540
DB 181 TATCATCATCAGATTAACAGGGATCAGGCTATGACGGGATCAAAAAGCACACAAAT 240
QY 541 GCCATGACCAATTCATGGGAATTCAGAGGGTAAATCGAGAGAGCAAGCAAAATTC 600
DB 241 GCCATTAAACGGATTTCAAAACAAGGTAACTGTATTCGAGAAAATGAACACTCAATTC 300
QY 601 CATCAATCGAAAGCAATTCAGAGTGAAGGGGATTCAGGACCTCGAGAAATAC 660
DB 301 ACAGCTGTGGTAAATATTCACAAATTAAGAAAAAGATGAGAAATTTAAATAAAAA 360
QY 661 GTTGAAGACACTAAATAGATCTCTGGTCTTACATCGGAGGCTCTTGTGCTCTGGAG 720
DB 361 GTTGAATGATGATTTTGTGACATTTGACATATATATGACGAATTTGTTAGTTCTACTGAA 420
QY 721 AATCAACATCAATTA 737
DB 421 AATGAAGGACTCTGGA 437

Search completed: August 9, 2003, 19:22:43
Job time: 180.294 secs

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(GenCore version 5.1.6)
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OM nucleic - nucleic search, using sw model

Run on: August 10, 2003, 06:17:35 : Search time 156.256 Seconds
(without alignments)
7190.265 Million cell updates/sec

Title: US-09-918-568-46
Perfect score: 1783
Sequence: 1 CGCGTAGCAAA/SCAGGGGT.....ACCCCTGTTCTGCTAGCCG 1783

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 646752 seqs, 315065167 residues

Total number of hits satisfying chosen parameters: 1293504

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New :
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2: /cgn2_6/ptbdata/1/pna/US06_NEW_COMB.seq :
3: /cgn2_6/ptbdata/1/pna/US07_NEW_COMB.seq :
4: /cgn2_6/ptbdata/1/pna/US08_NEW_COMB.seq :
5: /cgn2_6/ptbdata/1/pna/US09_NEW_COMB.seq :
6: /cgn2_6/ptbdata/1/pna/US10_NEW_COMB.seq :
7: /cgn2_6/ptbdata/1/pna/US60_NEW_COMB.seq :

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	833	46.7	1741	US-60-470-920-19	Sequence 19, Appl
2	489.4	27.4	1714	US-60-470-920-21	Sequence 21, Appl
3	467.4	26.2	1220	US-60-470-920-17	Sequence 17, Appl
4	103.6	5.8	1884	PCT-US03-12728-94	Sequence 94, Appl
5	49.2	2.8	124326	US-60-487-610-19458	Sequence 19458, A
6	48.4	2.7	201	US-60-487-610-42952	Sequence 42952, A
7	48.4	2.7	201	US-60-487-610-42953	Sequence 42953, A
8	48	2.7	201	US-60-487-610-42953	Sequence 42953, A
9	45.2	2.5	1946141	US-09-947-914-42	Sequence 42, Appl
10	44.8	2.5	201	US-60-487-610-42954	Sequence 42954, A
11	41.8	2.3	1837	US-10-286-897-4024	Sequence 4024, App
12	41.8	2.3	3423	US-10-105-837-126	Sequence 126, App
13	41.8	2.3	3423	US-10-286-897-452	Sequence 452, App
14	41.8	2.3	11116	US-10-286-897-1473	Sequence 1473, App
15	41.6	2.3	160592	US-60-487-610-19897	Sequence 19897, A
16	40.4	2.3	564	US-10-603-113-2884	Sequence 2884, App
17	40.2	2.3	282	US-10-603-113-11955	Sequence 11955, A
18	40	2.2	300	US-10-085-783A-47731	Sequence 47731, A
19	40	2.2	1777	US-10-042-417A-51	Sequence 51, Appl
20	40	2.2	2435	US-10-357-930-22543	Sequence 22543, A
21	40	2.2	2435	US-10-357-930-2493	Sequence 2493, A
22	40	2.2	2435	US-10-357-930-25291	Sequence 25291, A
23	40	2.2	2435	US-10-357-930-28380	Sequence 28380, A
24	38.6	2.2	13831263	US-09-947-914-41	Sequence 41, Appl
25	38.4	2.2	1176	US-10-603-114-1147	Sequence 1147, App
26	38	2.1	54233	US-60-485-450-12257	Sequence 12257, A

27	37.2	2.1	201	7	US-60-487-610-42930	Sequence 42930, A
28	37	2.1	6837	6	US-10-357-930-25433	Sequence 25433, A
29	37	2.1	152321	7	US-60-485-450-12128	Sequence 12128, A
30	36.8	2.1	357	6	US-10-085-783A-49736	Sequence 49736, A
31	36.6	2.1	1314	6	US-10-273-573-2516	Sequence 2516, App
32	36.6	2.1	1791310	5	US-09-947-914-46	Sequence 46, Appl
33	36.4	2.0	201	7	US-60-487-610-10158	Sequence 10158, A
34	36.4	2.0	9517	7	US-60-487-610-636	Sequence 636, App
35	36.4	2.0	27112	7	US-60-485-450-11992	Sequence 11992, A
36	36.2	2.0	1215	6	US-10-603-113-6183	Sequence 6183, App
37	36	2.0	201007	7	US-60-487-610-19435	Sequence 19435, A
38	35.8	2.0	95427	7	US-60-485-450-12224	Sequence 12224, A
39	35.6	2.0	412	6	US-10-085-783A-50134	Sequence 50134, A
40	35.6	2.0	508	6	US-10-085-783A-45358	Sequence 45358, A
41	35.6	2.0	2433	6	US-10-603-113-6178	Sequence 6178, App
42	35.4	2.0	500	6	US-10-621-901-46	Sequence 46, Appl
43	35.4	2.0	7677	6	US-10-357-930-23194	Sequence 23194, A
44	35.4	2.0	7677	6	US-10-357-930-29060	Sequence 29060, A
45	35.4	2.0	79786	1	PCT-US02-38582-175	Sequence 175, App

ALIGNMENTS

RESULT 1
US-60-470-920-19
Sequence 19, Application US/60470920
GENERAL INFORMATION:
APPLICANT: Luke, Catherine, J.
APPLICANT: Villalta, Adrian
APPLICANT: Wiloch, Mary K.
APPLICANT: Evans, Thomas G.
APPLICANT: Geall, Andrew J.
TITLE OF INVENTION: DNA Influenza Vaccine Compositions
FILE REFERENCE: 1530.0640000
CURRENT APPLICATION NUMBER: US/60/470,920
CURRENT FILING DATE: 2003-05-16
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19
LENGTH: 1741
TYPE: DNA
ORGANISM: Influenza A virus
US-60-470-920-19

Query Match 46.7%; Score 833; DB 7; Length 1741;
Best Local Similarity 68.8%; Pred. No. 7e-245;
Matches 1180; Conservative 0; Mismatches 520; Indels 15; Gaps 2;

QY	42	CAAAACATGCGCATCTTATCTCATCTCTCTGTTACACAGAGTGAGGAGGACCGAT	101
DB	5	CAAAATGAGAAATATGCTCTCTTTCGACAGACGATCTTAAAGTATGATCGAT	64
QY	102	ATGCATTGGATTACCATGCCAATTAATTCACAGAGAGGTCGACACATTTAGAGCGAA	161
DB	65	TTTCATTGGTTTACCATGCCAACAACCTGCAGAGAGGTTGACACATATATGAAAGAA	124
QY	162	CGTCACTGTGATCATATGCCAGACATCTTGAAGAACCCATACGGAAGTTATGCAAA	221
DB	125	TGTTCAGTGTACATGACATGCCCAAGACATACGGAAGACACAGCGAAGCTCTGCGA	184
QY	222	ACATAACGGAATCCCTCCATTAACATGAGGAGGATGAGCATGCCGAGGCTCTCTGG	281
DB	185	TTTAAATGAGTAAACCTCTCAATTTTGAAGGATTTAGTGTAGCTGATGCTCTCGG	244
QY	282	AAATCCAAATGTATAGGCTTCTAAGTGTGCCAGAACGCTCTATATATTGAGAAAGA	341
DB	245	AAACCCATGTGTAGAGAAATTCATCAATGTCCGGAATGTCTTACATATGAGAAAGC	304
QY	342	AAACCCGAGAGAGGTTTGTGTTATCCAGGACCTTCATGATTTATGACATTTGAAACA	401
DB	305	CAGTCAGCCAAATGACCTGTGTATTCACAGGAGGATTTTCAAGACTATGAGAACTGAAACA	364

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OY 402 TCTCTCAGACGCTGAACATTTTCGAGAAAGTAAGATTTCTGCCAAGAATAGATGG - 459
    || || || || || || || || || || || || || || || || || || || || ||
Db 365 CCTATTGAGCAGATTAACCATTTTGGAGAAATTCATCATCCCCAAAAGTTCTGTGTC 424
OY 460 -ACACAGCATACAACACTGAGGTTTCACGGGCTGGCGGTGCTGTATCCATCATTT 518
    || || || || || || || || || || || || || || || || || || || || ||
Db 425 CATTCATGATGCTCATCAGGGGAGAGCTGACATGTCATACCTTGGAGGTCCTCTT 484
OY 519 TTTCAGAACATGCTCTGCTGACAAAGAGATTCAGATTATCCGTTGCCAAGATC 578
    || || || || || || || || || || || || || || || || || || || || ||
Db 485 TTTCAGAAATGTGTTATGCTTATCAAAAAGAACAGTCATACCACATTAAGAGAG 544
OY 579 GTTCAACATACAGCGGAGACAACATGCTAATATTTGGGGGTGCACATCCCATTTGA 638
    || || || || || || || || || || || || || || || || || || || || ||
Db 545 GTACAAATTAATGACACCAACCAAAATCTTTTGTGATCTGTGGGGATTCACCATCTAATGA 604
OY 639 TGACAGAGAAACAAGACATTTGTACCGAATGTGGAACTGATGTTCCGTAGGACATC 698
    || || || || || || || || || || || || || || || || || || || || ||
Db 605 TCGGAGACAGACAGACAAAGCTCTATCAAAATCCACACCTACCTTTCCGTTGGAACATC 664
OY 699 AACATTGAACAAAGGTCAACCCAGAAATAGCAACAAAGGCTTAATGTAATGACAAAG 758
    || || || || || || || || || || || || || || || || || || || || ||
Db 665 AACACTGAACAGAGATTTGGTTCCAGAAATAGCTACTAGAACCCAAAGTAAGGGCAAG 724
OY 759 AGGTAGAATGGAATTTCTTTGGACCTCTTGGATATGTGGGACACATAATTTTGAGAG 818
    || || || || || || || || || || || || || || || || || || || || ||
Db 725 TCGAAAGAAATGGAGTTTCTGTGCAATTTTAAAGCCGAATGATCCATCAATTTCCGAGAG 784
OY 819 TACTGTATCTATTTGACACAGATAGTGGATTCAAAATTCGAAAAAGAGTGTTCAGG 878
    || || || || || || || || || || || || || || || || || || || || ||
Db 785 TATATGAATTTTCATTTGCCCCAGAAATATGTCATCAAAATTTGTCAAGAAAGGAGCTAAC 844
OY 879 GATCATGAAAGAGAAAGAACTGTGAGAACTGTGAGACCAAAATGCCAACTCTTTGGG 938
    || || || || || || || || || || || || || || || || || || || || ||
Db 845 AATTATGAAGAGATTTGGAATATGTGTAACCTGCAACACCAACTGTCAAACTCCATGGG 904
OY 939 AACATTAATACAACTTACCTTTTCACAATGTCACACCTGACATCAATAGTAGTCCG 998
    || || || || || || || || || || || || || || || || || || || || ||
Db 905 GCGGATAACTAGATATCCCATTCACAAACATACACCCCTCCACCATCGGGAATGCCC 964
OY 999 CAATATGTAAATATCGAGAAAGTTGTCTTAGCAACAGACATTAAGAAATGTTCCCGCAT 1058
    || || || || || || || || || || || || || || || || || || || || ||
Db 965 CAATATGTGAATCAACACAGATTTCTTGGACATGACATGAGAAATACCCCTCAAG 1024
OY 1059 TG-----AATCAAGAGATTTGTTGGGCAATAGCTGTTTATAGAAAGAG 1106
    || || || || || || || || || || || || || || || || || || || || ||
Db 1025 GGAGAGAAAGAAAGAAAGAGAGACTATTTGGAGCTATAGCAGTTTATAGAGGAGG 1084
OY 1107 ATGGCAAGAGATGTTGAGGTTGATGATGATACCATTCACAGCAATGACCAAGGATCAGG 1166
    || || || || || || || || || || || || || || || || || || || || ||
Db 1085 ATGGCAGGGCATGTATGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 1144
OY 1167 GTATCAGCAGACAAAGAAATCCATCAAAAGCATTTGATGATGATGATGATGATGATGATG 1226
    || || || || || || || || || || || || || || || || || || || || ||
Db 1145 ATAGCTGTGAGACAAAGATTCACATCAAAAGCAATGATGATGATGATGATGATGATGATG 1204
OY 1227 TTCTGTGATGAAAGATTAACACCCATTTGAGCTGTTGGAAAGAAATTCGCTAACTT 1286
    || || || || || || || || || || || || || || || || || || || || ||
Db 1205 CTGCTGATTTAAACAAATGACACATCAGTTTGAAGCGCTTGGAAAGGAAATTAATTAATCT 1264
OY 1287 AGAGAAAGACTGAGAGAACTTGAACAAAGATGGAAGACGGTTTCTGATGATGATGATG 1346
    || || || || || || || || || || || || || || || || || || || || ||
Db 1265 AGAAAGAGAAATGAGAAATTTAAACAAAGAAATGGAAGAGGAAATTCCTGATGATGATG 1324
OY 1347 ATACATGCTGAGCTTTTATGTTCTGATGGAATATGAGAGACATGTTTCATGATGATG 1406
    || || || || || || || || || || || || || || || || || || || || ||
Db 1345 TTACATGCTGATGATGTTGTTCTTATGAGAAATGAGAGAACTCTGATGATGATGATGATG 1384
OY 1407 TAAATGCAAGATCTGTATAGTAAAGTCAAGATGAGATGAGACAACTCAAGAAAGT 1466
    || || || || || || || || || || || || || || || || || || || || ||
Db 1385 AAATGTCAAGAACTTTAGCAGAGAGTCCGACTACAGCTTAAAGATTAATGCAAGAAAGT 1444
OY 1467 AGGAATGATGTTTGAATTTTATCACAATGTGATGATGATGATGATGATGATGATG 1526

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Db 1445 GGGTAATGTTGTTTGAATTTATCACAATGTATTAATGATATGAAAGTGAAGTGA 1504
OY 1527 AAAGGACATATGATTTATCCCAAGATATGAAGAGTCTAAACTAAATAGAAAT 1586
    || || || || || || || || || || || || || || || || || || || || ||
Db 1505 AAAGGACATATGATTTATCCCAAGATATGAAGAGTCTAAACTAAATAGAAAT 1564
OY 1587 CAAAGGGTAAATTTGAGAGATGAGAGGTTTATCAATCTTGGCATTTATGATGAT 1646
    || || || || || || || || || || || || || || || || || || || || ||
Db 1565 AAGGAGATTAATTTGGAATCATTTGGGAACTTACCAAAATCTGTCAATTTATCAAGAT 1624
OY 1647 AGAGGTTTATGTCATGAGCAATCATGATGCTGGGATCTCTTCTGGGTGCTCCAA 1706
    || || || || || || || || || || || || || || || || || || || || ||
Db 1625 GCGGAGTTCCCTAGACTGAGCAATCATGATGCTGCTATCTTATGATGATGCTCCAA 1684
OY 1707 CGGCTCTGCTGAGCAGATCGCATATGATAT 1741
    || || || || || || || || || || || || || || || || || || || || ||
Db 1685 TGGATCTTACATGACGAATTTGCAATTAATTT 1719

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RESULT 2
US-60-470-920-21
; Sequence 21. Application US/60470920
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine, J.
; APPLICANT: Villalta, Adrian
; APPLICANT: Wiloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; TITLE OF INVENTION: DNA Influenza Vaccine Compositions
; FILE REFERENCE: 1530.0640000
; CURRENT APPLICATION NUMBER: US/60/470,920
; CURRENT FILING DATE: 2003-05-16
; NUMBER OF SEQ. ID NOS.: 45
; SOFTWARE: PatentIn version 3.2
; SEQ. ID NO. 21
; LENGTH: 1714
; TYPE: DNA
; ORGANISM: Influenza A virus
US-60-470-920-21

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Query Match 27.4%; Score 489.4; DB 7; Length 1714;
Best Local Similarity 56.5%; Pred. No. 139;
Matches 978; Conservative 0; Mismatches 736; Indels 17; Gaps 3;

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OY 7 GCAAAGCAGGGGTTATACCATAGAAACCAAAACCAAAACAGGCGCATATTAATCTC 66
    || || || || || || || || || || || || || || || || || || || || ||
Db 1 GCAAAGCAGGGGATTTAC--TTAACTAGCAAAATGGAACAAATATCTAATTAATCTA 58
OY 67 ATTCTCTGTTCAGACGACTGAGAGGAGCCAGATATGATGATGATGATGATGATGATGAT 126
    || || || || || || || || || || || || || || || || || || || || ||
Db 59 CTACTAGTAGTAAACGACGACGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 118
OY 127 TCACAGAGAAAGTGCACCAATTTTAAAGCGGAAACGTCAGTGTACTCATGCAAGAGAC 186
    || || || || || || || || || || || || || || || || || || || || ||
Db 119 TCCACAGAAACGTGTGACACGCTTAAACAGAACTGTTCTGTGACACATGACCAAGAA 178
OY 187 ATCTCTGAGAGACCATTAAGCAAGTATGATGATGATGATGATGATGATGATGATGATG 246
    || || || || || || || || || || || || || || || || || || || || ||
Db 179 TTGCTTCACACAGACCATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 238
OY 247 CTAGGGGACTGTAGCATGCTGCGATGCTCTTGGAAATGCCAAATGATAGCTTCTA 306
    || || || || || || || || || || || || || || || || || || || || ||
Db 239 CTAGACACATGACATTAATGAGAGTACTGATGATGATGATGATGATGATGATGATGATG 298
OY 307 AGTGTCCAGAAAGTCTCTATATATTTGAGAAAGAAACCCGAGAGACGTTGTGTAT 366
    || || || || || || || || || || || || || || || || || || || || ||
Db 299 GGAGGAAGAGATGTTCTTACATGCTGCAAGATCATAGCTGTAATATGGAACGTTTAC 358
OY 367 CGAGGAGGTTAATGATTTATGAAATTTGAACATCTCTGACAGAGGTAACATTTTC 426
    || || || || || || || || || || || || || || || || || || || || ||
Db 359 CCGGGAATGTAGAAACCTAGAGAGACTGAGACACTTTTATGTTAGTTCGGTACTGCTAC 418

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OY	427	GAGAAAGTAAAGATCTTCCCAAAAGATGATGACACAGCATACAACTGAGGACTCA	486
OY	428	GAGAAAGTAAAGATCTTCCCAAAAGATGATGACACAGCATACAACTGAGGACTCA	486
Db	419	CAAGAAATCCAAATCTTCCAGACACAACTGG-----AATGTACTTACA	464
OY	487	CGGCGCTGCGCGTGTCTGTGATATCCATCATTTTTCAGGAACATGTGCTGGCTGCACAA	546
Db	465	CTGGAAACAGACAGAGCATGTGTCA--GGTTCATTTCTACAGAGTATGATGATGCTGCATCA	523
OY	547	GAAGATACAGTTATTCGGTTGGCCAAAGATGCTACCAACATACAGGAGGAGAACAAATG	606
Db	524	AAGAGCGGTTTTTACCTGTCTTCAGACGCCCAATACACAAATATACAGGGGAAAGCATTT	583
OY	607	CTAATTAATTTGGGGGTGTCACCATTCCTCATGTATGAGACAGAAAGAACTTGTACCAG	666
Db	584	CTTTTCGTGTGGGCGTACATCACCCACCACCTATATCCAGGACAAATTTGTACATA	643
OY	667	AATGTGGGAACCTATCTTCCGTAGGACATTCACATTTGAACAAAGSTCAACCCACAA	726
Db	644	AGAAACGACAAACATCAAGCGTGACAAACAAAGATTAAGATAGACCTTCAAAACAGTG	703
OY	727	ATAGCAACAAAGCCCTTAAGTAAATGACAAAGAGGTAAATGAATCTCTTGGACCTTC	786
Db	704	ATAGGGCCAAAGCCCTTGTCTCATGTGCTGCAGGAAACATTTGATTTATTGTGCGTA	763
OY	787	TTGGATATGTGGGACCTCATTAATTTTGAAGTACTGGTAACTTAATTTGACCCAGAGTAT	846
Db	764	CTAAACCCAGGCCAAATCATTCGAGTAGATATCCATGGGAATCTTAATGTCTCATGTAT	823
OY	847	GGATTCAAAATATGTGTAAGAGAGTATGTCAGAGGATCATGAACAAAGAAAGAACTTCAG	906
Db	824	GGACACGCTTTCTTCAGAGAGGACCCATGAAAGAAATCTGAAGACTGATTTAAAGGTGGT	883
OY	907	AACGTGTAGACCAAAATGCCAAACTCTCTTTGGAGCAATTAATACAACTTATACCTTTTCAC	966
Db	884	AATGTGTAGTGAATGTCTACAGATGAAAGAGTGGCTTAAACAGTATGTCATTCAC	943
OY	967	AATGTGCCACCATGTGCAATAGTGTAGTGGCCCCCAATATGTAAAAATCGGAGAAATTGGTC	1026
Db	944	AATATCAGTAATATGTGCAATTTTGAACCTGGCCCCCAATATGTAAAGTAAATAGTTCAAA	1003
OY	1027	TTAGCAACAGGACTAABGAAATGTTCCCCAGATTGATCAAGAGATTTTGGGGCAATA	1086
Db	1004	CTGGCAGTCGCTGAGGAGACGTGGCTGCTATGATCAACTAGAGAGCTATTTGGAGCCATA	1065
OY	1087	GCTGCTTTATAGAAGAGAGATGCGACAGAAATGTTGTCGCTGTGTATGATACCATCAC	1148
Db	1064	GCTGATTCATAGAAGAGAGGTGGCCAGACGTAGCTGCTGTGTATGATGTTTCAGCAT	1123
OY	1147	AGCAATGACCCGGGATTAAGGTATGACACAGACAAAGATCAGTCAAAAGAGCATTTGAT	1206
Db	1124	TCAATATGTCAGGGGTTGTATGTGCTGCAATAGGATTTAACTTCAAAAGGCATTTAT	1183
OY	1207	GGAAATCCCAACAGGTAATTTCTGTGTTGAAAAAGATTAACACCCCAATTTGAAGCTGT	1266
Db	1184	AAAATTAACATCCCAAGTGAAATTAATATAGTGCACAAAGATGAACAAAGCATATGAATAATT	1243
OY	1267	GGGAAGAAATTCGTAACCTTAGAAGAAAAGATGAGAACTTGAACAAAGAAATGAGAGAC	1328
Db	1244	GATATGATGATCAGTGGTGGTTGAACCTAGCTCAATATATGATCAATTAATTAAGATTTGATGAC	1303
OY	1327	GGGTTTTCAGATGTGTGACATTAACATGCTAGCTTTAGTTAGTTCGATGGAAGAAATGAGAGG	1386
Db	1304	CAATTAACAAGCGTATGCGCATTAATATGACAGAAATTCGTAAGTACTGTTGAAAATTCAAAAA	1366
OY	1387	ACACTTGACTTCAATGTTCTTAATGTCAAGATCTGTATAGTAAAGTCAAGATGCAGCTG	1448
Db	1364	ACACTCGATGACATGATGCGCAACGTGCAACATCTATATTAACAAGGTGMAAGGGCACTGT	1423
OY	1447	AGAGACAACTGCAAGAACTAGAAATGAGATTTTGAATTTTCAACAAATGATGATAT	1506
Db	1424	GGCTCCAAATGCTATAGGAAAGATGGGAAGGCTGTTCCAGCTATACCAATTAATTTGTATGAT	1483
OY	1507	GAATGCAATGATAGTGTCAAAACCGGCAATATATATATCCCAAGTATGAAGAAAGTCT	1566

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Db      1484 CAGTGCATGGAAACAATTTCCGAGACGGGACCTATATATAGAGAAAGTATAGAGAGAAATCA 1544
QY      1567 AAATCAATAGAAATGAATCAATCAAGGGGTAAAAATTGAGCAGCATGGGGCTTTATCAATC 1626
Db      1544 AGACTGAAAGGCGAGAAATGAGGGGGTTAAGCTGGAATCTGAGGGAATTTACAAAATC 1603
QY      1527 CTTGCCATTTATGCTACAGTAGCAGAGGTTCTATGTCACATGGCAATCATGATGGCTGGGATC 1688
Db      1604 CTCACCATTTATTTGACTGTGCTCATCTTGTGCTTGGAAATGGGGTTTGCTGCCCTTC 1666
QY      1687 TCTTTCTGGGTGTGCTCCACAGGGCTCTCTGCAGTGCAGAGATCTGCATATGA 1737
Db      1664 CTGTTCTGGGCGCATGTCCAAATGATCTTGCAGATGCAACATTTGATATTA 1714

RESULT 3
US-60-470-920-17
: Sequence 17, Application US/60470920
: GENERAL INFORMATION:
: APPLICANT: Luke, Catherine, J.
: APPLICANT: Vialalta, Adrian
: APPLICANT: Wlooh, Mary K.
: APPLICANT: Evans, Thomas G.
: APPLICANT: Geall, Andrew J.
: TITLE OF INVENTION: DNA Influenza Vaccine Compositions
: FILE REFERENCE: 1530 0640000
: CURRENT APPLICATION NUMBER: US/60/470, 920
: CURRENT FILING DATE: 2003-05-16
: NUMBER OF SEQ ID NOS: 45
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 17
: LENGTH: 1220
: TYPE: DNA
: ORGANISM: Influenza A virus
: US-60-470-920-17

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Query Match	26.2%;	Score 467.4;	DB 7;	Length 1220;
Best Local Similarity	62.8%;	Pred. No. 6e-13;		
Matches 745;	Conservative 0;	Mismatches 436;	Indels 6;	Gaps 1;

OY		76	TTCCACAGCAGGAGGAGGCACAATATGCACTTGGATGCACTGTGCCAATAATTCCACAG	135
Db		34	TTTGCACTACAAATTCAGACACACAATATGTTAGGCTACCATGGCAATTAACCTAACCGAC	93
OY		136	AAGGTGCACACAATTTCTAGAGCGGAACGTCACCTGACTCATGGCCAAGACATCCTTAG	195
Db		94	ACTGTTGACACAGTACTCGAAAAAATGTGACCCTGCACACCTCTGTTAACTCCTGCGAA	153
OY		196	AAGGCCATTAACGGAAAGTTATGGAACCTAACCGGAATCCTCCACTTGAACCTAGGSGAC	255
Db		154	GACAGCCACAACGGAAAACCTATGTAAATTAAGAAGAAATAGCCCATTAACAATTTGGGAAA	213
OY		256	TGTAGCAATTTCCGGGATGGCTCCTTGGAATCAAAATGTGATAGGCTCTTAAGTGTGCA	315
Db		214	TGTAATATTCGCGGATGGCTCTTGGGAAACCCGGAATTCGCAATTACTGCTCACACGACG	273
OY		316	GAMCGTCTATATATTGGAGAAAGAAACC CGAGAGCGGTTTGTTATCCAGCGACG	375
Db		274	TCATGCTTCCTAATATTGTAGAAACATCGCAACATCAGAAATGGAACTGTACC GAGAT	333
OY		376	TTCAATGATTTATGAGAAATGGAACATCTCCTCGACGCGTGAACATTTTCGAGAAATA	435
Db		334	TTCTTCACATATGAGAACTGAGGAGCAATTTGAGCTACAGTCACTGTTGAAAATAATC	393
OY		436	AAGATTCGCCCAAAGATAGATGG - - - - ACACAGCATACMAACACTGAGAGTTTCACG	489
Db		394	GAAATATTTTCCCAAGACAGCTCGTGCCCCCAATCATGAAACMACCAAGGTGTAA CGCA	453
OY		490	GCTCGCGCGGTGTCTGTAATCCATCAATTTTTCAGGAACATGCTGTGGCTATACAAAGAA	549
Db		454	GCAATGCTCTATGCGGGAGGAAGCATGTTTTTAACGAAATTTGCTGTGGCTATACAAAG	513

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QY 550 GGATCAGATTATCCGGTTGCCAAGAGATCCGACAAATACAGCGGAGCAATATGCTA 609
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 514 GGAAGCATATACCAAAAGCTTTAGCAAGTCTTGTGTGAACATTAAGGGAAAGTCTT 573
QY 610 ATAAATTTGGGGGTGACCATCCATTGATGAGACAGAAACAAATCTTACAGAT 669
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 574 GTACTATGGGGTGTTCATCATCCGCTACCGGTACTGATCAACAGAGCTCTATCAGAT 633
QY 670 GTGGGAACCTATGTTTCCGTAAGCAGATCAACATTTGAACAAAGGTCAACCCGAAATA 729
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 634 GCAGATGCTTATGTCTGTAGGGTCAATAATTAACAGAGATTCACCCCGAAATA 693
QY 730 GCACAAAGCCTAAAGTAATGGACAAAGAGGTGATGATGATCTCTTGACCTCTTG 789
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 694 GCAGCGAGACCAAGTAAGAGGTCAAGCTGGAGATGAACCTTACTGGACATTTACTA 753
QY 790 GATATGTGGACACCATTAATTTTGAAGTACTGTAATCTAATTTGACAGATATGGA 849
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 754 GAACCCGAGACCAATTAACATTTAGGCAACTGGAATCTAATAGCACCATGCTATGCT 813
QY 850 TTCAAAATATCGAAAAGAGTACTTCAGGATCATGAAAACAGAGAACACTTGAGAAC 909
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 814 TTGCACTGATAGAGGTCTGTGATCGGTATCATCTTCAGACGACAGTGCATGAT 873
QY 910 TGTGAGACCAAAATGCCAACTCTTTGGAGCAATTAATTAACATTAACCTTTGACAAT 969
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 874 TGTAAACAGAGTGTCAAAACCCCAAGTGTCTTAATTAACAGCACTCTCCCTTCCAAAT 933
QY 970 GTCCACCCACTGCAATAGGTGATGATGCCCAAAATATGTAATCGAAGAGTGTGCTTA 1029
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 934 ATACATCCAGTCACAGTAGAGAGTGCCTCAAAATACGTACAGATACCAATTTGAGATG 993
QY 1030 GCAACGAGCATAGATGTTCCCGAGATGATCAAGAGATTTGTTGGGCAATGCT 1089
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 994 GCTACGAGCATAGAAACATTTCCATCTATTCAATCCAGGGGTCTATTGGAGCATTTGCC 1053
QY 1090 GGTTTTATGAAGAGAGATGGCAAGAAATGTTGAGTGTGATGATACCATGACAGC 1149
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1054 GGTTTTATGAGGGGATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1113
QY 1150 AATGACGAGGATGAGGATGATGAGCAGACAAAGAAATCCACTCAAAAAGCATTTGATGA 1209
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1114 AATGAACAGGAGTACAGGTATGACAGGATCAAAAAAGCACAAATGSCATTTGACGGG 1173
QY 1210 ATCAACCAAGATTAATCTGTGATTAAGAAATTAACACCAATTT 1256
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1174 ATTAACCAAGATTAATCTGTGATTAAGAAATTAACACCAATTT 1220

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RESULT 4
PCT-US03-12728-94
; Sequence 94, Application PC/TUS0312728
; GENERAL INFORMATION:
; APPLICANT: MedImmune Vaccines, Inc.
; APPLICANT: Hoffman, Erich
; APPLICANT: Jin, Hong
; APPLICANT: Lu, Bin
; APPLICANT: Kemble, George
; APPLICANT: Duke, Greg
; TITLE OF INVENTION: MULTI PLASMID SYSTEM FOR THE PRODUCTION OF INFLUENZA VIRUS
; FILE REFERENCE: 26-00027005/PC
; CURRENT APPLICATION NUMBER: PCT/US03/12728
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/375,675
; PRIOR FILING DATE: 26-04-2002
; PRIOR APPLICATION NUMBER: 60/394,983
; PRIOR FILING DATE: 09-07-2002
; PRIOR APPLICATION NUMBER: 60/410,576
; PRIOR FILING DATE: 12-09-2002
; PRIOR APPLICATION NUMBER: 60/419,802
; PRIOR FILING DATE: 18-10-2002
; PRIOR APPLICATION NUMBER: 60/420,708
; PRIOR FILING DATE: 23-10-2002

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; PRIOR APPLICATION NUMBER: 60/457,699
; PRIOR FILING DATE: 24-03-2003
; PRIOR APPLICATION NUMBER: 60/462,361
; PRIOR FILING DATE: 10-04-2003
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 1884
; TYPE: DNA
; ORGANISM: Influenza B virus
PCT-US03-12728-94

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Query Match
Best Local Similarity 51.0%; Score 103.6; DB 1; Length 1884;
Matches 244; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

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QY 1065 AAGAGATGTTGTTGGGCATATGCTGTTTATAGAAGAGATGCGAAGATGCTTGA 1124
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1116 AAGGGTTTCTTCGACATATGCTGTTTCTTGGAAAGGAGTGGAAAGATGATTCG 1175
QY 1125 CGTTGGTATGATACCATCAACAGCAATGACCGAGTACGCTATGACAGACAAAGA 1184
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1176 AGTTGGCAGGATACACATCTCATGAGACATGAGTGGCAGTGGACGACCTTAA 1235
QY 1185 ATCCACTCAAAAGCATTTGATGATGATCAACAAAGTAATTTGATGATGAAAGAT 1244
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1236 GAGTACCAAGAAAGCTTAACAAAGATTAACAAAAATCTCAATTTTAAAGTACCTAGA 1295
QY 1245 AAACACCAATTTGAAGCTGTTGGAAAGATTTGCTTAATTAAGAAAGATGAGAGA 1304
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1296 AGTAAGAAATCTTCAAGACTTAAGCGGTGCAATGATGATCAACAAAGAAATCTGCA 1355
QY 1305 CTGTAACAAAGATGGAACCGGTTTCTAGATGTTGAGACATACAAATGCTGACCTTTT 1364
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1356 GCTGATGAGAAAGTGGATGATCTCAGAGCTGATTAACAAATGCTGCAATGAGCTTGC 1415
QY 1365 AGTTGATGGAAGATGAGAGCACTTGAATTTCAATGATGATGATGATGATGATGATGAT 1424
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1416 AGTCTTCTTCTTCAACGAAGATTAATTAACAGTGAAGTGAAGTCTTCTTGGCACTTGA 1475
QY 1425 TAGTAAGTCAGAAATGACCTGAGACAGCAACAGTCAAGAAATGATGATGATGATGATGAT 1484
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1476 AAGAAACATGAGAAATGCTGGGCCCTCTGCTGTAGACATAGGAAGATGCTTGA 1535
QY 1485 ATTTTATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1542
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1536 AACCAACAAATGCAACACGACTTGCCTAGACAGAGATGATGATGATGATGATGATGATGAT 1593

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RESULT 5
US-60-487-610-19458
; Sequence 19458, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; PRIOR FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19458
; LENGTH: 124326
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-487-610-19458

```

```

Query Match
Best Local Similarity 55.6%; Score 49.2; DB 7; Length 124326;
Matches 90; Conservative 2; Mismatches 70; Indels 0; Gaps 0;

```

[illegible]

```

RESULT 6
US-60-487-610-42952
: Sequence 42952, Application US/6048761.0
: GENERAL INFORMATION:
: APPLICANT: CARGILE, Michels
: APPLICANT: HUANG, Hongjin
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS
: TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C1001469
: CURRENT APPLICATION NUMBER: US/60/487,610
: CURRENT FILING DATE: 2003-07-17
: NUMBER OF SEQ ID NOS: 97101
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 42952
: LENGTH: 201
: TYPE: DNA
: ORGANISM: Homo sapiens
US-60-487-610-42952

```

[illegible]

```

RESULT 7
US-60-487-610-42953
? Sequence 42953, Applicator US/60487610
? GENERAL INFORMATION:
? APPLICANT: CARGILL, Mich[e]
? APPLICANT: HUANG, Hongji
? TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
? TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-
? TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
? FILE REFERENCE: CL001469
? CURRENT APPLICATION NUMBER: US/60/487,610
? CURRENT FILING DATE: 2003-07-17
? NUMBER OF SEQ ID NOS: 97141
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 42953
? LENGTH: 201
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-60-487-610-42953

```

Query Match	27%	Score 48.4	DB 7	Length 201
Best Local Similarity	56.2%	Pred. No. 6.3e-05		
Matches 91	Conservative 0	Mismatches 71	Indels 0	Gaps 0

[illegible]

```

RESULT 8
US-60-487-610-42923
; Sequence 42923, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LAYER FIBROSIS IN HEPATITIS C VIRUS-
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001469
; CURRENT APPLICATION NUMBER: US/60/487, 610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42923
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-487-610-42923

```

[illegible]

```

RESULT 9
US-09-947-914-42
: Sequence 42, Application US/0947914
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig
: TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPS) LOCATED ON
: TITLE OF INVENTION: 21, METHODS OF DETECTION, AND USES THEREOF
: FILE REFERENCE: C0001298
: CURRENT APPLICATION NUMBER: US/09/947,914
: CURRENT FILING DATE: 2001-09-07
: NUMBER OF SEQ ID NOS: 75
: SEQ ID NO 42
: LENGTH: 1946141
: TYPE: DNA
: ORGANISM: HUMAN
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(1946141)
: OTHER INFORMATION: n = A,T,C OR G
US-09-947-914-42

```

Query Match 2.58; Score 45.2; DB 5; Length 1946141;

Best Local Similarity 45.5%; Pred. No. 0.032;
Matches 161; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

QY 1248 CACCAATTTGAAGCTGTGGAAAGAAATTCGTAACCTTAAGAGAAAGCTGGAGACTT 1307
Db 489693 CTCACATTTGGACATATATAAAAAATTTTAAATTTATTTGAAAAAGAAAAATACACAG 490022
QY 1308 GAACAAAAGATGAGAGACGGGTTCTAGATGTGTGACATACAAATGCTGACTTTAGT 1367
Db 490023 AGAAAAACCAAAACAAATGATTTAAATGATTAACAAAAACCATTAATGACTAAAAAG 490082
QY 1368 TCGATGGAATGAGAGACACTTTCATGATTTCTAATGTCAGAAATCTGTATAG 1427
Db 490083 ATTCTTTTAAAGAGAGACACTTATTAACCAATTAACCAATTAATGATGGA 490142
QY 1428 TAAATGAGATGAGAGACACTTTCATGATTTCTAATGTCAGAAATCTGTATAG 1487
Db 490143 CATATACATATATATTTCTTACATACATCCAAAGCTTATAGAAAAATTTTCAGCAAT 490202
QY 1488 TTATCAAAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1547
Db 490203 TTATACCAATTAATTTGATTAATTAACAAAAATTTCTTGAATTAACACAAATTC 490262
QY 1548 CAAGTATGAGAGAGAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1601
Db 490263 AAGTGACACAAAAGAGACATGTGATGATGATGATGATGATGATGATGATGATGAT 490316

RESULT 10
US-60-487-610-42954
; Sequence 42954, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CANGIL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: CI001469
; CURRENT APPLICATION NUMBER: US/60/487, 610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42954
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-487-610-42954

Query Match 2.5%; Score 44.8; DB 7; Length 201;
Best Local Similarity 59.8%; Pred. No. 0.0008;
Matches 73; Conservative 1; Mismatches 48; Indels 0; Gaps 0;

QY 1494 CAAATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1553
Db 75 CACTTGTATGAGAGGATTCAGACASCTCGCCCATGATGATGATGATGATGATGATGATGAT 134
QY 1554 TGAAGAGAGGCTTAACTAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 1613
Db 135 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 194
QY 1614 GG 1615
Db 195 GG 196

RESULT 11
US-10-286-897-4024
; Sequence 4024, Application US/10286897
; GENERAL INFORMATION:
; APPLICANT: Hysq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/10/286, 897

CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552, 317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US/09/598, 042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US/09/620, 312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US/09/653, 450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US/09/662, 191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US/09/693, 036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US/09/727, 344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7143
; SOFTWARE: PL_Fl_genes_b Versions 1.0
; SEQ ID NO 4024
; LENGTH: 1837
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-286-897-4024

Query Match 2.3%; Score 41.8; DB 6; Length 1837;
Best Local Similarity 48.2%; Pred. No. 0.017;
Matches 118; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 1191 TCAAAAGCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1250
Db 86 TCTAGAAATTTACAGAAAGATGCTTGAAGCTTTGATGATGATGATGATGATGATGATGAT 145
QY 1251 CCAATTTGAGCTGTGGGAAAGAAATTCGTAACCTTAAGAGAAAGCTGAGAACTTGA 1310
Db 146 CTTTAAATACATGAGGAAAGCTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTA 205
QY 1311 CAAAAGATGAGAGAGCGGTTTCTAGATGTGTGACATCAATGCTGACCTTTTAGTCT 1370
Db 206 TGAAGAAATGATGAGAGAGGTTTACACAGATGATGAGAAAGCCACAGCTTTGAGAGA 265
QY 1371 GATGAAATGAGAGAGCACTTCTATGATGATGATGATGATGATGATGATGATGATGAT 1430
Db 266 AGTGAAGAGAGAGAGATGAGATGCTTCTGATGAGAGATGATGATGATGATGATGATGAT 325
QY 1431 AGTCA 1435
Db 326 GGACA 330

RESULT 12
US-10-105-837-126
; Sequence 126, Application US/10105837
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhao, Qing A.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/10/105, 837
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 09/620, 312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552, 317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488, 725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: PL_Fl_genes Version 1.0
; SEQ ID NO 126

```

; LENGTH: 3423
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (53)..(2800)
US-10-105-837-126

```

Query Match	2.88;	Score 41.8;	DB 6;	Length 3423;
Best Local Similarity	48.28;	Pred. No. 0.023;		
Matches 118; Conservative	0;	Mismatches 127;	Indels	0

QY	1191	TCAAAAGCACTTTTA	TGGAATCCACCAACAGTAATTTCTGTATTGAAAGATTAACAC	1250
Db	1246	TCTGGAATAATTTACA	AGAAAAGCTCTTGAGCATTTGAAGCCCTTTTGTAGTGAGATGATGC	1305
QY	1251	CCAAATTTGAAGCTGT	TGGAAAAGAAATTCGGTAACTTAGAGAAAAGACTGGAGAACTTGAA	1310
Db	1306	CTTTTAAATACCAT	TGAGGAAAACCTGTAGTAAAAAATGAGAAAAGCGCTAGAAAGAACGAA	1365
QY	1311	CAAAAACATGGAGAA	TGGTTTCTAGAGATGTGGACATACAAATGCTGACCTTTTAGTTCT	1370
Db	1366	TGAGGAATATGTGAA	TAAGTTTATTAGCACATATGATGAGAAAGCCCAAGACCTTTGAGAA	1425
QY	1371	GATGAAAATGAGAG	TACACTTGACCTTCTGATTTCAATCTCAAGAATCTGTATTAGTAA	1430
Db	1426	AGTGAAGAAGAGAA	TATGAGTTCCTCGATGACACAGATGCTCCACTTTCTGCAGACGAT	1485
QY	1431	AGTCA 1435		
Db	1486	GGACA 1490		

RESULT 13
US-10-286-897-452

Sequence 452, Application US/10286897	
GENERAL INFORMATION:	
APPLICANT: Hyseq Inc	
TITLE OF INVENTION: Novel	Nucleic Acid and Polypeptides
FILE REFERENCE: 784FLPCT	
CURRENT APPLICATION NUMBER: US/10/286,897	
CURRENT FILING DATE: 2002-11-01	
PRIOR APPLICATION NUMBER: US/09/488,725	
PRIOR FILING DATE: 2000-01-21	
PRIOR APPLICATION NUMBER: US/09/552,317	
PRIOR FILING DATE: 2000-04-25	
PRIOR APPLICATION NUMBER: US/09/598,042	
PRIOR FILING DATE: 2000-06-20	
PRIOR APPLICATION NUMBER: US/09/620,312	
PRIOR FILING DATE: 2000-07-19	
PRIOR APPLICATION NUMBER: US/09/653,450	
PRIOR FILING DATE: 2000-08-31	
PRIOR APPLICATION NUMBER: US/09/662,191	
PRIOR FILING DATE: 2000-09-14	
PRIOR APPLICATION NUMBER: US/09/693,036	
PRIOR FILING DATE: 2000-10-19	
PRIOR APPLICATION NUMBER: US/09/727,344	
PRIOR FILING DATE: 2000-11-29	
NUMBER OF SEQ ID NOS: 7143	
SOFTWARE: pc_fl_genes_b Versions 1.0	
SEQ ID NO 452	
LENGTH: 3423	
TYPE: DNA	
ORGANISM: Homo sapiens	
FEATURE:	
NAME/KEY: CDS	
LOCATION: (53)..(2800)	
US-10-286-897-452	

Query Match	2.3%	Score 41.8;	DB 6;	Length 3423;
Best Local Similarity	48.2%	Pred. No. 0.023;		
Matches 118; Conservative	0;	Mismatches 127;	Indels 0;	Gaps 0;

OY	1191	TCAAAAGCATTTATGGAATCACCAACAAAGGTAAATTCTGTGATTCAAAAAAGAATAACAC	1250
Dd	1246	TCTTGAAAATTTACACAAGAAAGTCCCTTGAGCATTGGAACCCTTTCTTGTGTGATGATGAAATC	1305
OY	1251	CCAATTTGAACCTGTTGGGAAAGAATTCGGTAACCTAGAGAGAAAAGACTGGAGAATCGAA	1310
Dd	1306	CTTTTTTAATACCATTTGAGGAAAACCTGATGAAAAATGAGAAAAGGCTAGAGAACAAGAA	1365
OY	1311	CAAAAAGATGGAACACGGGTTTCTAGATGCTGACATACAAATGCATGACCTTTTAGTTCCT	1370
Dd	1366	TGAGGAAATGTTGNAAGAGTTTITTAGCACATATGATGACGAAACCCACGACCTTGTGAGA	1425
OY	1371	GATGAAAATGAGAGGACACTTGACTTTCATGATTTCAATTCATCAAGAATCTGATATAA	1430
Dd	1426	AGTGAAAGAGAGAAGATGAGATTCCTCATGATGACAGATGTCCTCATTCTCGAGACAT	1485
OY	1431	AGTCA	1435
Dd	1486	GGACA	1490

```

RESULT 14
US-10-286-897-1473
; Sequence 1473, Application US/10286897
GENERAL INFORMATION:
; APPLICANT : Hyseq Inc.
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
CURRENT APPLICATION NUMBER: US/10/286,897
CURRENT FILING DATE: 2002-11-01
PRIORITY APPLICATION NUMBER: US/09/488,725
PRIORITY FILING DATE: 2000-01-21
PRIORITY APPLICATION NUMBER: US/09/552,317
PRIORITY FILING DATE: 2000-04-25
PRIORITY APPLICATION NUMBER: US/09/598,042
PRIORITY FILING DATE: 2000-06-20
PRIORITY APPLICATION NUMBER: US/09/620,312
PRIORITY FILING DATE: 2000-07-19
PRIORITY APPLICATION NUMBER: US/09/653,450
PRIORITY FILING DATE: 2000-08-31
PRIORITY APPLICATION NUMBER: US/09/662,191
PRIORITY FILING DATE: 2000-09-14
PRIORITY APPLICATION NUMBER: US/09/693,036
PRIORITY FILING DATE: 2000-10-19
PRIORITY APPLICATION NUMBER: US/09/727,344
PRIORITY FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7143
SOFTWARE: pt_fl_genes_b Versions 1.0
SEQ ID NO 1473
LENGTH: 1116
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS (4552)..(11116)
LOCATION: (4552)..(11116)
US-10-286-897-1473

```

Query Match	2.3%	Score	41.8	DB	6	Length	1116
Best Local Similarity	48.2%	Pred. No.	0.038				
Matches	118	Conservative	0	Mismatches	127	Indels	0
						Gaps	0

[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search: using sw model

Run on: August 10, 2003, 02:11:24 ; Search time 3938.27 Seconds
(without alignments)
14835.212 Million cell updates/sec

Title: US-09-918-568-46

Perfect score: 1783
Sequence: 1 CGCGTAGCAAAAGCAGGCGT.....ACCCCTGTTCTGCTAGCCG 1783

Scoring table: IDENTITY_NUC

Gapop 10.0 , (apex 1.0

Searched: 32997241 seqs, 16383922548 residues

Total number of hits satisfying chosen parameters: 65994482

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_NA_Main: *
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2: /cgn2_6/p/oddata/2/pna/PCRTUS_COMB.seq: *
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4: /cgn2_6/p/oddata/2/pna/US080_COMB.seq: *
5: /cgn2_6/p/oddata/2/pna/US081_COMB.seq: *
6: /cgn2_6/p/oddata/2/pna/US082_COMB.seq: *
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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1783	100.0	1783	9	US-08-443-862-46
2	1783	100.0	1783	38	US-09-918-568-46
3	1723.4	96.7	1773	10	US-08-573-569-17
4	1718.6	96.4	1773	10	US-08-573-569-35

5 1606.4 90.1 1728 9 US-08-443-862-28
6 1606.4 90.1 1728 38 US-09-918-568-28
7 908.8 51.0 1135 9 US-08-443-862-49
8 908.8 51.0 1135 38 US-09-918-568-49
9 732.4 41.1 1733 1 PCT-US03-09287-13
10 732.4 41.1 1733 2 PCT-US03-09287-13
11 732.4 41.1 1733 51 US-10-397-635-13
12 728.2 40.8 1738 4 US-07-773-597-14
13 714 40.0 1698 15 US-09-040-944-1
14 714 40.0 1698 15 US-09-045-042-1
15 703.4 39.5 1770 5 US-08-063-818-1
16 695.6 39.0 1754 9 US-08-443-862-27
17 695.6 39.0 1754 38 US-09-918-568-27
18 463.2 26.0 1757 51 US-10-381-085-12
19 460 25.8 1753 51 US-10-381-085-9
20 460 25.8 1753 51 US-10-381-085-11
21 453.8 25.5 1697 51 US-10-381-085-10
22 400 22.4 400 9 US-08-443-862-33
23 400 22.4 400 38 US-09-918-568-33
24 397 22.3 409 9 US-08-443-862-34
25 397 22.3 409 38 US-09-918-568-34
26 382.4 21.4 410 9 US-08-443-862-35
27 382.4 21.4 410 38 US-09-918-568-35
28 379.6 21.3 394 9 US-08-443-862-36
29 379.6 21.3 394 38 US-09-918-568-36
30 373 20.9 924 4 US-07-751-896-1
31 373 20.9 924 4 US-07-837-773-15
32 373 20.9 924 4 US-07-837-773-15
33 372.6 20.9 810 4 US-07-751-896-5
34 372.6 20.9 810 4 US-07-837-773-19
35 372.6 20.9 810 4 US-08-391-315-19
36 368.2 20.7 670 4 US-07-837-773-5
37 368.2 20.7 670 8 US-08-391-315-5
38 361.4 20.3 912 4 US-07-751-896-17
39 361.4 20.3 912 4 US-07-837-773-31
40 361.4 20.3 912 8 US-08-391-315-31
41 318.6 17.9 1777 9 US-08-443-862-54
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43 312.8 17.5 2005 38 US-09-914-658B-3
44 312.8 17.5 4930 38 US-09-914-658B-1
45 312.4 17.5 4610 38 US-09-914-658B-6

ALIGNMENTS

Sequence 28, Appl
Sequence 28, Appl
Sequence 49, Appl
Sequence 49, Appl
Sequence 13, Appl
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Sequence 14, Appl
Sequence 1, Appl
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Sequence 5, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 6, Appl

FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: A/Okuda/57
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLER:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:

RESULT 1
US-08-443-862-46
Sequence 46, Application US/08443862
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,862
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016

Query Match 100.0%; Score 1783; DB 9; Length 1783;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-08-443-862-46

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Oy 1261 GCTGTGGGAAAGATTCGTAATCTTGAGAAAAAGACTGGAACCTTGGAACAAAAGATG 1320
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Oy 1441 CAGCTGAGACACACGCTCAAGAACCTAGGAATGATGTTTGAATTTATCACAATGT 1500
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Oy 1561 GAGTCTAAACTAAATAGAAATGAATCAAGGGGTAAATTTAGACAGCATGGGGTTTAT 1620
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Db 1741 TAAATCATTTTATATTAATAAACACCCCTGTTCTGCTAGCGG 1783

RESULT 2
US-09-918-568-46
Sequence 46, Application US/09918568
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESS: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918, 568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004, 422.
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443, 862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229, 781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054, 016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200

TELEFAX: 202-721-8250
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1783 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to genomic RNA
 HYPOTHETICAL: <Unknown>
 ANTI-SENSE: <Unknown>
 FRAGMENT TYPE: <Unknown>
 ORIGINAL SOURCE:
 ORGANISM: A/Okuda/57
 STRAIN: <Unknown>
 INDIVIDUAL ISOLATE: <Unknown>
 DEVELOPMENTAL STAGE: <Unknown>
 HAPOTYPE: <Unknown>
 TISSUE TYPE: <Unknown>
 CELL TYPE: <Unknown>
 CELL LINE: <Unknown>
 ORGANELLER: <Unknown>
 IMMEDIATE SOURCE:
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 MAP POSITION: <Unknown>
 UNITS: <Unknown>
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 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION:
 PUBLICATION INFORMATION:
 AUTHORS:
 TITLE:
 JOURNAL:
 VOLUME:
 ISSUE:
 PAGES:
 DATE:
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 FILING DATE:
 PUBLICATION DATE:
 RELEVANT RESIDUES IN SEQ ID NO:
 SEQUENCE DESCRIPTION: SEQ ID NO: 46:
 US-09-918-568-46

Query Match 100.0%; Score 1783; DB 38; Length 1783;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 121 AATATTCACAGAGAGGTGACACATATCTTAGAGCGGAGAGTCACTGTGACTCATGCC 180
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 1081 GCAATAGCTGTGTTTATGAAGAGAGTGAAGAAATGTTGAGAGGTGTGATGAGATC 1140
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Db 1441 GAGGGAACAACGTCAAAGAACTAGAAATGGAATGATGTTTGAATTTTATCAAAATGTATGA 1500
QY 1506 TGAATGCAATGATGTAAGAAACGAGCATATGATTTTCCAGTATGAGAGAGTC 1565
Db 1501 UGAUUGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1560

QY 1566 TAACTAATAGAAATGAATCAAGGAGTAAATTTGAGCAGCATGGGGTTTATCAAT 1625
Db 1561 UAAACUAAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1620
QY 1626 CCTTGCAATTTATGCTACAGTACAGGTTTCTATGTCATGCAATCATGATGCTGGAT 1685
Db 1621 CUUGCCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1680
QY 1686 CTCTTCTGCGGTGCTCCACAGGCTCTGCAAGTGCAGATCTGATATATTAAT 1745
Db 1681 CUUUCUUGAUUGUGUCCCAAGGUCUUGCAGUGCAGACUUCGUAUUAUUAUUAU 1740
QY 1746 CATTTAATTAATAAAACACCTTGTCTGCT 1778
Db 1741 CAUUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1773

RESULT 4
US-08-573-569-35
Sequence 35, Application US/08573569
GENERAL INFORMATION:
APPLICANT: Maesab, Hunein F
APPLICANT: Heliocher, Martha L
TITLE OF INVENTION: Cold-adapted Influenza Virus
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anna M Lewak
STREET: 5445 Corporate Drive
CITY: Troy
STATE: MI
COUNTRY: USA
ZIP: 48098
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/573, 569
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082, 846
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lewak, Anna M
REGISTRATION NUMBER: 33006
REFERENCE/DOCKET NUMBER: 2115-00257
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-641-1600
TELEFAX: 313-641-0270
INFORMATION FOR SEQ. ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 1773 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Influenza virus
STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)
IMMEDIATE SOURCE:
CLONE: HA
FEATURE:
NAME/KEY: mutation
LOCATION: replace(144, "a")
OTHER INFORMATION: /gene= "HA"
OTHER INFORMATION: /note= "u in ca "master" strain; a in wt(3)"
FEATURE:
NAME/KEY: mutation
LOCATION: replace(455, "g")

OTHER INFORMATION: /gene= "HA"
OTHER INFORMATION: /note= "a in ca "master" strain; g in wt2(3)"
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FEATURE:
NAME/KEY: mutation
LOCATION: replace(729, "a")
OTHER INFORMATION: /gene= "HA"
OTHER INFORMATION: /note= "c in ca "master" strain; a in wt2(3)"
OTHER INFORMATION: /c:lation= ([1])
FEATURE:
NAME/KEY: CDS
LOCATION: 44..1729
OTHER INFORMATION: /product= "hemagglutinin"
OTHER INFORMATION: /gene= "HA"
OTHER INFORMATION: /note= "hemagglutinin protein"
OTHER INFORMATION: /c:lation= ([1])
PUBLICATION INFORMATION:
AUTHORS: Herlocher, M L
AUTHORS: Maassab, H F
AUTHORS: Webster, R G
TITLE: Molecular and biological changes in the cold
TITLE: adapted master strain A/A/6/60 (H2N2) Influenza
TITLE: virus
JOURNAL: Proceedings of the National Academy of Sciences of the USA
DATE: 1993
RELEVANT RESIDUES IN SIQ ID NO: 35: FROM 1 TO 1773
US-08-573-569-35

Query Match 96.48; Score 1718.6; DB 10; Length 1773;
Best Local Similarity 74.8; Pred. No. 0;
Matches 1318; Conservative 421; Mismatches 34; Indels 0; Gaps 0;

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DB 1 AGCAAAAGCGAGGGGTATACCATGAAACCAAGCAAAACATGGCCATATTCT 60
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DB 61 CAUUCUCCUGUACGAGTGAAGGGGACAGATATGATGATGATGATGATGAT 120
QY 126 TTCACAGAGAGAGTGCACACATTTCTAGACCGGACAGTCTGATCTGATG 185
DB 121 UGCCACGAGACGGUACACAAAUUCAGACGGGACGUCACUUGACUUGCCAA 180
QY 186 CATCTCTGAGAGAGCATATACGGAAGTTATGCAAACTAAAGCAATCCCTCA 245
DB 181 CAUUCUUGAGAGAGCATATACGGAAGTTATGCAAACTAAAGCAATCCCTCA 240
QY 246 ACTAGGGGAGTGTAGATTGCGCGAGTCTCTTGAATCCAAATGTATAGCTT 305
DB 241 ACUAGGGGAGTGTAGATTGCGCGAGTCTCTTGAATCCAAATGTATAGCTT 300
QY 306 AAGTGTCCGAGAGCTTCTATATATTGAGAAAGAAACCCGAGAGAGCGTTT 365
DB 301 AAGGTGCGAGAGTGTCTATATATTGAGAAAGAAACCCGAGAGAGCGTTT 360
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DB 361 UCCAGGAGGTTCAAGTATGAGAAATGAAACATCTCTCAAGCGGCTGAAAC 420
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DB 421 CGAAGAAAGTAAAGATCTGCCCAAGATAGATGACACAGCATCAACAATG 480
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QY 726 AATGCAACAGGCGCTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 785
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QY 786 CTTCGATATGTTGGGACACATATATTTTGAAGTACTGTAATGATGATG 845
DB 781 CUUGAUAUUGGGGACACCAUAAUUGUAGAGUACUGUAUUCUAUUGCACA 840
QY 846 TGAATTCAAATATCGAAAGAGGTACTTCAGGATCATGAACAGAGACAT 905
DB 841 UGGAUUCAAAUUACGAAAGAGGAGUAGUUCUGGAGCAUAGAAACAGAA 900
QY 906 GAATGTGAGACCAATGCCCAACTCTTGGGAGCAATATATCAATACATT 965
DB 901 GAACUUGAGACCAAUUCCCAACUCCUUGGGAGCAUAAUACCAUUGCC 960
QY 966 CAATGTCCACCCATGACATATGATGATGATGATGATGATGATGATG 1025
DB 961 CAUUGUCCACCCACACUAGACAAUAGUGAGUGGCCCCCAUAAUUGG 1020
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||||| 781 AAATTTGAGAGCAGTGGTATCTAGTTGCACCGAGATGATGATTTCAAAATATGAAAG 840
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QY 987 AGGTAGTGGCCCAATATGTAATGAGAGAACTGGTCTTACCAAGAGCTAAGAA 1046
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Db 1081 ATGCAAGAGATGTTGACGGTTGTATGATACCATCACAGCAATGACCGAGATCAGG 1140
QY 1167 GATGACAGACAGCAATCAATCCACTCAAAAGGCAATTTGATGATCAACCAAGGTAAA 1226
Db 1141 GATGACAGACAGCAATCAATCCACTCAAAAGGCAATTTGATGATCAACCAAGGTAAA 1200
QY 1227 TTTCTGTATGAAAAATTAACACCCCAATTTGAAGCTGTGGGAAAGAAATTCGTAACCTT 1286
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Db 1261 AGAGAAAAAGATGGAATCAAAAGATGGAAGAGAGGGTTCTAGATGTGTGAC 1320
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Db 1321 ATACCAATGCTGAGCTTTAGTCTGATGAGAAATGAGAGACACTTGCATGTATTC 1380
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Db 1381 TAATGTCAAGAACTTATAGTAAAGTCAGAAATGACAGTCAAGCTCAAGAACT 1440
QY 1467 AGGAATGAGATGTTTGAATTTATCACAATGATGATGAATGATGATGATGAA 1526
Db 1441 AGGAATGAGATGTTTGAATTTATCACAATGATGATGAATGATGATGATGAA 1500
QY 1527 AAACGGGACATATGATATCCCAAGTATGAAAGAGCTAAACTAAATGAAATGAAT 1586
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QY 1647 AGCAGGTTCTATGCTACTGCGCAATCATGATGGCTGGGATCTCTTGGGGTGGCTCCAA 1706
Db 1621 TGCAGGTTCTCTGCTACTGCGCAATCATGATGGCTGGGATCTCTTGGGATGGCTCCAA 1680
QY 1707 CGGCTCTCTGCACTGATGATCTGCATATGATTAATGATGATTTATA 1754
Db 1681 CGGCTCTCTGCACTGATGATCTGCATATGATTAATGATGATTTATA 1728

RESULT 6

US-09-918-568-28
Sequence 28, Application US/09918568
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ. ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1728 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/12um1/5/65
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:

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1026 GCTACAGAGATTAGAAATATCCGCTATTCAATCTAGAGGTCTGTTGGAGCCATTGCT 1085
QY 1090 GGTATTATAGAGAGAGATGGCAAGGAATGGTGGATGGTATGATGATCATTACAGC 1149
1086 GGTATTATAGAGAGAGATGGCAAGGAATGGTGGATGGTATGATGATCATTACAGC 1145
QY 1150 AATGACGAGGATCAGGATGATGAGCAGACAAAGAAATCCACTCAAAAGCAATTTGATGA 1209
1146 AATGGGACAGGATCAGGATGATGAGCAGACAAAGAAAGACACAGAAATGCCATTGACGG 1205
QY 1210 ATCACCACAGGATTAATTTCTGATTTGAAAACATTAACACCCATTGAACTGTTGG 1269
1206 ATCCTAACAAAGTAATTTCTGATTTGAAAAGATGAACACACGTTACACGCGTGGT 1265
QY 1270 AAGAATTCGATCTAGAGAAAGACTGAGAACTTGAACAAAAGATGGAAGAGGG 1329
1266 AAGAATTCACACCTTGGAAAGAGATAGAGATTTAAACAAAAGTTGATGATGG 1325
QY 1330 TTTCTAGATGCTGACATACAAATGCTGACCTTTAGTCTGATGAAAATGACAGACA 1389
1326 TTTCTGATGTTGGACTTACATGCCGAACTTTGGTCTCTATTGAAAATGAAAGACT 1385
QY 1390 CTGACTTTCATGATCTATGTCAGAAATCTGATAGTAAGTCAGATGCACTGAGA 1449
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1506 TGTATGAGAGTGTCAAAAATGGGACTTATGATTACTCAAAATATCTCAGAAAGTCAAAA 1565
QY 1570 CTAATATGAAATGAATCAAGGGGTAAATTTAGCAGCATGGGGTTTATCAATCTT 1629
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QY 1690 TTCTGGGTGTCTCCACGCGTCTCTGACGTGAGATCTGATATGATTAATGATCATT 1749
1686 TTCTGGATGTCTCCATGCGTCTTACAGTGCAGATATGATTTAAATTTAGATTTTC 1745
QY 1750 TTATATTAATAAACA 1764
1746 AGAGACATGAGAAA 1760
Db

Search completed: August 10, 2003, 18:58:40
Job time : 3943.27 secs

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Core version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 9, 2003, 19:11:43 ; Search time 1703.58 Seconds
(without alignments)
15836.045 Million cell updates/sec

Title: US-09-918-568-57

Perfect score: 1110

Sequence: 1 CTAGAGACAAACAGGGGAT.....TAAACACCCCTGTTTCG 1110

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database: EST:

1: em_estbda:
2: em_estbda:
3: em_estbda:
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5: em_estbda:
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25: em_estbda:
26: em_estbda:
27: em_estbda:
28: em_estbda:
29: em_estbda:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	56.4	5.1	997	29	CNS005TE
C 2	50.6	4.6	878	29	CNS0187R
C 3	49.2	4.4	1101	29	CNS0039G
C 4	47.4	4.3	1159	29	CNS015XR

C 5	47	4.2	1101	29	CNS00KIB	AL077812 Drosophila
C 6	47	4.2	1101	29	CNS017KX	AL180171 Drosophila
C 7	44.2	4.0	662	28	AZ839792	AZ839792 2M0136N02
C 8	44	4.0	901	28	AZ537973	AZ537973 ENTPT76TF
C 9	43.6	3.9	904	28	AZ535715	AZ535715 ENTBS23TF
C 10	43.2	3.9	528	28	BH095442	BH095442 RPT-24-2
C 11	43.2	3.9	1001	29	CNS01400	AL103554 Drosophila
C 12	43	3.9	634	28	AZ676094	AZ676094 2M0237E23
C 13	43	3.9	664	28	AZ724344	AZ724344 RPT-24-1
C 14	42.8	3.9	1201	13	BX399653	BX399653 BX399653
C 15	42.6	3.8	1201	13	BX461310	BX461310 BX461310
C 16	42.4	3.8	936	28	BH160320	BH160320 ENTST12TF
C 17	42.4	3.8	1101	29	CNS0181N	AL108771 Drosophila
C 18	42.4	3.8	1201	13	BX376097	BX376097 BX376097
C 19	42.2	3.8	632	28	AG166064	AG166064 Pan troy1
C 20	41.8	3.8	816	28	AZ528212	AZ528212 ENTDA70TF
C 21	41.8	3.8	1115	9	AL551400	AL551400 AL551400
C 22	41.6	3.7	634	10	BF426967	BF426967 df73f09.y
C 23	41.6	3.7	838	29	CNS03W9J	AL263440 Tetraodon
C 24	41.6	3.7	1101	29	CNS017KE	AL108152 Drosophila
C 25	41.4	3.7	747	29	CNS011RO	AL100640 Drosophila
C 26	41.4	3.7	844	28	AZ675008	AZ675008 ENTBS57TF
C 27	41.2	3.7	500	12	BM279971	BM279971 zah6149.z
C 28	41.2	3.7	604	29	FR0042754	AL130246 Fugu rubr
C 29	41.2	3.7	622	12	BM168204	BM168204 EST570727
C 30	41	3.7	356	28	AO296270	AO296270 HS_2166.B
C 31	41	3.7	816	14	CA463791	CA463791 AGENCOURT
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C 33	41	3.7	987	29	CNS00418	AL065537 Drosophila
C 34	40.8	3.7	713	29	BX241460	BX241460 Danio rer
C 35	40.8	3.7	822	13	BU620988	BU620988 UI-H-FL1-
C 36	40.8	3.7	867	29	CNS0054A	AL057618 Drosophila
C 37	40.8	3.7	971	29	CNS000297	AL068026 Drosophila
C 38	40.6	3.7	972	14	CD389021	CD389021 AGENCOURT
C 39	40.4	3.6	885	13	BX425603	BX425603 BX425603
C 40	40.4	3.6	974	29	CNS001WT	AL075432 Drosophila
C 41	40.4	3.6	1101	29	CNS00YYG	AL096994 Drosophila
C 42	40.2	3.6	532	14	CA301599	CA301599 taa05d10.
C 43	40.2	3.6	566	28	BH113964	BH113964 RPT-24-2
C 44	40.2	3.6	670	29	AG168925	AG168925 Pan troy1
C 45	40	3.6	500	28	AO374391	AO374391 RPT11-14

ALIGNMENTS

RESULT 1
CNS005TE/C
LOCUS
DEFINITION
BACRI2K22 of RPT-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION
AL060767
VERSION
AL060767.1 GI:4943573
KEYWORDS
GSS.
ORGANISM
Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 997)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammosier in Pieter de Jong's laboratory in the Department of

COMMENT

AL060767 Drosophila
AL108993 Drosophila
AL063921 Drosophila
AL106041 Drosophila

ACCESSION AL108993
 VERSION AL108993.1
 KEYWORDS GSS.
 GI: 5629297

ORGANISM
Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPc1-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bcpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source
Location/Qualifiers

1. 1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR08K10"
/clone_1b="RPc1-98"
/note="end : TET3"
BASE COUNT 201 a 64 c 131 g 202 t 503 others

Query Match 4.38; Score 49.2; DB 29; Length 1101;
Best Local Similarity 17.7%; Pred. No. 0.27;
Matches 100; Conservative 230; Mismatches 234; Indels 2; Gaps 1;

OY 544 ATGACCAATCAATGGAATTTGAACAGGTAATGAGAAAGCAAGCAATTCAT 603
Db 999 RDGAGAKRBDATDADGAGRRDGRKRDKRRKGGDDKKKKKAAKAAKATKW 940
OY 604 CAATCGAAAAGAAATTCAGAGTGAAGGAGAAATTCAGACCTCGAATACTGT 663
Db 939 DDDMDKDKWKDGAKRRKADDDGAGDDGKRDADDDTGTGKDDDKKDDMDKAK 880
OY 664 GAAGACATTAATATATCTGCTTACATCGCGAGCTTTGCTGCTGCGAAT 723
Db 879 GTWGDATWMAAATDWMWGWADADWMTWAAADDMWADDMWAMKWDAMAGARTAD 820
OY 724 CAACATACAAATGACCTGACCTGACGAAATGACAAAGCTTTGAAAAACAAAGAG 783
Db 819 RRMWRBARKRGARRRDRKRRDKRDAADDDADATTTTTRTDDKMTDTW 760
OY 784 CAACGTAGGGAATCTGTAAGAGATGGCAATGTTGTTCAAAATATACCAATGT 843
Db 759 TRWAADRTMDRDDDDBRAGTAGRKMRRTWKRRMRRTDTRMDADADTARDBRRRKG 700
OY 844 GACACGCTTCCTAATGATCACAATG--TACTATGACCATGATGTATACAG 901
Db 699 DGADAKGKTKGRRRRRBRATWDRDAMWADAMWTTTDTDDMDKRRRRKARRR 640
OY 902 ACAACATTAACACCGGTTTCAGATCAAGAGTGTGACAGAGTGGATACAAAG 961
Db 639 RTTARAAMWMTYKADMAKMDKTRADRRDAADTWDARAKADDMAKARWRARRDR 580
OY 962 ACTGATCTGTGATTTCTCTTGCATATCATCTTTTGTCTGTGTTTCTGCG 1021
Db 579 ARARADRRMTTGTATATTTWAARAAMWAMATTTATTTTWTWTWTWT 520
OY 1022 GGTTCATCATGTGGCTCGCAGAGGCAACATTTGCGCAATTTGATTTGAGT 1081
Db 519 TWTTTAAWMAWMTATWAAWMTAAWMAAAWMAATTTTWTWTWTAAWMA 460

OY 1082 ATAGTAATTAACACCTTGT 1107
Db 459 WTTTWTWTWTWTWMAATTTTWTWT 434

RESULT 4
CNS015XR/c
LOCUS
DEFINITION
CNS015XR 1159 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence 77 end of BAC
BACN15017 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION
AL106041
GI:5619746
GSS.
Drosophila melanogaster (fruit fly)

VERSION
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
1 (bases 1 to 1159)

AUTHORS
TITLE
JOURNAL
COMMENT

Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
<http://www.edgp.edi.ac.uk> - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES

source
Location/Qualifiers

1. 1159
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN15017"
/clone_1b="DrosBAC"
/plasmid="pBelobAC11"
/note="end : T7"
BASE COUNT 448 a 36 c 7 g 178 t 490 others

Query Match 4.38; Score 47.4; DB 29; Length 1159;
Best Local Similarity 21.7%; Pred. No. 0.77;
Matches 95; Conservative 173; Mismatches 167; Indels 3; Gaps 2;

OY 270 CACTCAATGAGAGATTCCTCAATGCAAGCCCTTCAAAAGCTTAACAGATCAT 329
Db 1087 SAIVSVVAAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSA 1028
OY 330 TGGAGCATGCCCAATATGTTAAGCAAAACACCTGAGTTGCAACAGATCGGAA 389
Db 1027 SASAVSVSAVSVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSS 968
OY 390 TGTACAGAGAAACAATAGAGGCTATTTCGCGCAATAGCAGGTTTATAGAAATG 449
Db 967 SCRMSCA-ASASASVSCGMSMSMSAGASVSAASASASASASASASAS 909
OY 450 TTGGAGAGGAATGATGACCGTTGATGAGTTTCAGCATCAAAATTCGAGGCGAC 509
Db 908 ASASASVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSA 849
OY 510 ACAAGCAGAGATCTTAAGAGCACTCAGACGACCATGCAATCAATGGAATTTGAA 569
Db 848 AVTVVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSA 791
OY 570 CAGGTAATCGACAGACGAGAAATTCATCAATGCAAAAGCAATTTCTCAGACT 629
Db 790 HASRVAVASASRSVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSAVSA 731

Db 910 GAWMTKTRKRGCGGAAAD-WGRTDWMWMDKRAAAAGKDGCKKARTWGAAAAA 852

QY 683 TCTGCTTACATGAGAGCTCTTGCGCTCGAGATCAACATACATGACCTGA 742

Db 851 WTKTKATTKKTKTKTGRAWMAAGTTRTWDATAMKTKRAAAAGRAAAAMAKDGTGR 792

QY 743 CTGACTCGGAATGACCAAGCTTTGAAA-AAACAGAGGAGCACTGAGGAGAAATGC 800

Db 791 GKRKRKGTGDTGKTGKTKTTTWTATAAARRARAANKWTKTKDGRARAAMDAMT 732

QY 801 TGAAGAGAGGCGCAATGCTTCAATATACCAATATGACACCGCTTGATAGA 860

Db 731 TTRKGAATRRGAAATAATRGAAAAATGKTTDGAATAATAMVRRTWMDWMAAR 672

QY 861 GTCATCAGAAATGTAATGACCATGATGACATGATACAGAGAGAG 907

Db 671 AAGAAWMAKAAWDAADAKKKGRRKRAAAATAARRAKKAKDR 625

RESULT 7

LOCUS AZ839792/c 662 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0136N02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0136N2 F, genomic survey sequence.

ACCESSION AZ839792

VERSION AZ839792.1 GI:1309700

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 662)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weils,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0136 row: N column: 02
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 662.

FEATURES

source

1. 662

Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0136N02"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

BASE COUNT 131 a 116 c 106 g 309 t

ORIGIN

Query Match

Best Local Similarity 60.3%; Pred. No. 4.4;

Matches 73; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 556 AATGGAAATTTGACAGCGGTAATCGAGACAGACAGAAATTCATCAATGAAAG 615

Db 561 AATGGAAGTTGAGTGAACCAACAGCAATATCAACCAAGAAAGAAATGAGAG 502

QY 616 GAATTCACAGAGAGAGAGCAATTCAGACCTCGAATAATACGTTGAACACTAA 675

Db 501 AAATATCAGATGTTGAGACACACATCGAAGACATGATACATCAGTCAAGAAATGAA 442

QY 676 A 676

Db 441 A 441

RESULT 8

LOCUS AZ537973/c 901 bp DNA linear GSS 14-NOV-2000

DEFINITION ENTFT76TF Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.

ACCESSION AZ537973

VERSION AZ537973.1 GI:1142468

KEYWORDS GSS.

SOURCE Entamoeba histolytica

ORGANISM Entamoeba histolytica

REFERENCE Eukaryota; Entamoebidae; Entamoeba. 1 (bases 1 to 901)

AUTHORS Loftus,B., Van Aken,S. and Fraser,C.

TITLE Determination of clone end sequences from Entamoeba histolytica HMI:IMSS sheared DNA library

JOURNAL Unpublished

COMMENT Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjoftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library

FEATURES

source

1. 901

Location/Qualifiers

/organism="Entamoeba histolytica"

/mol_type="genomic DNA"

/strain="HMI:IMSS"

/db_xref="taxon:5759"

/clone_lib="Entamoeba histolytica Sheared DNA"

/note="Vector: PHOS1; Site:1; Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith,

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gil473211419b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Bartell, Oxford University Press, 1999). "

BASE COUNT 108 a 192 c 67 g 534 t

Query Match 4.0%; Score 44; DB 28; Length 901;
Best Local Similarity 54.3%; Pred. No. 5.2;
Matches 89; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 513 AGCAGCATCTTTAAAGCAGCTCAGCCATCGACCAATCATGGAATTGGAACAG 572
11
Db 206 AGAAGAGAAATTAAGAAACAAATTAAGATGACAGATTAAAGAGAGAGAGAA 147
11
QY 573 GGTATTCGAGAGACAGAGAAATTCATCAATCGAAAGAGAAATTCGCAAGATAG 632
11
Db 146 GAAATAGAGATGAAAGACAGATTAATAGAGAGAGAAAGAAATTAATAGAAAA 87
11
QY 633 AGGAGAAATTCAGACCTCGAGAAATTCGTTGAGAGACTTAAAG 676
11
Db 86 AGAAAGAAATGAAAGAAACAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 43

RESULT 9 904 bp DNA linear GSS:03-NOV-2000
A2535715
LOCUS ENTB523TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
DEFINITION genomic, genomic survey sequence.
ACCESSION A2535715
VERSION A2535715.1 GI:11092662
KEYWORDS GSS.
SOURCE Entamoeba histolytica
ORGANISM Entamoeba histolytica
REFERENCE 1 (bases 1 to 904)
AUTHORS Loftus, B., Van Aken, S. and Fraser, C.
TITLE Determination of clone end sequences from Entamoeba histolytica
JOURNAL HMI:IMSS sheared DNA library
COMMENT Unpublished
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b.loftus@tigr.org

Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library
Seq primer: M13-Forward
Class: shotgun
High quality sequence start: 19
High quality sequence stop: 795.
Location/Qualifiers

FEATURES
Source 1..904
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HMI:IMSS"
/db_xref="taxon:5759"

/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOSt1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Bartell, Oxford University Press, 1999). "

BASE COUNT 489 a 76 c 108 g 231 t

Query Match 3.9%; Score 43.6; DB 28; Length 904;
Best Local Similarity 50.8%; Pred. No. 6.5;
Matches 129; Conservative 0; Mismatches 124; Indels 1; Gaps 1;

QY 532 ACTCAAGCAGCCATCGACCAATTCATGGAATGGAACAGGTAATGAGAGAGAG 591
11
Db 228 AATTATTAAGAAAGAAATAGAAATTAATAGAAATGAATGATATGTACACAAAAC 287
11
QY 592 GAGAAATTCATCAATCGAAAGAAATTCGAGAGAGAGAGAGAGAGAGAGAG 651
11
Db 288 ATTAAGCAAAAT-AAATAGAGAGAAATTAAGAGAGAGAGAGAGAGAGAGAG 346
11
QY 652 GAGAAATTCATCAATCGAAAGAAATTCGAGAGAGAGAGAGAGAGAGAGAG 711
11
Db 347 AACCAATTCAGCAATCTAATAGAGAAATTAATTAATTAATTAATTAATTAAT 406
11
QY 712 GCTCTGAGAGATCAATCAATTCATGCTGACTGAGAGAGAGAGAGAGAGAG 771
11
Db 407 AATCTTCATTAATTAATCAAGAAATGAAATTAATTAATTAATTAATTAATTAAT 466
11
QY 772 AAAACAGAGAGCA 785
11
Db 467 TAAAAAAGAGAA 480

RESULT 10 528 bp DNA linear GSS:18-JUL-2001
BH095442/c
LOCUS RPCI-24-271C12.TV RPCI-24 Mus musculus genomic clone RPCI-24-271C12
DEFINITION genomic survey sequence.
ACCESSION BH095442
VERSION BH095442.1 GI:14915347
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 528)
AUTHORS Zhao, S., Niernan, W., Malek, J., Shatsman, S., Akintet, B., Levins, M., Tsagaye, G., Geier, K., Kroll, M., Shvartsbeyn, A., Gebregorgis, E., Russell, D., de Jong, P. and Fraser, C.M.
TITLE Mouse BAC End Sequences from Library RPCI-24
JOURNAL Unpublished
Other_GSSs: RPCI-24-271C12.TV
COMMENT Contact: Shanying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdjong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choi.org/bacpac/orderinframe.htm>). BAC end plate: 271 row: C column: 12
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers

FEATURES
Source 1..528
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

/clone="RPCI-24-271C12"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pVBARBAC1; Site_1: BamHI; Site_2: BamHI;

RCPI-24 mouse BAC library produced by Pieter de Jong. The library was cloned in the pARBAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA.

BASE COUNT 110 a 108 c 101 g 209 t

Query Match 3.4%; Score 43.2; DB 28; Length 528;
Best Local Similarity 55.4%; Pred. No. 7.5;
Matches 84; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 525 TAAAGCCTCAGAGC/GCCATCGACCAATTCGGAATTCAGAGGCTAATCGAGAA 584
||||| - - - - - || - - - - - || - - - - - || - - - - - ||
DB 466 TAAAGCCTCAGAGC/TCCCAAGAGGAAACCTCGATATCGAAACATAGAGAGAA 407
- - - - - || - - - - - || - - - - - || - - - - - || - - - - - ||
QY 585 GAGCAAGGAGAAATTCATCAATTCGAAAGAAATTCGAGAGTGAAGAGGAAATTC 644
- - - - - || - - - - - || - - - - - || - - - - - || - - - - - ||
DB 406 TACAGCAGCTACATTCAGAAATTCGAGAGAAATTCGAGTGAAGATACCATAGA 347
- - - - - || - - - - - || - - - - - || - - - - - || - - - - - ||
QY 645 GGACCTCGAGAAATTCGTTGAGACACTAAAA 676
- - - - - || - - - - - || - - - - - || - - - - - || - - - - - ||
DB 346 AGATATTGAGCATC/GTCGAGAGAAATTCAAA 315
- - - - - || - - - - - || - - - - - || - - - - - || - - - - - ||

RESULT 11
CNS01400 1001 bp DNA linear GSS 26-JUL-1999
LOCUS CNS01400
DEFINITION Drosophila melanogaster genome survey sequence Sp6 end of BAC
BACN11806 of Drosophila library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL103554
VERSION AL103554.1 GI:5615165
KEYWORDS GSS.

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1001)

AUTHORS

TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : secrete@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billard at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payat. It has been constructed in the vector pBelobAC11.

FEATURES Location/Qualifiers

1..1001
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="BACN11806"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : Sp6"
BASE COUNT 263 a 70 c 145 g 236 t 287 others

Query Match 3.9%; Score 43.2; DB 29; Length 1001;
Best Local Similarity 22.5%; Pred. No. 8.4;
Matches 82; Conservative 114; Mismatches 168; Indels 0; Gaps 0;

QY 605 AATTCAGAAAGAAATTCGAGAGTGAAGGAGAAATTCGAGACCTCGAGAAATTCAGTTG 664
||||| - - - - - || - - - - - || - - - - - || - - - - - ||
DB 596 AAATVTEMBANGNRCINHAATBTNKTGKRGKTKMDTRABAMARRRRKATATRTWTTTKR 655
- - - - - || - - - - - || - - - - - || - - - - - || - - - - - ||
QY 665 AAGACACTAAATATGATCTCTGCTTACAAATCGAGCTTCTTCTGCTCTGAGAAATC 724
- - - - - || - - - - - || - - - - - || - - - - - || - - - - - ||

DB 656 TDGAKATADAAARAAVKAQKRTNGWMAWMAATATADATADTDATDTGTWGTAKA 715
- - - - - || - - - - - || - - - - - || - - - - - || - - - - - ||
QY 725 AACATCAATTCAGCTTACGACCGGCAATTCGAGAGCTGTTGAAAAAACAAGAGGC 784
- - - - - || - - - - - || - - - - - || - - - - - || - - - - - ||
DB 716 WADMTTKMANKRRKAGRRKAKDKRDKDWMKATRTGKMGAGATWDKDKNRKAGAG 775
- - - - - || - - - - - || - - - - - || - - - - - || - - - - - ||
QY 785 AACTGAGGAGAAATTCGAGAGAGATGGCAATGCTTCAAAATATACCAAAATGTG 844
- - - - - || - - - - - || - - - - - || - - - - - || - - - - - ||
DB 776 AGAGAGKGDARARRRRRAGARWMTAKADTATMKNRHHHTATATATMAADTAKAAMD 835
- - - - - || - - - - - || - - - - - || - - - - - || - - - - - ||
QY 845 ACAAGCTTCATAGATCAATCAGAAATGTAATTCAGACATGATGTATACAGAGC 904
- - - - - || - - - - - || - - - - - || - - - - - || - - - - - ||
DB 836 GWMAAATATDWMTKMKADADTTATAKAKMABABAKAHDHTAAMWADKMAAARRANAA 895
- - - - - || - - - - - || - - - - - || - - - - - || - - - - - ||
QY 905 AAGCATTAACCAACCGCTTCAGATCAACAGTGTGTAAGCTCGATACAAACT 964
- - - - - || - - - - - || - - - - - || - - - - - || - - - - - ||
DB 896 DATTAATMADNMWAKMGAABADBDHGGAGAKADWAKAAKAAWTAADAAWAKW 955
- - - - - || - - - - - || - - - - - || - - - - - || - - - - - ||
QY 965 GCAT 968
- - - - - || - - - - - || - - - - - || - - - - - || - - - - - ||
DB 956 AGAK 959
- - - - - || - - - - - || - - - - - || - - - - - || - - - - - ||

RESULT 12
A2967094 634 bp DNA linear GSS 27-APR-2001
LOCUS A2967094
DEFINITION 2M0237E23R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0237E23 R, genomic survey sequence.

ACCESSION A2967094
VERSION A2967094.1 GI:13838321
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 634)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00
Plate: 0237 row: E column: 23
Seq primer: CACACACGAAACAGCTATGACG
Class: plasmid ends
High quality sequence stop: 634.

FEATURES Location/Qualifiers

1..634
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0237E23"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PMD42nv. Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory mouse DNA resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrotynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (9147321419b1AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 277 a 132 c 92 g 133 t

Query Match 3.9% Score 43; DB 28; Length 634;
Best Local Similarity 47.6%; Pred. No. 8.7;
Matches 127; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

OY 526 AAAAGCACTCAAGCAGCCATGACCAATCAATGGAATTGACAGGTAATCGAGAAG 585
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OY 586 ACGAAGCAGAAATTCATCAATGAAAGAAATTCAGAGTAGAAGGAGAAATTCAG 645
DB 259 ATTCTGACATCATGTGCTCCAAATGAGTGCACCCACATTCATTAAGAACTTTACAA 318
OY 646 GACCTGAGAAATTCGTTGAAGACATTAATAGATCTGCTTCAATGCGAGCTT 705
DB 319 AACCTCAAAACACACACTGAAACTCAGCAATTAATGAAATTTAAACCACTCTT 378
OY 706 CTGTGCTCTGGAGATCAACATATGACCTGACTGAGAAATGAAAGAGCTG 765
DB 379 GCCAATGCTGAGCAGATTGATACGAAGTCAACAAAGGCAGACTGAATTAACAGATT 438
OY 766 TTGAAAAAACAAGAGGCAACTGAGG 792
DB 439 TATGAACCAATTTGAATTTAACAAGATG 465

RESULT 13
LOCUS A2724344 664 bp DNA linear GSS 24-JAN-2001
DEFINITION RPCI-24-145C19.TJ RPCI-24 Mus musculus genomic clone RPCI-24-145C19
ACCESSION A2724344
VERSION A2724344.1 GI:12469888
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
1 (bases 1 to 664)
Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akiret,B., Levins,M.,
Tsengaye,G., Geer,K., Krol,M., Shvartsdey,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished
Other GSSs: RPCI-24-145C19.TJ
Contact: Shaying Zhao

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@igf.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end
page: http://www.tigr.org/db/bac_ends/mouse/bac_end_intro.html
Plate: 145 row: C column: 19

Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
1. 664
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-145C19"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTRBAC1; Site-1: BamHI; Site-2: BamHI;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTRBAC1 cloning vector at the
BamHI sites using MboI partially digested male C57BL/6J
DNA."

BASE COUNT 308 a 138 c 89 g 129 t

Query Match 3.9% Score 43; DB 28; Length 664;
Best Local Similarity 47.6%; Pred. No. 8.7;
Matches 127; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

OY 526 AAAAGCACTCAAGCAGCCATGACCAATCAATGGAATTGACAGGTAATCGAGAAG 585
DB 120 AGAGACAAAAAAGAGACATTTCTATCTATCAAGAAATCTCCACCAAGATGAGTCAA 179
OY 586 ACGAAGCAGAAATTCATCAATGAAAGAAATTCAGAGTAGAAGGAGAAATTCAG 645
DB 180 ATTCTGACATCATGTGCTCCAAATGAGTGCACCCACATTCATTAAGAACTTTACAA 239
OY 646 GACCTGAGAAATTCGTTGAAGACATTAATAGATCTGCTTCAATGCGAGCTT 705
DB 240 AACCTCAAAACACACACTGAAACTCAGCAATTAATGAAATTTAAACCACTCTT 299
OY 706 CTGTGCTCTGGAGATCAACATATGACCTGACTGAGAAATGAAAGAGCTG 765
DB 300 GCCAATGCTGAGCAGATTGATACGAAGTCAACAAAGGCAGACTGAATTAACAGATT 359
OY 766 TTGAAAAAACAAGAGGCAACTGAGG 792
DB 360 TATGAACCAATTTGAATTTAACAAGATG 386

RESULT 14
LOCUS BX399653/c 1201 bp mRNA linear EST 13-MAY-2003
DEFINITION BX399653 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
ACCESSION BX399653
VERSION BX399653.1 GI:30629850
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4309.f. For
more information about this cluster, see
<http://www.genoscope.cns.fr/cgl-bin/cluster.cgi?seq=CS0D1080BC030P1&cluster=4309.f>
Feng Liang Email : liang@lifetech.com URL :
<http://fulllength.invitrogen.com/InvitrogenCorporation1600>
Paradise Avenue Genoscope, sequence ID : CS0D1080BC030P1.

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QY 766 GTCAAGATCTGTATAGTAAGTCAGANTCAGCTGAGACACAGCTCAAGAACTAGCA 825
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QY 826 AATGATGTTTGAATTTTATCACAATGTGATGATGATGATGATGATGATGATGATGAT 885
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Db 1435 AATGATGTTTGAATTTTATCACAATGTGATGATGATGATGATGATGATGATGATGAT 1494
1111111111 1111 1111 1111 1111 1111 1111 1111 1111 1111
QY 886 GGGACATATGATTTTCCAGATGAGAGAGCTAACTAAATAGAAATGAATGAAA 945
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Db 1495 GGGACATATGATTTTCCAGATGAGAGAGCTAACTAAATAGAAATGAATGAAA 1554
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QY 946 GGGTAAATTAAGCAGCATGGGGGTTTATCAATCCTTGCATTTATGCTACAGTAGCA 1005
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QY 1006 GGTCTATGCTACTGCAATCATGATGCTGGGATCTCTTCTGGGCTGCTCCACGGG 1065
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Db 1615 AGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1674
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QY 1066 TCTCTGAGTCAGAGATCTGCAT 1088
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Db 1675 TCTTTCAGTCAGAGATCTGCAT 1697
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RESULT 12
US-09-045-042-1
Sequence 1, Application US/09045042
GENERAL INFORMATION:
APPLICANT: TAUBENBERGER, Jeffery K.
APPLICANT: REID, Ann H.
APPLICANT: FANNING, Thomas G.
TITLE OF INVENTION: HEMAGGLUTININ GENE OF THE 1918 INFLUENZA
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: BELLAMY, Werten, F.W.
STREET: 901 North Stuart Street, N.W., Suite 700
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22203-1837
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09/045,042
FILING DATE: 19-MAR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BELLAMY, Werten, F.W.
REGISTRATION NUMBER: 27,029
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-696-8119
TELEFAX: 703-696-8116
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1698 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Influenza virus
STRAIN: Influenza A/South Carolina/1/18 (H1N1)
IMMEDIATE SOURCE:
CLONE: Hemagglutinin
US-09-045-042-1

Query Match 40.1%; Score 455; DB 15; Length 1698;
Best Local Similarity 70.5%; Pred. No. 2.5e-108;
Matches 608; Conservative 0; Mismatches 255; Indels 0; Gaps 0;
QY 226 GGATCCGGGATCATGAAGAGAGAAAGCACTTGAGAACTGTGAGACCAATGCAAACT 285
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QY 1066 TCTCTGAGTCAGAGATCTGCAT 1088
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Db 1675 TCTTTCAGTCAGAGATCTGCAT 1697
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RESULT 13
PCT-US03-09287-13
Sequence 13, Application PC/TUS0309287
GENERAL INFORMATION:
APPLICANT: ZHANG, XIAOLIU
TITLE OF INVENTION: POTENT ONCOLYTIC HERPES SIMPLEX VIRUS FOR CANCER
US-09-045-042-1

Db	1410	AGAAATTATATGAG	AAGGTCAAATGCGAATTGAGAAATATATGCCAAGAATTTGGAAAT	1465
Qy	829	GGATGTTTTCGAATTTAT	CACAATTCGATGATGATGAATAGTCATGAATAGTGTGTAACAAACGGG	888
Db	1470	GGTGTGTTTTCAGTTCTC	ACCAACATGTCATGATATAGTCAGAAAGTGTAAAGAACGGC	1529
Qy	889	ACATATGATTTATCCCA	TAGTATGAAGAAGAGCTCTAACTAAATATAGAAATGAATCAAAAGG	948
Db	1530	ACATAGCAGTACCCCA	TAGTATTCAGAAAGTCCCAATTTGATTCGAGAAAGAATATAGACGG	1589
Qy	949	GTAATTTGAGCAGCA	TGGGGGTTATCAATTCCTGGCATTTATGCTACAGTACAGCT	1008
Db	1590	GTCGAACTCAGATCA	TGGGAGCTTTATCAAAATTTTGGGAGCTATATCCACAGTGCACAGT	1649
Qy	1009	TCTATGTCACGTGCGA	TTCATGATGATGGCTGGGAGATCTCTTTCTTGGGGATGTCCTCCACAGGAGCT	1068
Db	1650	TCTCTACTGTTGTTAA	TCTCCCTGGGGGCAATCAGCTTCTGATGTGTCTTAATGGGTCA	1709
Qy	1069	CTGCAGTGCAGGATCT	GCATATGA	1092
Db	1710	TTGCAATGCAGAAATAT	GCATTTAA	1733

US-RESULT 15
US-10-397-635-13
Sequence 13, Application US/10397635
GENERAL INFORMATION:
APPLICANT: ZHANG, XIAOLI
APPLICANT: FU, XUPING
TITLE OF INVENTION: POTENT ONCOLYTIC HERPES SIMPLEX VIRUS FOR CANCER
TITLE OF INVENTION: THERAPY
FILE REFERENCE: P02410052
CURRENT APPLICATION NUMBER: US/10/397,635
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: 60/367,788
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 60/410,024
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 1733
TYPE: DNA
ORGANISM: Influenza virus
US-10-397-635-13

Query Match	39.8%;	Score 452.8;	DB 51;	Length 1733;
Best Local Similarity	70.8%;	Pred. No. 9.7e-108;		
Matches 607; Conservative	0;	Mismatches 257;	Indels 0;	Gaps 0;

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Search completed: August 10, 2003, 18:58:42
Job time : 2508.97 secs

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COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/063.818
FILING DATE: 19930520
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Brady Jr., James W.
REGISTRATION NUMBER: 32,115
REFERENCE/DOCKET NUMBER: N0610.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)785-9700
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1770 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-063-818-1

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Query Match 41.4%; Score 470; DB 5; Length 1770;

Best Local Similarity 70.4%; Pred. No. 2,9e-113; Mismatches 265; Indels 0; Gaps 0;

Matches 629; Conservative 0; Mismatches 265; Indels 0; Gaps 0;

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QY 346 GAGTGGCCCAATATGTAAATCGAGAACTTGTCTAGCAACAGAGACTAAGAAATGT 405
DB 987 GAATGTCCAAAGTATGTCAAAAGCAAGAAATTTGAGAAATGCTACAGATTAAGAAATATC 1046
QY 406 CCCCAATTTGATTAAGAGATTTGTTGGGCAATAGCTGTTTATAGAAAGAGAGATG 465
DB 1047 CCGTCTATTCAATGTAGAGTCTGTTGGAGCCATTCGTTGTTATTTGAAGGGGGTGG 1106
QY 466 CAAGGATGGTGGGTTGGTATGATGATACATCAGACACAGAGAGAGAGAT 525
DB 1107 ACAGGATGTAGATGGTGTAGCGTTATCACCACAAATGGGAGGATCAGGTTAC 1166
QY 526 GCAGCAGACAAAGATCCACTCAAAAGGATTTGATGATGATCACCACAAAGGTAATCT 585
DB 1167 GCAGCTGACCAAAAGAGACACAGATGCCATTTGAGGGGATCAGTCAAAAGGTAATCT 1226
QY 586 GTGATTAAAAAGATTAACCCCAATTTGAGCTGTTGGGAAAGAAATTCGTAAGT 645
DB 1227 GTTATTAAAAAGATGAACACACAGTTCACAGCGGGGTTAAAGAAATTCACACCTT 1286
QY 646 AAAAGACTGGAGCTGAACAAAAAAGATGAAGGAGGTTTATGATGTGGGACATAC 705
DB 1287 AAGGAATTAAGATTTTAACAAAAAGTTGATGATGATGATGATGATGATGATGATGAT 1346
QY 706 AATGCTGAGCTTTAGTTTGTGATGAGAAATGAGAGACACTTGTGATGATGATGAT 765
DB 1347 AATGCCCACTTTGTTGTTCTTTGTAATAAAGAACTTTGATTTTCAATGACTCAAT 1406
QY 766 GTCAAGATCTGTATTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 825
DB 1407 GTGAAGAACCTATATGAAGAAAGTAAAGACGAGTCAAGAACAAATGCCAAGAAAT 1466
QY 826 AATGATGTTTGAATTTTATCACAATGTGATGATGATGATGATGATGATGATGAT 885
DB 1467 AATGATGCTTTGATTTCTATCACAATGTGATGATGATGATGATGATGATGATGAT 1526

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QY 886 GGACATATGATATCCCAAGTAGAAGAGAGTCTAACTAATAGAAATGAATCAAA 945
DB 1527 GGGACTTTGATTTACTCAAAATACAGAAAGTCAAAACAAAGAGAGATATGAT 1586
QY 946 GGGTAAATTTGAGCAGATGGGGTTTATCAATCTTGCCATTTATGCTACAGTACA 1005
DB 1587 GGGTAAATTTGAGCAGATGGGGTTTATCAATCTTGCCATTTATGCTACAGTACA 1065
QY 1006 GGTCTATGTCATGCGCAATCATGATGATGATGATGATGATGATGATGATGAT 1065
DB 1647 AGTTCATTTGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1706
QY 1066 TCTCTGACGTCAGATGTCATATGATTAATGATTTTAAATTAATAAACA 1119
DB 1707 TCTTACAGTTCAGATATGATTTTAAATTAATGATTTTCAAGACATGACAAAA 1760

```

RESULT 10

US-07-773-597-14

Sequence 14, Application US/07773597

GENERAL INFORMATION:

APPLICANT: INGLIS, Stephen C.

APPLICANT: BRIERLEY, Ian

TITLE OF INVENTION: RIBOSOMAL FRAMESHIFT SIGNALS AND USES

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Walter H. Dreyer

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/773.597

FILING DATE: 19920106

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Dreyer, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-55784/RHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 1778 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 33..1730

US-07-773-597-14

Query Match 41.1%; Score 466.8; DB 4; Length 1778;

Best Local Similarity 51.4%; Pred. No. 2e-111;

Matches 469; Conservative 172; Mismatches 267; Indels 4; Gaps 1;

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QY 226 GGATCGGGGATCATGAAACAGAGAACTGTGAGAACTGTGAGACCAATGCCAACT 285
DB 867 GGGGCGGCAACUACACCUCAAGCAUUGAGUGUAAACAGAGUGUCAAACA 926
QY 286 CCTTTGGAGCAATTAACAACTTACCTTTTCAATGTCCACCCACTGACAAATAGT 345
DB 927 CCGGCGGCAUUAACAGAGAGGUCUCCUUCAGAAUUAUACCCAGUCACAAUAGGA 986

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REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1728 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: A/12um1/5/65
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-443-862-28

Query Match 73.8%; Score 838; DB 9; Length 1728;
Best Local Similarity 95.6%; Pred. No. 4.7e-209;
Matches 862; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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DB 1067 TTATAGAGAGAGATGGCAGAGATGGTTGATGGTATGATGATACATCAGACCAAT 1126
QY 508 GACCAAGCATACAGCGATGACAGACAGCAAGATCCACTCAAGCGATTGATGATC 567
DB 1127 GACCAAGCATACAGCGATGACAGACAGCAAGATCCACTCAAGCGATTGATGATC 1186
QY 568 ACCAACAAGGTAAATCTCTGATGAGAAAGATTAACACCAATTTGAAGCTGTGGAAA 627
DB 1187 ACCAACAAGGTAAATCTCTGATGAGAAAGATTAACACCAATTTGAAGCTGTGGAAA 1246
QY 628 GAATTCGCTACTTGAGAGAAAGCTGGAGAACTTTGAACAAAAGATGAGAGCGGTTT 687
DB 1247 GAATTCAAATTAATTTAGAGAAAAGACTGGAGAACTTTGAACAAAAGATGAGAGCGGTTT 1306
QY 688 CTAGATGTTGGACATACATGCTGAGCTTTAGTCTGATGAGAAATGAGAGCACTT 747
DB 1307 CTAGATGTTGGACATACATGCTGAGCTTTAGTCTGATGAGAAATGAGAGCACTT 1366
QY 748 GACTTTCATGATTCTAATGTCAGAAATCTGTATAGTAAAGTCAGAAATGACAGTGAAGAC 807
DB 1367 GACTTTCATGATTCTAATGTCAGAAATCTGTATAGTAAAGTCAGAAATGACAGTGAAGAC 1426
QY 808 AACGTCAAGAACTGAGAAATGATGTTTGAATTTTATCAAAATGATGATGAATGC 867
DB 1427 AACGTCAAGAACTGAGAAATGATGTTTGAATTTTATCAAAATGATGATGAATGC 1486
QY 868 ATGATGATGTTGAGAAACGGGACATATGATTCACCAAGTATGAAGAAGTCAAACTA 927
DB 1487 ATGATGATGTTGAGAAACGGGACATATGATTCACCAAGTATGAAGAAGTCAAACTA 1546
QY 928 AATGAATGAAATCAAGGGGTAAATTTAGAGACATGGGGTTTATCAAACTCTTGC 987
DB 1547 AATGAATGAAATCAAGGGGTAAATTTAGAGACATGGGGTTTATCAAACTCTTGC 1606
QY 988 ATTATGCTACAGTACAGTGTCTATGTCACCTGCAATCATGATGCTGGATCTTTC 1047
DB 1607 ATTATGCTACAGTACAGTGTCTATGTCACCTGCAATCATGATGCTGGATCTTTC 1666
QY 1048 TGGGTGCTCCACAGGGGTCTCTGACGAGCAATGCAATGATATATTAAGCATTTTA 1107
DB 1667 TGGGTGCTCCACAGGGGTCTCTGACGAGCAATGCAATGATATATTAAGCATTTTA 1726
QY 1108 TA 1109
DB 1727 TA 1728

RESULT 8
US-09-918-568-28
Sequence 28, Application US/09918568
GENERAL INFORMATION:
APPLICANT: yoshiobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESSES:
ADDRESS: Wenderoth, Lind & Bonack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918, 568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422

```

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Influenza virus
STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)
IMMEDIATE SOURCE:
CLONE: HA
FEATURE:
NAME/KEY: mutation
LOCATION: replace(144, "a")
OTHER INFORMATION: /gene= "HA"
OTHER INFORMATION: /note= "u in ca "master" strain; a in wt2(3)"
OTHER INFORMATION: /citation= (11)
FEATURE:
NAME/KEY: mutation
LOCATION: replace(455, "g")
OTHER INFORMATION: /gene= "HA"
OTHER INFORMATION: /note= "a in ca "master" strain; g in wt2(3)"
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FEATURE:
NAME/KEY: mutation
LOCATION: replace(729, "a")
OTHER INFORMATION: /gene= "HA"
OTHER INFORMATION: /note= "c in ca "master" strain; a in wt2(3)"
OTHER INFORMATION: /citation= (11)
FEATURE:
NAME/KEY: CDS
LOCATION: 44..1729
OTHER INFORMATION: /product= "hemagglutinin"
OTHER INFORMATION: /gene= "HA"
OTHER INFORMATION: /note= "hemagglutinin protein"
OTHER INFORMATION: /citation= (11)
PUBLICATION INFORMATION:
AUTHORS: Herlocher, M L
AUTHORS: Maassab, H F
AUTHORS: Webster, R G
TITLE: Molecular and biological changes in the cold
TITLE: adapted master strain A/AA/6/60 (H2N2) influenza
TITLE: virus
JOURNAL: Proceedings of the National Academy of Sciences of the USA
DATE: 1993
RELEVANT RESIDUES IN SEQ ID NO: 35: FROM 1 TO 1773
US-08-573-569-35
Query Match 77.8%; Score 882.8; DB 10; Length 1773;
Best Local Similarity 71.8%; Pred. No. 7.9e-221;
Matches 665; Conservative 234; Mismatches 27; Indels 0; Gaps 0;
QY 208 AAGTTATGCAACTAAACGATCGGATCATGAAACAGAGAACACTTGAGACTGT 267
DB 848 AAAAUAUCGAAAGABGUAUUCUGGAAUUAUAAACAGACACUCUGAACUCUG 907
QY 268 GAGACCAATGCCAATCTCTTTGGAGCAATAAATACACATTACTTTTCAATGTC 327
DB 908 GAGACCAAAUGCCAAACUCUUGGAGCAUUAUAAACAAUUGCCUUUUCACAAUUC 967
QY 328 CACCCACTGCATATAGTAGTCCCAATATGTAAATCGAGAAAGTTGCTTACGA 387
DB 968 CACCCACUGCAUUAUGUGAGUCGCCAAUUAUGUAAUUCGAGAAUGUGGUCUAGCA 1027
QY 388 ACAGGACTAGGAATGTCCCGCATTTGATGATCAAGAGATTTGTTGGGCAATAGCTGG 447
DB 1028 ACAGGACUAAAGATGTCUCCCGCAUUAUUAUUAUUAUUAUUAUUAUUAUUAUUA 1087
QY 448 TTTATAGAAAGGAGATGGCAAGGAATGTTGACGTTGATGATACATACACCAAT 507
DB 1088 UUUUAUUAAGAGAGATGGCAAGGAUUGUUUGAUUGUUAUUAUUAUUAUUAUUA 1147
QY 508 GACGAGGATCAGGATATGACAGACAAAGAAATCCATCTCAAAAGCATTTGATGAAATC 567
DB 1148 GACGAGGATCAGGATATGACAGACAAAGAAATCCATCTCAAAAGCATTTGATGAAATC 1207

QY 568 ACCACAGGTAATTTCTGATGATGAAAAATATAACACCCATTTGAGCTGTGGGAAA 627
DB 1208 ACCACAGGTAATTTCTGATGATGAAAAATATAACACCCATTTGAGCTGTGGGAAA 1267
QY 628 GAATTCGTTAATCTTAGAGAAAGACGAGACACTTGAACAAAAGATGGAAGACGGGTTT 687
DB 1268 GAATTCGTTAATCTTAGAGAAAGACGAGACACTTGAACAAAAGATGGAAGACGGGTTT 1327
QY 688 CTAGATGTGTGACATACAAATGCTGAGCTTTTGAATTTATGCAAAATGATGATGATG 747
DB 1328 CTAGATGTGTGACATACAAATGCTGAGCTTTTGAATTTATGCAAAATGATGATGATG 1387
QY 748 GACTTCATCATCTTATATGCAAGATCTGTATAGTAAGTCAAGATGCAAGCTGACAGAC 807
DB 1388 GACTTCATCATCTTATATGCAAGATCTGTATAGTAAGTCAAGATGCAAGCTGACAGAC 1447
QY 808 AACGCAAGAACTAGCAAAATGATGTTGATTTATGCAAAATGATGATGATGATGATG 867
DB 1448 AACGCAAGAACTAGCAAAATGATGTTGATTTATGCAAAATGATGATGATGATGATG 1507
QY 868 ATGATATGTTGAAAAACGGGACATATGATTTATCCCAAGTATGAAAGAGTCTAAACAT 927
DB 1508 ATGATATGTTGAAAAACGGGACATATGATTTATCCCAAGTATGAAAGAGTCTAAACAT 1567
QY 928 AATGAAATGATGAAAAACGGGACATATGATTTATCCCAAGTATGAAAGAGTCTAAACAT 987
DB 1568 AATGAAATGATGAAAAACGGGACATATGATTTATCCCAAGTATGAAAGAGTCTAAACAT 1627
QY 988 AATTATGCTACAGTACAGTTCTATATGTCACATGATGATGATGATGATGATGATG 1047
DB 1628 AATTATGCTACAGTACAGTTCTATATGTCACATGATGATGATGATGATGATGATG 1687
QY 1048 TGGGTGCTCTCAACGGGCTCTGTCAGTGCAGATGTCATATGATTTATGATTTA 1107
DB 1688 TGGGTGCTCTCAACGGGCTCTGTCAGTGCAGATGTCATATGATTTATGATTTA 11747
QY 1108 TAATTAATAAACACCTGTTCTGCT 1133
DB 1748 TAATTAATAAACACCTGTTCTGCT 1773
RESULT 7
US-08-443-862-28
; Sequence 28, Application US/08443862
; GENERAL INFORMATION:
; APPLICANT: Yoshinobu OKUNO et al.
; TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,862
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,781
; FILING DATE: April 19, 1994
; APPLICATION NUMBER: 08/054,016
; FILING DATE: April 29, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367

```

? STRAIN:
? IMMEDIATE SOURCE:
? CLONE: HA
? FEATURE:
? NAME/KEY: mutation
? LOCATION: replace(144, "u")
? OTHER INFORMATION: /gene= "HA"
? OTHER INFORMATION: /note= "u in ca "master" strain; a in w2(3)"
? OTHER INFORMATION: /citation= ([1])
? FEATURE:
? NAME/KEY: mutation
? LOCATION: replace(455, "a")
? OTHER INFORMATION: /gene= "HA"
? OTHER INFORMATION: /note= "a in ca "master" strain; g in wt2(3)"
? OTHER INFORMATION: /citation= ([1])
? FEATURE:
? NAME/KEY: mutation
? LOCATION: replace(729, "c")
? OTHER INFORMATION: /gene= "HA"
? OTHER INFORMATION: /note= "c in ca "master" strain; a in wt2(3)"
? OTHER INFORMATION: /citation= ([1])
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 44..1729
? OTHER INFORMATION: /product= "hemagglutinin"
? OTHER INFORMATION: /gene= "HA"
? OTHER INFORMATION: /note= "hemagglutinin protein"
? OTHER INFORMATION: /citation= ([1])
? PUBLICATION INFORMATION:
? AUTHORS: Herlocher, M L
? AUTHORS: Maassab, H F
? AUTHORS: Webster, R G
? TITLE: Molecular and biological changes in the cold
? TITLE: adapted master strain A/Aa/6/60 (H2N2) influenza
? TITLE: virus
? JOURNAL: Proceedings of the National Academy of Sciences of the USA
? DATE: 1993
? RELEVANT RESIDUES IN SEQ ID NO: 17: FROM 1 TO 1773
? US-08-573-569-17

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Query Match 77.8%; Score 882.8; DB 10; Length 1773;
Best Local Similarity 71.8%; Pred. No. 7.9e-221;
Matches 665; Conservative 234; Mismatches 27; Indels 0; Gaps 0:

? 208 AAGTTATGCAACTAAGCGATCCGGATCATGAAAAAGAGAACTTGAGAACTG 267
? 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
? 848 AAAAUAUCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
? 268 GAGACCAATGCAAACTCTTTGGAGAGCAATAATACATTAACCTTTTCACAAATGC 327
? 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
? 908 GAGACCAAAUUGCCAAACUCUUGGGAGCAUAAAUAACAAACUUCUUCACAAUUGUC 967
? 328 CACCCACTGCAATAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 387
? 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
? 968 CACCCACUUGCAAAUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1027
? 388 ACAGAGTAAAGATGTTCCCAAGATGATCAAGAGAGATGTTGGGCAATAGCTGCT 447
? 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
? 1028 ACAGAGCUAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1087
? 448 TTTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 507
? 1088 UUUUAUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1147
? 508 GACCAGGAGATCAGGATGATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 567
? 1148 GACCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1207
? 568 ACCAACAAGGTAATTCGTGATGAAAGATTAACACCAATTCAGAGCTGGTGGGAAA 627
? 1208 ACCAACAAGGTAATTCGTGATGAAAGATTAACACCAATTCAGAGCTGGTGGGAAA 1267
? 628 GAATTCGTAACCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 687

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? 1268 GAAUUCAGUAAACUUGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1327
? 688 CTAGATGCTGAGACATACATGCTGAGCTTTTATGCTGATGAGAAATGAGAGACACT 747
? 1328 CUGAGAGGUGGAGACUACAAUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1387
? 748 GACTTTCATGATTCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 807
? 1388 GACUUCUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1447
? 808 AACGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 867
? 1448 AACGUCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1507
? 868 ATGATAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 927
? 1508 AUGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1567
? 928 AATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 987
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? 988 ATTATGCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1047
? 1628 AUUUAUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1687
? 1048 TGGCGTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1107
? 1688 UGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1747
? 1108 TAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1133
? 1748 UAAUUAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1773

```

```

RESULT 6
US-08-573-569-35
? Sequence 35, Application US/08573569
? GENERAL INFORMATION:
? APPLICANT: Maassab, Hunein F
? APPLICANT: Herlocher, Martha L
? TITLE OF INVENTION: Cold-adapted Influenza Virus
? NUMBER OF SEQUENCES: 40
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Anna M Lewak
? STREET: 5445 Corporate Drive
? CITY: Troy
? STATE: MI
? COUNTRY: USA
? ZIP: 48098
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/573.569
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/082.846
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Lewak, Anna M
? REGISTRATION NUMBER: 33006
? REFERENCE/DOCKET NUMBER: 2115-00257
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 313-641-1600
? TELEFAX: 313-641-0270
? INFORMATION FOR SEQ ID NO: 35:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1773 base pairs

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DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-09-918-568-46

Query Match 80.1%; Score 908.8; DB 38; Length 1783;
Best Local Similarity 98.7%; Pred. No. 1.2e-227;
Matches 916; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY	208	AAGTATGCAAACTAAACGATCCGGATCATGAAAACAGAGAACTTGGAATGT	267
DB	853	AAATATCGAAAAGABSTAGTTTCAGGATCATGAAAACAGAGAACTTGGAATGT	912
QY	268	GAGACCAATGCCAATCTCTTGGGAGCAATAATACAACTTACCTTTCAACATGTC	327
DB	913	GAGACCAATGCCAATCTCTTGGGAGCAATAATACAACTTACCTTTCAACATGTC	972
QY	328	CACCACTGACATAATGTAGTGTGCCCCCAATATGTAAATCGAGAACTTGCTTACGA	387
DB	973	CACCACTGACATAATGTAGTGTGCCCCCAATATGTAAATCGAGAACTTGCTTACGA	1032
QY	388	ACAGACTAAGAAATTTTCCCAAGATGATCAAGAGATTTTGGGCAATAGCTGCT	447
DB	1033	ACAGACTAAGAAATTTTCCCAAGATGATCAAGAGATTTTGGGCAATAGCTGCT	1092
QY	448	TTTATAGAGAGAGATGCAAGAAATGTTGACGTTGTTATGATACATCAGCAAT	507
DB	1093	TTTATAGAGAGAGATGCAAGAAATGTTGACGTTGTTATGATACATCAGCAAT	1152
QY	508	GACAGGAGATCAGGATGTCAGAGCAACAAATCCACTAAAAGCATTTGATGATC	567
DB	1153	GACAGGAGATCAGGATGTCAGAGCAACAAATCCACTAAAAGCATTTGATGATC	1212
QY	568	ACCAACAGGTAATTTCTGTGATTGAAAAGATTAACACCAATTTGAAGCTGTGGAAA	627
DB	1213	ACCAACAGGTAATTTCTGTGATTGAAAAGATTAACACCAATTTGAAGCTGTGGAAA	1272
QY	628	GAATTCGTAACCTTGAGAAAGACTGAGAACTTGAAACAAAAGAGAGACGGGTTT	687
DB	1273	GAATTCGTAACCTTGAGAAAGACTGAGAACTTGAAACAAAAGAGAGACGGGTTT	1332
QY	688	CTAGATGTGGACATTCATATGCTGAGCTTTTGTGTTGATGAAAATGAGAGACCTT	747
DB	1333	CTAGATGTGGACATTCATATGCTGAGCTTTTGTGTTGATGAAAATGAGAGACCTT	1392

QY	748	GACTTCATGATCTAATGTCAGAAATCTGTATGTAAGTCAGAAATGACGTGAGAC	807
DB	1393	GACTTCATGATCTAATGTCAGAAATCTGTATGTAAGTCAGAAATGACGTGAGAC	1452
QY	808	AACGTCAAGAACTAGGAAATGATGTTTGAATTTTATCACAATGTGATGATGTC	867
DB	1453	AACGTCAAGAACTAGGAAATGATGTTTGAATTTTATCACAATGTGATGATGTC	1512
QY	868	ATGATATGTGAAAAACGGGACATATGATTTATCCCAAGTATGAGAAAGTCTAACTA	927
DB	1513	ATGATATGTGAAAAACGGGACATATGATTTATCCCAAGTATGAGAAAGTCTAACTA	1572
QY	928	AATGAATGAAATCAAGGGGTAAATGTAGCAGATGGGGGTTTATCAATCTTGCC	987
DB	1573	AATGAATGAAATCAAGGGGTAAATGTAGCAGATGGGGGTTTATCAATCTTGCC	1632
QY	988	ATTATGCTACAGTAGCAGGTTTATGTCATGCAATCAATGATGCTGGATCTTTC	1047
DB	1633	ATTATGCTACAGTAGCAGGTTTATGTCATGCAATCAATGATGCTGGATCTTTC	1692
QY	1048	TGGGTGTCTCCAAAGGGTCTCTGCACTGAGATTCGATATGATTAATGATTTTA	1107
DB	1693	TGGGTGTCTCCAAAGGGTCTCTGCACTGAGATTCGATATGATTAATGATTTTA	1752
QY	1108	TAATTAATAACACCTGTTTCTGCTAG	1135
DB	1753	TAATTAATAACACCTGTTTCTGCTAG	1780

RESULT 5
US-08-573-569-17
Sequence 17, Application US/08573569
GENERAL INFORMATION:
APPLICANT: Maassab, Hunein F
APPLICANT: Herlocher, Martha L
TITLE OF INVENTION: Cold-adapted Influenza Virus
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anna M Lewak
STREET: 5445 Corporate Drive
CITY: Troy
STATE: MI
COUNTRY: USA
ZIP: 48068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/573,569
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/082,846
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lewak, Anna M
REGISTRATION NUMBER: 33006
REFERENCE/DOCKET NUMBER: 2115-00257
TELECOMMUNICATION INFORMATION:
TELEPHONE: 313-641-1600
TELEFAX: 313-641-0270
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1773 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Influenza virus
STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI

CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-443-862-46

Query Match 80.1%; Score 908.8; DB 9; Length 1783;
Best Local Similarity 98.7%; Pred. No. 1.2e-227;
Matches 916; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 208 AAGTTATGCAACTAAGCGATCCGATCATGAAACAGAGAACTTGAGAACTGT 267
DB 853 AAATATGCAAGAGAGTAGTTCAGCGATCATGAAACAGAGAACTTGAGAACTGT 912
QY 268 GAGACCAATGCCAACTCTTTGGGAGCAATTAATACACATTAACCTTTTCACAATGTC 327
DB 913 GAGACCAATGCCAACTCTTTGGGAGCAATTAATACACATTAACCTTTTCACAATGTC 972
QY 328 CACCACATGCAATAGTGTGAGTCCCAATATGTAATGAGAGAGTGTCTTAGCA 387
DB 973 CACCACATGCAATAGTGTGAGTCCCAATATGTAATGAGAGAGTGTCTTAGCA 1032
QY 388 ACAGGACTAAGGAATGTTCCCGAGATTGAATCAAGAGATTGTTGGGCAATAGCTGT 447
DB 1033 ACAGGACTAAGGAATGTTCCCGAGATTGAATCAAGAGATTGTTGGGCAATAGCTGT 1092
QY 448 TTTATAGAGAGATGCGCAAGGAATGTTGACGTTGTAAGATACCATCAGACAAAT 507
DB 1093 TTTATAGAGAGATGCGCAAGGAATGTTGACGTTGTAAGATACCATCAGACAAAT 1152
QY 508 GACCAGGATCAGGATGATGCGCAAGGAATGTTGACGTTGTAAGATACCATCAGACAAAT 567
DB 1153 GACCAGGATCAGGATGATGCGCAAGGAATGTTGACGTTGTAAGATACCATCAGACAAAT 1212
QY 568 ACCAACAAGTAATTTCTGTATTGAAAGATAACACCAATTTGAAGCTTTGGGAAA 627
DB 1213 ACCAACAAGTAATTTCTGTATTGAAAGATAACACCAATTTGAAGCTTTGGGAAA 1272
QY 628 GAATTCGTAACCTAGAGAAAAGATGAGAACTTGAACAAAAGATGGAAGAGCGGTTT 687
DB 1273 GAATTCGTAACCTAGAGAAAAGATGAGAACTTGAACAAAAGATGGAAGAGCGGTTT 1332
QY 688 CTAGATGTGTGAGATCAATGCTGAGCTTTTACTGTCGATGGAAGATGAGAGACACTT 747
DB 1333 CTAGATGTGTGAGATCAATGCTGAGCTTTTACTGTCGATGGAAGATGAGAGACACTT 1392
QY 748 GACTTTCATGATCTAATGTCAGCAATCTGTATAGTAAGTCAGAACTCAGCTGAGAGAC 807
DB 1393 GACTTTCATGATCTAATGTCAGCAATCTGTATAGTAAGTCAGAACTCAGCTGAGAGAC 1452
QY 808 AACGTCAAAGACTAGAGAAATGATGTTTGAATTTTATCAGAAATGTCAGATGAATGC 867
DB 1453 AACGTCAAAGACTAGAGAAATGATGTTTGAATTTTATCAGAAATGTCAGATGAATGC 1512
QY 868 ATGAATAGTGTGAAGAAACGGGACATATGATATCCCAAGTATGAAGAGAGCTTAACCTA 927
DB 1513 ATGAATAGTGTGAAGAAACGGGACATATGATATCCCAAGTATGAAGAGAGCTTAACCTA 1572

QY 928 AATAGAAATGAATCAAGGGGTAAATTTGACACACAGGAGGCTTTATCAAAATCCTTCCC 987
DB 1573 AATAGAAATGAATCAAGGGGTAAATTTGACACACAGGAGGCTTTATCAAAATCCTTCCC 1632
QY 988 ATTATGCTACAGTACAGGCTTCTATGTCACATGCGCAATCATGATGCGGATCTCTTTC 1047
DB 1633 ATTATGCTACAGTACAGGCTTCTATGTCACATGCGCAATCATGATGCGGATCTCTTTC 1692
QY 1048 TGGGTGTGCTCCAGGGGTCTGTCAGTGCAGGATCTGATATGATTAAGTCAATTTTA 1107
DB 1693 TGGGTGTGCTCCAGGGGTCTGTCAGTGCAGGATCTGATATGATTAAGTCAATTTTA 1752
QY 1108 TAATTAACACACCTTTTCTGCTAG 1135
DB 1753 TAATTAACACACCTTTTCTGCTAG 1780

RESULT 4

US-09-918-568-46

Sequence 46, Application US/09918568

GENERAL INFORMATION:

APPLICANT: Yoshinobu OKUNO et al.

TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSER: Wenderoth, Lind & Ponack, L.L.P.

STREET: 2033 K Street, N.W., #800

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/918,568

FILING DATE: 02-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/004,422

FILING DATE: January 8, 1998

APPLICATION NUMBER: 08/443,862

FILING DATE: May 22, 1995

APPLICATION NUMBER: 08/229,781

FILING DATE: April 19, 1994

APPLICATION NUMBER: 08/054,016

FILING DATE: April 29, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER: <Unknown>

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-721-8200

TELEFAX: 202-721-8250

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:

LENGTH: 1783 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to genomic RNA

HYPOTHETICAL: <Unknown>

ANTI-SENSE: <Unknown>

FRAGMENT TYPE: <Unknown>

ORIGINAL SOURCE:

ORGANISM: A/Okuda/57

STRAIN: <Unknown>

INDIVIDUAL ISOLATE: <Unknown>

PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-918-568-49

Query Match 100.0%; Score 1135; DB 38; Length 1135;
Best Local Similarity 100.0%; Pred. No. 3,1e-287;
Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CTAGCAAAAGCAGGGGTTATACCATAGAAAACCAAGCAAAACATGGCCATCTTTAT 60
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DB 121 AATTCACAGAGAGAGGTTGACACCAATTTCTAGAGCGGAACGTCTGCTGCTATGCCAAG 180
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DB 181 GACATCCCTTGAGAGGAGGCCATTAACGGAAGTTATGCAACTTAACGGATCCGGGATCTG 240
QY 241 AAAACAGAGAGAGAGGTTGAGAGAGCTGTGAGACCAAAATGCCAAACTCTTTGGAGACATA 300
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QY 301 AATACACATTACCTTTTACCAATGTCCACCCACTGACAAATAGGTGATGATGCCCAAAATAT 360
DB 301 AATACACATTACCTTTTACCAATGTCCACCCACTGACAAATAGGTGATGATGCCCAAAATAT 360
QY 361 GTAAATGSGAGAGGTTGGCTTTAGCAACAGAGACTAAGGATGTTCCCAATTTGAACA 420
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QY 421 AGAGGATTTGTTGGGTCATAGCTGTTTATAGAGAGGATGAGCAAGATGTTGATGAC 480
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QY 481 GGTGGTATGATGATACATACAGCAATGACAGGATGATGAGATGACAGCAAAAGAA 540
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DB 541 TCCACTCAAAAGGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
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DB 601 AACACCCATTTGAATCTGTTGGCAAAAGATTCGTAATCTAGAGAAAAGACTGGAGAC 660
QY 661 TTGAACAAAAGATGAGAGAGGCTTTCTAGATGTTGAGATGATGATGATGATGATGATGAT 720
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QY 721 GTTCTGATGAGAAAATGAGAGAGACTGATGATGATGATGATGATGATGATGATGATGATGAT 780
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QY 781 AGTAAGTCAAGATGACAGTGAAGACAGCTCAAAAGACTAGGAATGATGATGATGATGATGAT 840
DB 781 AGTAAGTCAAGATGACAGTGAAGACAGCTCAAAAGACTAGGAATGATGATGATGATGATGAT 840
QY 841 TTTTATACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 841 TTTTATACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 CCCAAGATGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
DB 901 CCCAAGATGAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960

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QY 961 AGCATGGGGGTTTATCAAAATCCTTCATTTATGCTACAGTAGAGGTTCTATGCTACTG 1020
DB 961 AGCATGGGGGTTTATCAAAATCCTTCATTTATGCTACAGTAGAGGTTCTATGCTACTG 1020
QY 1021 GCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 GCAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 ATCTGATATGATATTAAGTCAATTTTATTAATTAATAAACACCCCTGTTCTGCTAG 1135
DB 1081 ATCTGATATGATATTAAGTCAATTTTATTAATTAATAAACACCCCTGTTCTGCTAG 1135

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RESULT 3

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US-08-443-862-46
; Sequence 46, Application US/08443862
; GENERAL INFORMATION:
; APPLICANT: Yoshinobu OKUNO et al.
; TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,862
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,781
; FILING DATE: April 19, 1994
; APPLICATION NUMBER: 08/054,016
; FILING DATE: April 29, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1783 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: A/Okuda/57
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLER:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:

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241 AAAACAGAGAGAACACTTGAGAACTGTGAGACCAATGCGAAATCTCTTTGGAGCAATA 300
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301 AATACACATTACCTTTTACACAAATGTCCACCCACTGACAAATAGGTAGTGTCCCAAAATAT 360
361 GTAAATGGAGAACTGTGCTTACAGACAGCAATGAGAAATGTTCCCAAGATGTAATCA 420
361 GTAAATGGAGAACTGTGCTTACAGACAGCAATGAGAAATGTTCCCAAGATGTAATCA 420
421 AGAGATTTGTTGGGGCAATACCTGTTTTATAGAAGAGAGATGCCAAGAAATGTTGAC 480
421 AGAGATTTGTTGGGGCAATACCTGTTTTATAGAAGAGAGATGCCAAGAAATGTTGAC 480
481 GGTGGTATGATACCATCAGCAATGACAGGATCAGGGATGATGACAGCAAGAA 540
481 GGTGGTATGATACCATCAGCAATGACAGGATCAGGGATGATGACAGCAAGAA 540
541 TCCACTCAAAAGGCAATTTGATGGAATCACCACAAAGTAATTTCTGATGTAAGAAATA 600
541 TCCACTCAAAAGGCAATTTGATGGAATCACCACAAAGTAATTTCTGATGTAAGAAATA 600
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601 AACACCCCAATTTGAGCTGTTGGGAAAGAAATTCGGTAATCTTGAAGAAAGACTGGAGAC 660
661 TTGAACAAAAGATGGAAGACGGGTTTCTAGATGTGTGACATACAACTGAGCTTTTA 720
661 TTGAACAAAAGATGGAAGACGGGTTTCTAGATGTGTGACATACAACTGAGCTTTTA 720
721 GTTCGATGAGAAAAGAGAGGACACTTGTGATCTTCAATGATCTCAAGATCTGAT 780
721 GTTCGATGAGAAAAGAGAGGACACTTGTGATCTTCAATGATCTCAAGATCTGAT 780
781 AGTAAGTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
781 AGTAAGTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
841 TTTTATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
841 TTTTATCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
901 CCCAAGTATGAAGAGAGTCTAACTAAATAGAAATGAATGAAGGGGTAATATGAGC 960
901 CCCAAGTATGAAGAGAGTCTAACTAAATAGAAATGAATGAAGGGGTAATATGAGC 960
961 AGCATGGGGGTTTATCAATCTTCCATTTATGCTAGACAGAGTCTATGTCACGT 1020
961 AGCATGGGGGTTTATCAATCTTCCATTTATGCTAGACAGAGTCTATGTCACGT 1020
1021 GCAATCATGATGCTGGGATCTCTTGGGGTGTCTCCACAGGGTCTCTGACGTGACG 1080
1021 GCAATCATGATGCTGGGATCTCTTGGGGTGTCTCCACAGGGTCTCTGACGTGACG 1080
1081 ATCGCATATGATATATGATATTTATTAATTAATAAACACCTTGTCTGTCTAG 1135
1081 ATCGCATATGATATATGATATTTATTAATTAATAAACACCTTGTCTGTCTAG 1135

RESULT 2
US-09-918-568-49

Sequence 49, Application US/09918568
GENERAL INFORMATION:
APPLICANT: Yoshiyoshi OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.

STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 1135 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A/Okuda/57
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:

5 882.8 77.8 1773 10 US-08-573-569-17 Sequence 17, Appl
6 882.8 77.8 1773 10 US-08-573-569-35 Sequence 35, Appl
7 838 73.8 1728 9 US-08-443-862-28 Sequence 28, Appl
8 838 73.8 1728 36 US-09-918-568-28 Sequence 28, Appl
9 470 41.1 1770 5 US-08-063-818-1 Sequence 1, Appl
10 466.8 41.1 1778 4 US-07-773-597-14 Sequence 14, Appl
11 455 40.1 1698 15 US-09-040-944-1 Sequence 1, Appl
12 455 40.1 1698 15 US-09-045-042-1 Sequence 1, Appl
13 452.8 39.9 1733 1 PCT-US03-09287-13 Sequence 13, Appl
14 452.8 39.9 1733 2 PCT-US03-09287-13 Sequence 13, Appl
15 452.8 39.9 1733 51 US-10-397-635-13 Sequence 13, Appl
16 447.8 39.5 1754 9 US-08-443-862-27 Sequence 27, Appl
17 447.8 39.5 1754 38 US-09-918-568-27 Sequence 27, Appl
18 400 35.2 400 9 US-08-443-862-33 Sequence 33, Appl
19 400 35.2 400 38 US-09-918-568-33 Sequence 33, Appl
20 397 35.0 409 9 US-08-443-862-34 Sequence 34, Appl
21 397 35.0 409 38 US-09-918-568-34 Sequence 34, Appl
22 382.4 33.7 410 9 US-08-443-862-35 Sequence 35, Appl
23 382.4 33.7 410 38 US-09-918-568-35 Sequence 35, Appl
24 379.6 33.4 394 9 US-08-443-862-36 Sequence 36, Appl
25 379.6 33.4 394 38 US-09-918-568-36 Sequence 36, Appl
26 373 32.9 924 4 US-07-751-886-1 Sequence 1, Appl
27 373 32.9 924 4 US-07-837-773-15 Sequence 15, Appl
28 373 32.9 924 8 US-08-391-315-15 Sequence 15, Appl
29 372.6 32.8 810 4 US-07-751-896-5 Sequence 5, Appl
30 372.6 32.8 810 4 US-07-837-773-19 Sequence 19, Appl
31 372.6 32.8 810 8 US-08-391-315-19 Sequence 19, Appl
32 368.2 32.4 670 4 US-07-837-773-5 Sequence 5, Appl
33 368.2 32.4 670 8 US-08-391-315-5 Sequence 5, Appl
34 361.4 31.8 912 4 US-07-751-896-17 Sequence 17, Appl
35 361.4 31.8 912 4 US-07-837-773-31 Sequence 31, Appl
36 361.4 31.8 912 8 US-08-391-315-31 Sequence 31, Appl
37 293.6 25.9 1697 51 US-10-381-085-10 Sequence 10, Appl
38 293.6 25.9 1753 51 US-10-381-085-9 Sequence 9, Appl
39 293.6 25.9 1753 51 US-10-381-085-11 Sequence 11, Appl
40 280.2 24.7 1757 51 US-10-381-085-12 Sequence 12, Appl
41 263.8 23.2 729 4 US-07-751-896-3 Sequence 3, Appl
42 263.8 23.2 729 4 US-07-751-899-3 Sequence 3, Appl
43 263.8 23.2 729 4 US-07-837-773-17 Sequence 17, Appl
44 263.8 23.2 729 5 US-08-021-535-3 Sequence 3, Appl
45 263.8 23.2 729 5 US-08-021-617-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-443-862-49
Sequence 49, Application US/08443862
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,862
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,781
FILING DATE: April 15, 1994
APPLICATION NUMBER: 08/034,016

FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 1135 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: A/Okuda/57
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-443-862-49
Query Match 100.0%; Score 1135; DB 9; Length 1135;
Best Local Similarity 100.0%; Pred. No. 3,1e-287;
Matches 1135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTAGCAAAAGCAGGGGTTATACCATAGAAAACCAAAAGCAAAACATGGCCATCATTTAT 60
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Db 1 CTAGCAAAAGCAGGGGTTATACCATAGAAAACCAAAAGCAAAACATGGCCATCATTTAT 60
QY 61 CTATTTCTCTGTTTCACAGCAGTGAAGGGGACCAATATGATTTGGATTCATGCCAAT 120
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Db 61 CTATTTCTCTGTTTCACAGCAGTGAAGGGGACCAATATGATTTGGATTCATGCCAAT 120
QY 121 AATTCCAGAGAGAGGTCGACACATTTAGAGCGGAGTCGTCGCTACTATGCCAAG 180
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Db 121 AATTCCAGAGAGAGGTCGACACATTTAGAGCGGAGTCGTCGCTACTATGCCAAG 180
QY 181 GACATCTTGAGAGAGCCATACGGAAGGTTATGCAAACTAAACGATCCGGGATCANG 240
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OM nucleic - nucleic search, using sw model

Run on: August 10, 2003, 02:11:24 ; Search time 2506.97 Seconds
(without alignments)
14835.212 Million cell updates/sec

Title: US-09-918-568-49
Perfect score: 1135
Sequence: 1 CTAGCAACAGCAGCGTTAT.....AACACCCCTGTTCTGCTAG 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32997241 seqs, 16383922548 residues

Total number of hits satisfying chosen parameters: 65994482

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 41: /cgn2_6/ptodata/2/pna/US099D_COMB.seq.*
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- 43: /cgn2_6/ptodata/2/pna/US099F_COMB.seq.*

Result No.	Score	% Match	Query Length	ID	Description
1	1135	100.0	1135	US-08-443-862-49	Sequence 49, Appl
2	1135	100.0	1135	US-09-918-568-49	Sequence 49, Appl
3	908.8	80.1	1783	US-08-443-862-46	Sequence 46, Appl
4	908.8	80.1	1783	US-09-918-568-46	Sequence 46, Appl

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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```

: FILE REFERENCE: CU001469
: CURRENT APPLICATION NUMBER: US/60/487,610
: CURRENT FILING DATE: 2003-07-17
: NUMBER OF SEQ ID NOS: 97101
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 19897
: LENGTH: 160592
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(160592)
: OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-60-487-610-19897

```


Db 1306 CTTTTTAATACCATTTAGCAAAACTGTAGTAAATAATGAGAAAGGCTAGAAAGACGAA 1365
QY 666 CAAAAGATGAGAGCGGTTCTAGATGTGTGACATACATGCGTACCTTTTACTTCT 725
Db 1366 TGGGGAAGATGAGAAAGAGTTTACACAGATATGATGAGAAAGCCAGGCTTTCAGGA 1425
QY 726 GATGAAAATGAGAGACACTTGACTTTCATGATCTCTAATGTCAGAAATCTGTATAGTAA 785
Db 1426 AGTGAAGAAGAAAGAGATGAGATTCTCGATGACAGATGTCCTTCTCTGACAGCAT 1485
QY 786 AGTCA 790
Db 1486 GGACA 1490

RESULT 13
US-10-286-897-452
; Sequence 452, Application US/10286897
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/10/286,897
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US/09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US/09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US/09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US/09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US/09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US/09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7143
; SOFTWARE: PL_FL_genes_b Versions 1.0
; SEQ ID NO 452
; LENGTH: 3423
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (53)..(2800)
US-10-286-897-452

Query Match 3.7%; Score 41.8; DB 6; Length 3423;
Best Local Similarity 48.2%; Pred. No. 0.018; Indels 0; Gaps 0;
Matches 118; Conservative 0; Mismatches 127;

QY 546 TCAAAAGCATTGATGGAATCCACACAGTAATCTGTGATTGAAAGATAAAGAC 605
Db 1246 TCTAGAAATTTACAGAAAGTCTTGAGATTAAGGCTTTGTTAGAGATAGATG 1305
QY 606 CCAATTTGAGCTGTTGGGAAAGAAATTCGTAACCTTAGAGAAAGACTGGAGACTTGA 665
Db 1306 CTTTTTAAATCCATTGAGGAAAGAACTGTAGTAAATAGAGAAAGGCTAGAGAACAGAA 1365
QY 666 CAAAAGATGAGAAAGGGTTCTAGATGTGTGACATACATGCTGAGCTTTTACTTCT 725
Db 1366 TGAGAAATGATGAATGAAGCTTTTAGCACAGTATGATGAGAAAGCCAGGCTTTCAGGA 1425
QY 726 GATGAAAATGAGAGACACTTGACTTTCATGATCTCTAATGTCAGAAATCTGTATAGTAA 785
Db 1426 AGTGAAGAAGAAAGAGATGAGATTCTCGATGACAGATGTCCTTCTCTGACAGCAT 1485
QY 786 AGTCA 790
Db 1486 GGACA 1490

Db 1486 GGACA 1490

RESULT 14
US-10-286-897-1473
; Sequence 1473, Application US/10286897
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/10/286,897
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US/09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US/09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US/09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US/09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US/09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US/09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7143
; SOFTWARE: PL_FL_genes_b Versions 1.0
; SEQ ID NO 1473
; LENGTH: 11116
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4532)..(11116)
US-10-286-897-1473

Query Match 3.7%; Score 41.8; DB 6; Length 11116;
Best Local Similarity 48.2%; Pred. No. 0.03;
Matches 118; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 546 TCAAAAGCATTGATGGAATCCACACAGTAATCTGTGATTGAAAGATAAAGAC 605
Db 10060 TCTAGAAATTTACAGAAAGTCTTGAGATTAAGGCTTTGTTAGTGAATGAAATC 10119
QY 606 CCAATTTGAGCTGTTGGGAAAGAAATTCGTAACCTTAGAGAAAGACTGGAGACTTGA 665
Db 10120 CTTTTTAAATCCATTGAGGAAAGAACTGTAGTAAATAGAGAAAGGCTAGAGAACAGAA 10179
QY 666 CAAAAGATGAGAGAGCGGTTTCTAGATGTGTGACATACATGCTGAGCTTTTACTTCT 725
Db 10180 TGAGAAATGATGAAGAGGTTTGTAGCACAGTATGATGAGAAAGCCAGGCTTTCAGGA 10239
QY 726 GATGAAAATGAGAGACACTTGACTTTCATGATCTCTAATGTCAGAAATCTGTATAGTAA 785
Db 10240 AGTGAAGAAGAAAGATGAGATTCTCGATGACAGATGTCCTTCTCTGACAGCAT 10299
QY 786 AGTCA 790
Db 10300 GGACA 10304

RESULT 15
US-60-487-610-19897/c
; Sequence 19897, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF

Db	1116	AAGGGGTTCTTCGGAGAGTATTTGCTGGTTCTTGGAAAGAGATGGGAGAGATGATTCG	1175
QY	480	CGGTTGGTANGGATACCATCATCAGACAATGACCCAGGATCAGGGTATGCAAGACAAGA	539
Db	1176	AGGTTGGCACGGATACACATCTCATGGAGCCATGAGAGTGGCAGTGGCAGACCTTAA	1235
QY	540	ATCCACCTMAAAGGCATTTTGAATGGAATCCACAAGGTAAATTCGTGATTGAAAAAT	599
Db	1236	GAGTACGGAGAAACCTATAAACAAGATPACAAAAAATCTCAATTCCTTAAAGTGAAGCTAGA	1295
QY	600	AAACACCCAAATTTGAGAGCTGTGGGAAAAAATTTGGTAACTTAGAGAAAAGACTCGAGAA	659
Db	1296	AGTAAAGATGTTCAAGAGACTPACCGGGTGCATGGATGAACTCCACAACGAAATPACTCGA	1355
QY	660	CTTGAACAAAAGATGGAAGACGGGTTTCTAGATGTGTGACATACATCAATGCTGAGCTTTT	719
Db	1356	GCTGATGAGAAATGGATGATCTCAGAGCTATACATTAAGCTCGCAAAATGAGCTTGC	1415
QY	720	AGTTCGTGATGSAANAATGAGAGGACACTTGACTTCATGATTTCTAATGTCAAAGATCTGTA	779
Db	1416	AGTCTTCTCTTCCACACGAGGAATTAATTAACAGGAAGATGAGCATCTCTTGGCACCTTGA	1475
QY	780	TACTAAAGTCAAGATGACGCTGAGAGAGACAACGTCCTAAAGAACTAGAGAAATGGATTTTGA	839
Db	1476	AAGAAAATGAGAAANMGTGGGCCCTCGCTGTGACATAGGAATGGATGCTTCGA	1535
QY	840	ATTTTATCACAAATGTGATGATGATTCATGATGAATAGTGTGAAAAACGGGACATATGAT	897
Db	1536	AACCAAAACCAAAATGCAACGACTTCTCTTAGACAGAGATAGCTGCTGGACACTTTAAT	1593

```

RESULT 5
US-60-487-610-19458
; Sequence 19458, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT : CARGILL, Michele
; APPLICANT : HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19458
; LENGTH: 124326
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-487-610-19458

Query Match          4.3%; Score 49.2; DB 7; Length 124326;
Best Local Similarity 55.6%; Pred. No. 0.00046;
Matches 90; Conservative 2; Mismatches 70; Indels 0; Gaps 0;

OY      849   CAAAATGATGATGAATGCATGTAATTAGTGTCAAAAAACGGACATPATGATTATCCCAAAGTA    908
            ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       93443  CACTTGTCAGCAGAGAGTTCCAAGACCASCCTCGGCCAACATGTTAAAACCTCATCTCTAATTA    93502

OY      909   TGAAGAAGAGCTATAACTAATAATGAANAATGAAATCAAAAGGGGTAAATTTGAGCGACAGCATGGG    968
            ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       93503  AAAAAAAAAAATAAATAATTAATAATAANMAAATAAATAAATAAATAAATAAATAAAGCTTGCGATGGT    93562

OY      969   GGTTTTATCAAAATCCTTGCCATTTATGCTACAGTAGCAGGTTC    1010
            ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       93563  GGACATGCTACTATCCACCCTCACAGGCKCTGAGCGCAGCATG    93604

```

RESULT 6
US-60-487-610-42952
; Sequence 42952, Application US/60487610
; GENERAL INFORMATION:
APPLICANT: CARGILL, Michele

OY	583	TCTGATGATGAAAAGATTAACACCCCAATTTGAAAGCTGTGGGAAAGAAATTCGTAACTTA	642
Db	1206	TGCATCATTTAACAAATGACACACTAGTTTGAGGCCGTTGGAAAGGAAATTTATTAACCTTA	1265
OY	643	GAGAAAAGACTGGAGAACTGTGAACAAAAAGATGGAAGACGGGTTTCTAGATGTGTGACA	702
Db	1266	GAAAGCAAGAAATGAGAAATTTAAACAAAGAAAAATGGAAGACGGATTCCTGATGTGTGACT	1322
OY	703	TACAAATGCTGAGCTTTTATGTTCTGTATGGAAAAATGAGACACTTGACTTTTCATATCT	762
Db	1326	TACAAATGCTGAACTTTGTTGTTCTGTATGGAATAATGGAAGAACTCTGCACTTTCATACCTA	1385
OY	763	AATGTCAGAAATCTGTATAGTAAAGTCAAGAAATGCAGCTGAGAGACACAGCTCAAGAACTA	822
Db	1386	AATGTCAGAAACCTTTACGACAAAGTCCGACTACAGCTTAGGGAATATGCAAGAACTG	1444
OY	823	GGAATGATGATCTTTTAAATTTTATCACAATGTGATGAATGCATGAATAGTGTGAA	882
Db	1446	GCTAATGTTCTTTTCBAATCTTATCACAATAATGTGATGAATGATGAAGTGTAA	1505
OY	883	AACGGAGCATATGATATCCCAAGATGABAAGAGCTAAACCTAATAGAAATCAATC	942
Db	1506	AACGGAGCATGTGACTATCCCGCAGTATTCAGAAAGACGAAAGCTAAACAGAGAGAAATA	1565
OY	943	AAAGGGGTAAATATGACAGCATGGGGGTTTATCAATCCTTGGCATTTATGCTACAGTA	1002
Db	1566	AGTGAGATAAATTTGAAATCAATGGGAGCACTTACCAAAATATGTAATTTATCAACAGTG	1622
OY	1003	GCAGTTCATATGTCAATGGCAATCATATATGCTGGGATCTCTTTGGGCTGTCTCCAAC	1066
Db	1626	GCGAGTTCCTCAGAGATGGCAATATGATGTACTGCTATCTTTATGATGATGCTCCAAAT	1685
OY	1063	GGGTCTCTGCAGTGCAGGATCTGCATATGATTAAT	1096
Db	1686	GGATCGTTTACAAATCGAGATTTGCATTTAAATTT	1719
RESULT 2			
US-60-470-920-21			
Sequence 21, Application US/60470920			
GENERAL INFORMATION:			
APPLICANT: Luke, Catherine, J.			
APPLICANT: Vilalta, Adrian			
APPLICANT: Wiloch, Mary K.			
APPLICANT: Evans, Thomas S.			
APPLICANT: Geall, Andrew B.			
TITLE OF INVENTION: DNA Influenza Vaccine Compositions			
FILE REFERENCE: 1530 064000			
CURRENT APPLICATION NUMBER: US/60/470,920			
CURRENT FILING DATE: 2003-05-16			
SOFTWARE: PatentIn version 3.2			
SEQ ID NO 21			
LENGTH: 1714			
TYPE: DNA			
ORGANISM: Influenza A virus			
US-60-470-920-21			

	Query Match	29.4%	Score 333.6	DB 7	Length 1714
	Best Local Similarity	61.7%	Pred. No. 3.1e-91		
	Matches 531	Conservative	0	Mismatches 329	Indels 0
				Gaps 0	
QY	233 GGATCATGAAACGAGAGAACACTGTAGAACTGTAGACCAATGCGCAATCTCTTTGG	292			
Db	855 GAATCTGGAAGACGATTTAAAGGTGGTATTTGTAGTGCATATGTCAAGCTCAAAAAG	914			
QY	293 GAGCAATTAATACACATACCTTTTACAATGTCCACCCACTGACAAATAGTAGTGC	352			
Db	915 GTGCTTAAACAGTACATGTCATCCACAAATACAGTAATATGCAATTTGGAACCTGCC	974			
QY	353 CCAATATGTAATAATCGGAGAGTGTGCTTAGAACAGAGCTAAGAAATGTCCACAGA	412			
Db	975 CCAATATGTAGAGCTTAATATGTCTCAAAACGTGCGGTGTAGAGACCTGCTGCTA	1034			

OY	413	TTGAAATCAAGAGATTTGTTTGGGCAATGACGTGGTTTATGAAAGAGAGATGGCAAGAA	472
Db	1035	GATCAAGTAGAGGACTATTTGGAGCCATAGCTGGATTATAGAAAGAGGTTGGCCAGAC	1099
OY	473	TGGTTGACGGTTGGTAGGATACCATCAATGACAGCAATGACAGGAGTACAGGATGACAG	532
Db	1095	TAGTCGGCTGGGTATGGTTCCAGCAATTCATAATGATCAAGGGGTTGGTATGGCTCG	1154
OY	533	ACAAAGAAATCCATCAAAAGGCATTGGTAGATACCAACAGAGTAATCTGTGATG	592
Db	1155	ATAGGATTTCAACTCAAAAGCAATTTGTAATAATTAACATCCAAAGGTGATATATATAGTCG	1214
OY	593	AAAAGATPAACCCCAATTTTAAAGCTGTTGGGAAAGAAATTCGTTAACTTAGAGAAAGAC	652
Db	1215	ACAAGATGAACAGCAATATGTAATAATTTGATTCATGTAATTCAGTAGGTTGAACTAGAC	1274
OY	653	TGGAGACCTTAACAAAAAGATGCAAGACGGGTTTCTAGATGTGTGACATATACGTCTG	712
Db	1275	TCAAATATGATCAATTAATTAAGATTGATGACCAAAATPAACAAGACGTATGGCAATATATG	1334
OY	713	AGCTTTTAGTTCTGTATGGAAATAGAGAGCACTGTAATTCATGATTTCTATATGCAGA	772
Db	1335	AATTGCTAGTACTCTACTTGGAAATCAAAAACACTCGATGACATGATGCCAAGCTGAACA	1394
OY	773	ATCTGTAGTAAAGTCAAGTCAAGCTGAGAGACAAACGTCAAAAGACTAGAAATGGAT	832
Db	1395	ATCTATATTAACAAAGTGAAGAGGACACGTGGCTCCAAATGCTATGGAAAGATGGGAAAG	1454
OY	833	GTTTTGAATTTTATACCAAAATGTATGTGTAATGCATTAATTAAGTGTGAAAAACGGGACAT	892
Db	1455	GTTTCGAGCTATACCATTAATGTATGATGATGATGATGATGATGATGATGATGATGATGATG	1514
OY	893	ATGATTTATCCCAAGTATGAGAGAGAGTCTAAACTTAATAGAAATGAATGAATCAAGGGTAA	952
Db	1515	ATAATAGAGAGAAAGTATAGAGAGAAATCAACACTAGAAAGGCAACAAATAGAGGGGTTA	1574
OY	953	AATAGAGACATGGGGTTTATCAAAATCCCTGTCATTTATGTATGATGACAGTACAGGTTCTA	1012
Db	1575	AGCTGGAAATCTGAGAGGAACCTTACAAAAATCCCTCACCATTTATTCCAGATCTGGCTTCATCTC	1634
OY	1013	TGTCACTGGCAATCATGATGAGGCTGGGATCTCTTCTGTGGGTGCTGCCAAGGGTCTCTCGC	1072
Db	1635	TTGTGCTTGCATGGGGTTTGGCT	1694
OY	1073	AGTCAGAGATTCGATATGA 1092	
Db	1695	GATCAACATTTGTATATAA 1714	

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RESULT 3
US-60-470-920-17
: Sequence 17, Application US/60470920
: GENERAL INFORMATION:
: APPLICANT: Luke, Catherine, J.
: APPLICANT: Vilalta, Adrian
: APPLICANT: Wlooch, Mary K.
: APPLICANT: Evans, Thomas G.
: APPLICANT: Geall, Andrew J.
: TITLE OF INVENTION: DNA Influenza Vaccine Compositions
: FILE REFERENCE: 1530.0640000
: CURRENT APPLICATION NUMBER: US/60/470,920
: CURRENT FILING DATE: 2003-05-16
: NUMBER OF SEQ ID NOS: 45
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 17
: LENGTH: 1220
: TYPE: DNA
: ORGANISM: Influenza A virus
US-60-470-920-17

Query Match      17.9%   Score 203.6;   DB 7;   Length 1220;
Best Local Similarity 70.3%;   Pred. No. 8,4e-52;

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Db 792 GTCAAGATACAAGATTGATCTGTGATTTCTTTCATATCATGCTTTTGCTTG 851
OY 1008 TGTGTTTGTGCTGGCTTCATCATGTGGCCTGGCCAGAGGCAACATTTAGTGCACAT 1067
Db 852 TGTGTTTGTGCTGGCTTCATCATGTGTGGCCTGGCCAAAAGGCAACATTTAGTGCACAT 911
OY 1068 TTGCATT 1074
Db 912 TTGCATT 918

Search completed: August 10, 2003, 18:58:45
Job time : 2454.76 secs

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Db      252 TATGGCATATTCGGGGCAATAGCAGTTTCATAGAAAATGTTGGAGGAATGATAGA 311
QY      468 CGGTGGTACGGTTTCAGCATCAAAATCTGAGGGCACAGGCAAGCAATCTTAA 527
Db      312 CGGTGGTACGGTTTCAGCATCAAAATCTGAGGGCACAGGCAAGCAATCTTAA 371
QY      528 AAGCACTCAAGCAGCCATGACCAATCAATGAGGAATTCAGAGGGTATTCAGAGAAC 587
Db      372 AAGCACTCAAGCAGCCATGACCAATCAATGAGGAATTCAGAGGGTATTCAGAGAAC 431
QY      588 GAACGAGAAATTCATCAATCGAAAAGAAATTCAGAGAATTCAGAGAATTCAGAGA 647
Db      432 GAACGAGAAATTCATCAATCGAAAAGAAATTCAGAGAATTCAGAGAATTCAGAGA 491
QY      648 CCTGAGAAATTCAGTGAAGACATCAATAGATCTGCTTAAATGCGGAGCTTCT 707
Db      492 CCTGAGAAATTCAGTGAAGACATCAATAGATCTGCTTAAATGCGGAGCTTCT 551
QY      708 TGTGCTCTGAGAAATCAACATACAAATGACCTGACTCGGAATGCAACAGCTGT 767
Db      552 TGTGCTCTGAGAAATCAACATACAAATGACCTGACTCGGAATGCAACAGCTGT 611
QY      768 TGAATAAACAGAGGCAACTGAGGAAAATGCTGAGAGAGTGGCAATGTTGCTTCAA 827
Db      612 TGAATAAACAGAGGCAACTGAGGAAAATGCTGAGAGAGTGGCAATGTTGCTTCAA 671
QY      828 AATATACCAAAATGTCAGCAAGCTTGTAGTCAATACGAAATGACTATATACCA 887
Db      672 AATATACCAAAATGTCAGCAAGCTTGTAGTCAATACGAAATGACTATATACCA 731
QY      888 TGATGTATACAGAGCAAGCAATTAACACCGGTTTCAGATCAAAAGTGTGTAACGAA 947
Db      732 TGATGTATACAGAGCAAGCAATTAACACCGGTTTCAGATCAAAAGTGTGTAACGAA 791
QY      948 GTCTGTATACAAAGACTGATCCTGTGATTTCTTGCATATCATGCTTTTGTCTTG 1007
Db      792 GTCTGTATACAAAGACTGATCCTGTGATTTCTTGCATATCATGCTTTTGTCTTG 851
QY      1008 TGTGTTTGTGAGGATTCATGATGAGGCTGCGCAGAGAGCAATTAAGGTGCAACAT 1067
Db      852 TGTGTTTGTGAGGATTCATGATGAGGCTGCGCAGAGAGCAATTAAGGTGCAACAT 911
QY      1068 TTGCATT 1074
Db      912 TTGCATT 918

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RESULT 15

US-08-391-315-9
Sequence 9, Application US/08391315

GENERAL INFORMATION:

APPLICANT: Shatzman, Allan

APPLICANT: Scott, Miller B.

TITLE OF INVENTION: Vaccinal Polypeptides

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation - Corporate

STREET: U.S. Mailcode VW2220 - 709 Swedeland Road

CITY: King of Prussia

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19406-2799

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/391.315

FILING DATE:

```

CLASSIFICATION: 435
Prior APPLICATION DATA:
APPLICATION NUMBER: US/08/108, 914
FILING DATE:
APPLICATION NUMBER: US 837, 773
FILING DATE: 18-FEB-1992
Prior APPLICATION DATA:
APPLICATION NUMBER: US 751, 896
FILING DATE: 30-AUG-1991
Prior APPLICATION DATA:
APPLICATION NUMBER: US 387, 200
FILING DATE: 28-JUL-1989
ATTORNEY/AGENT INFORMATION:
NAME: Lentz, Edward T.
REGISTRATION NUMBER: 30,191
REFERENCE/DOCKET NUMBER: SBCL4224-8c1p
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-270-5013
TELEFAX: 215-270-5090
INFORMATION FOR SEQ. ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..918
US-08-391-315-9

Query Match      57.8%; Score 641.4; DB 8; Length 918;
Best Local Similarity 97.6%; Pred. No. 5.4e-170;
Matches 651; Conservative 0; Mismatches 16; Indels 0; Gaps 0:

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QY 592 GAGAAATTCATCAATGCAAGAAAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 651
|||||
DB 181 GAGAAATTCATCAATGCAAGAAAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 240
QY 652 GAGAAATTCATCAATGCAAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 711
|||||
DB 241 GAGAAATTCATCAATGCAAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 300
QY 712 GCTCTGGAGAAATTCATCAATGCAAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 771
|||||
DB 301 GCTCTGGAGAAATTCATCAATGCAAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 360
QY 772 AAAACAGAGGAGCAATGAGGAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 831
|||||
DB 361 AAAACAGAGGAGCAATGAGGAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 420
QY 832 TACCAACAATGTGACACGCTTGCATAGTCAATGAGAAATGTACTATTGACCATGAT 891
|||||
DB 421 TACCAACAATGTGACACGCTTGCATAGTCAATGAGAAATGTACTATTGACCATGAT 480
QY 892 GATATACAGAGCAATGAGGAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 951
|||||
DB 481 GATATACAGAGCAATGAGGAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 540
QY 952 GATATACAGAGCAATGAGGAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 1011
|||||
DB 541 GATATACAGAGCAATGAGGAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 600
QY 1012 GTTTTGGTGGGTTGATCATGTTGGGCTTCCAGAGGAGCAATGAGGAGAAATTCAGACCTC 1071
|||||
DB 601 GTTTTGGTGGGTTGATCATGTTGGGCTTCCAGAGGAGCAATGAGGAGAAATTCAGACCTC 660
QY 1072 ATTTGA 1077
|||||
DB 661 ATTTGA 666

RESULT 12
US-08-391-315-3
Sequence 3, Application US/08391315
GENERAL INFORMATION:
APPLICANT: Shatzman, Allan
APPLICANT: Scott, Miller
APPLICANT: Dillon, Susan B.
TITLE OF INVENTION: Vaccinal Polypeptides
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation - Corporate
STREET: U.S. Mailcode VM2220 - 709 Swedeland Road
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,315
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/108,914
FILING DATE:
APPLICATION NUMBER: US 837,773
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 751,896
FILING DATE: 30-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 387,200

FILING DATE: 28-JUL-1989
ATTORNEY/AGENT INFORMATION:
NAME: Lentz, Edward T.
REGISTRATION NUMBER: 30,191
TELEPHONE: 215-270-5090
TELEFAX: 215-270-5090
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 666 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..663
US-08-391-315-3

Query Match 57.8%; Score 642; DB 8; Length 666;
Best Local Similarity 97.7%; Pred. No. 3, 2e-170;
Matches 651; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 412 GGCTTATGCGGCAATAGACAGGTTTCATAGAAATGTTGGGAGGAGATGATAGACGT 471
|||
DB 1 GGATATTTGGCGGCAATAGACAGGTTTCATAGAAATGTTGGGAGGAGATGATAGACGT 60
QY 472 TGGTACGTTTACAGGATCAAAATTCAGAGGAGCAAGAGCAAGCAAGATCTTAAAGC 531
|||||
DB 61 TGGTACGTTTACAGGATCAAAATTCAGAGGAGCAAGAGCAAGCAAGATCTTAAAGC 120
QY 532 ACTCAAGCAGCCATGACCAATCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 591
|||||
DB 121 ACTCAAGCAGCCATGACCAATCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
QY 592 GAGAAATTCATCAATGCAAGAAAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 651
|||||
DB 181 GAGAAATTCATCAATGCAAGAAAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 240
QY 652 GAGAAATTCATCAATGCAAGAAAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 711
|||||
DB 241 GAGAAATTCATCAATGCAAGAAAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 300
QY 712 GCTCTGGAGAAATTCATCAATGCAAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 771
|||||
DB 301 GCTCTGGAGAAATTCATCAATGCAAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 360
QY 772 AAAACAGAGGAGCAATGAGGAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 831
|||||
DB 361 AAAACAGAGGAGCAATGAGGAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 420
QY 832 TACCAACAATGTGACACGCTTGCATAGTCAATGAGAAATGTACTATTGACCATGAT 891
|||||
DB 421 TACCAACAATGTGACACGCTTGCATAGTCAATGAGAAATGTACTATTGACCATGAT 480
QY 892 GATATACAGAGCAATGAGGAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 951
|||||
DB 481 GATATACAGAGCAATGAGGAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 540
QY 952 GATATACAGAGCAATGAGGAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 1011
|||||
DB 541 GATATACAGAGCAATGAGGAGAAATTCAGAGTAGAAGGAGAAATTCAGACCTC 600
QY 1012 GTTTTGGTGGGTTGATCATGTTGGGCTTCCAGAGGAGCAATGAGGAGAAATTCAGACCTC 1071
|||||
DB 601 GTTTTGGTGGGTTGATCATGTTGGGCTTCCAGAGGAGCAATGAGGAGAAATTCAGACCTC 660
QY 1072 ATTTGA 1077
|||||
DB 661 ATTTGA 666

ADDRESSEE: Patents
STREET: U.S. Mailcode VW2220 - 709 Swedeland Road
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/07/837,773
FILING DATE: 19920218
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Canter, Carol G.
REGISTRATION NUMBER: 31,151
REFERENCE/DOCKET NUMBER: SBC14224-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-270-5013
TELEFAX: 215-270-5090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 666 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..663
US-07-837-773-3

Query Match 57.8%; Score 642; DB 4; Length 666;
Best Local Similarity 97.7%; Pred. No. 3.2e-170;
Matches 651; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

412 GGCTATTGCGCCCAATGACAGGTTTCATGAAATGTTGGAGGAGATAGAGCGT 471
1 GGCATATTGCGCCCAATGACAGGTTTCATGAAATGTTGGAGGAGATAGAGCGT 60

472 TGGTACGTTTCAGGATATCAAAATCTGAGGCGACAGAGACAGATCTTAAAGC 531
1 TGGTACGTTTCAGGATATCAAAATCTGAGGCGACAGAGACAGATCTTAAAGC 120

61 TGGTACGTTTCAGGATATCAAAATCTGAGGCGACAGAGACAGATCTTAAAGC 120

532 ACTCAAGCAGCCATTCACCAATCAATGGAATTTGACGGGTAATCGAAGACGAC 591
1 ACTCAAGCAGCCATTCACCAATCAATGGAATTTGACGGGTAATCGAAGACGAC 180

121 ACTCAAGCAGCCATTCACCAATCAATGGAATTTGACGGGTAATCGAAGACGAC 180

592 GAGAAATTCATCAATTCGAAAAGGAATTCGAAAGTAGAAGGGAATTCAGGACCTG 651
1 GAGAAATTCATCAATTCGAAAAGGAATTCGAAAGTAGAAGGGAATTCAGGACCTG 240

181 GAGAAATTCATCAATTCGAAAAGGAATTCGAAAGTAGAAGGGAATTCAGGACCTG 240

652 GAGAAATTCATCAATTCGAAAAGGAATTCGAAAGTAGAAGGGAATTCAGGACCTG 711
241 GAGAAATTCATCAATTCGAAAAGGAATTCGAAAGTAGAAGGGAATTCAGGACCTG 300

712 GCTCTGAGAGATCAATATACAAATTTGACTGACTCGGAATTAAGCAAGCTTTGAA 771
301 GCTCTGAGAGATCAATATACAAATTTGACTGACTCGGAATTAAGCAAGCTTTGAA 360

772 AAACAAGAGGCAATTTGAGGAAATGCTGAGAGAGTGGCAATGTTCTTCAAAATA 831
361 AAACAAGAGGCAATTTGAGGAAATGCTGAGAGAGTGGCAATGTTCTTCAAAATA 420

832 TACCACAATGTGACACAGCTTGCATAGAGTCAATCAGAAATGTAATTTGACCATGAT 891
421 TACCACAATGTGACACAGCTTGCATAGAGTCAATCAGAAATGTAATTTGACCATGAT 480

892 GTTACAGAGAGCAATCATTAACAACCGGTTTCAGATCAAGAGTGTGACATGAGTCT 951
481 GTTACAGAGAGCAATCATTAACAACCGGTTTCAGATCAAGAGTGTGACATGAGTCT 540

952 GGATCAAGAGACATGATCCTGTGATTTCTTGGCCATATCATGCTTTTGTGTGTT 1011
541 GGATCAAGAGACATGATCCTGTGATTTCTTGGCCATATCATGCTTTTGTGTGTT 600

1012 GTTTGCTGGGTTTCATCATATGAGGCTGCGCAGAGAGCAACATTAAGTCAACATTGCG 1071
601 GTTTGCTGGGTTTCATCATATGAGGCTGCGCAGAGAGCAACATTAAGTCAACATTGCG 660

1072 ATTTGA 1077
661 ATTTGA 666

RESULT 11
US-08-013-415-3
Sequence 3, Application US/08013415
GENERAL INFORMATION:
APPLICANT: Shatzman, Allan
ATTORNEY/AGENT INFORMATION:
NAME: Canter, Carol G.
REGISTRATION NUMBER: 31,151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5015
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 666 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..663
US-08-013-415-3

Query Match 57.8%; Score 642; DB 5; Length 666;
Best Local Similarity 97.7%; Pred. No. 3.2e-170;
Matches 651; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

412 GGCTATTGCGCCCAATGACAGGTTTCATGAAATGTTGGAGGAGATAGAGCGT 471
1 GGCATATTGCGCCCAATGACAGGTTTCATGAAATGTTGGAGGAGATAGAGCGT 60

472 TGGTACGTTTCAGGATATCAAAATCTGAGGCGACAGAGACAGATCTTAAAGC 531
1 TGGTACGTTTCAGGATATCAAAATCTGAGGCGACAGAGACAGATCTTAAAGC 120

61 TGGTACGTTTCAGGATATCAAAATCTGAGGCGACAGAGACAGATCTTAAAGC 120

532 ACTCAAGCAGCCATTCACCAATCAATGGAATTTGACGGGTAATCGAAGACGAC 591
1 ACTCAAGCAGCCATTCACCAATCAATGGAATTTGACGGGTAATCGAAGACGAC 180

CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-443-862-54

Query Match 78.2%; Score 868; DB 9; Length 1777;
Best Local Similarity 100.0%; Pred. No. 5.4e-234;
Matches 868; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

243 TATTGATACCTGATTTCTGTAATGATCATCTCCAAATGGAAGCATTTCCCAATGACAAGCC 302
|||||
903 TATTGATACCTGATTTCTGTAATGATCATCTCCAAATGGAAGCATTTCCCAATGACAAGCC 962
303 CTTTCAAAAGCTAAACAGATCATATGAGCATGCCCAAGTATGTTAAAGCAAAACAC 362
|||||
963 CTTTCAAAAGCTAAACAGATCATATGAGCATGCCCAAGTATGTTAAAGCAAAACAC 1022
363 CCTGAAGTTGGCAACAGGATGCGGAATGTACCAAGAAACAACTAGAGGCGCTATTGGG 422
|||||
1023 CCTGAAGTTGGCAACAGGATGCGGAATGTACCAAGAAACAACTAGAGGCGCTATTGGG 1082
423 CGCAATAGCAGGTTTCATAGAAATGTTGGAGGGAATGATAGAGGTTGGTACGTTT 482
|||||
1083 CGCAATAGCAGGTTTCATAGAAATGTTGGAGGGAATGATAGAGGTTGGTACGTTT 1142
483 CAGGATCAAAATTTCTGAGGCGACAGACACAGCATCTTTAAAGCACTCAAGCAGC 542
|||||
1143 CAGGATCAAAATTTCTGAGGCGACAGACACAGCATCTTTAAAGCACTCAAGCAGC 1202
543 CATGACCAATTCATGGAATTTGAACAGGTTATCCAGAGAGCAAGCAAAATTTCA 602
|||||
1203 CATGACCAATTCATGGAATTTGAACAGGTTATCCGAGAGAGCAAGCAAAATTTCA 1262
603 TCAATCGAAAGGAATTTCTGAGAGTGAAGGGAATTTAGAGCTCGAGAAATACGT 662
|||||
1263 TCAATCGAAAGGAATTTCTGAGAGTGAAGGGAATTTAGAGCTCGAGAAATACGT 1322
663 TGAAGACACTAAATAGATCTCTGCTTCAATCGGAGCTTCTTGCTGCTGAGAA 722
|||||
1323 TGAAGACACTAAATAGATCTCTGCTTCAATCGGAGCTTCTTGCTGCTGAGAA 1382
723 TCAATCATCATTTGACTGACTGATCGGAATGAACAAGCTGTTGAAAAACAAGAG 782
|||||
1383 TCAATCATCATTTGACTGACTGATCGGAATGAACAAGCTGTTGAAAAACAAGAG 1442
783 GCAACTGAGGAAATGCTGAAGAGATGGCAATGTTGCTCAAAATATACCAAAATG 842
|||||
1443 GCAACTGAGGAAATGCTGAAGAGATGGCAATGTTGCTCAAAATATACCAAAATG 1502
843 TGACAGCGCTTGCATAGATCAATGAGATGTTACTTATGACATGATGTTATACAGAG 902
|||||
1503 TGACAGCGCTTGCATAGATCAATGAGATGTTACTTATGACATGATGTTATACAGAG 1562
903 CGAAGCATTTAAACAACCGGTTTCAATCAAAAGGTTTGAAGTCTGAGTATACAGAG 962
|||||
1563 CGAAGCATTTAAACAACCGGTTTCAATCAAAAGGTTTGAAGTCTGAGTATACAGAG 1622

963 CTGATCTCTGTGATTTCTCTTGCATATCATGCTTTTGTGCTTTGTGCTGCG 1022
|||||
1623 CTGATCTCTGTGATTTCTCTTGCATATCATGCTTTTGTGCTTTGTGCTGCG 1682
1023 GTTCATCATGTTGGGCTGCGACAGAGCAACATTTAGGCAACATTTGATGCTA 1082
|||||
1683 GTTCATCATGTTGGGCTGCGACAGAGCAACATTTAGGCAACATTTGATGCTA 1742
1083 TTAGTATTTAAACACCTGTTCTG 1110
|||||
1743 TTAGTATTTAAACACCTGTTCTG 1770
Db

RESULT 4
US-09-918-568-54
Sequence 54, Application US/09918568
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918, 568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004, 422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443, 862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229, 781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054, 016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A2/Aich1/2/68
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>

PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-918-568-57

Query Match 100.0%; Score 1110; DB 38; Length 1110;
Best Local Similarity 100.0%; Pred. No. 1.5e-302;
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CTAGAGCAAGCAGGAGATATTTCTATTATCATGAAGACCATTCCTTTGAGCTAC 60
DB 1 CTAGAGCAAGCAGGAGATATTTCTATTATCATGAAGACCATTCCTTTGAGCTAC 60
QY 61 ATTTCTGTGGCTCTGGCCAGACCTTCAGAAATGCAACAGACAGCAACGCTG 120
DB 61 ATTTCTGTGGCTCTGGCCAGACCTTCAGAAATGCAACAGACAGCAACGCTG 120
QY 121 TGCCCTGGACATCATGCGGTGCCAAAGCGAACACTAGTGAAGAACATCAGATGATCAG 180
DB 121 TGCCCTGGACATCATGCGGTGCCAAAGCGAACACTAGTGAAGAACATCAGATGATCAG 180
QY 181 ATTAGAGTACTAATGCTACTAGCTACTTACAGCTCTCTCAAGGGGAAATATGCAC 240
DB 181 ATTAGAGTACTAATGCTACTAGCTACTTACAGCTCTCTCAAGGGGAAATATGCAC 240
QY 241 AATATGATACCTGATTTCTGAATGCATCACTCCAAATGAGACATCCCAATGACACAG 300
DB 241 AATATGATACCTGATTTCTGAATGCATCACTCCAAATGAGACATCCCAATGACACAG 300
QY 301 CCCTTTCAAAAGCTTAAACAGATCATATGAGCATGCCCCAAGTATGTTAAGCAAAAC 360
DB 301 CCCTTTCAAAAGCTTAAACAGATCATATGAGCATGCCCCAAGTATGTTAAGCAAAAC 360
QY 361 ACCCTGAAGTGGCTACAGGAGTGGGATGTACCAAGAAACAACTAGAGGCTATTC 420
DB 361 ACCCTGAAGTGGCTACAGGAGTGGGATGTACCAAGAAACAACTAGAGGCTATTC 420
QY 421 GGGCAATAGCAGGTTTCATAGAAATGTTGGAGGAGATGATAGACGTTGTACGCT 480
DB 421 GGGCAATAGCAGGTTTCATAGAAATGTTGGAGGAGATGATAGACGTTGTACGCT 480
QY 481 TTCAGGATCAAAATTCAGAGGCAAGGACAGACAGCATGCTTTAAAGCCTCAAGCA 540
DB 481 TTCAGGATCAAAATTCAGAGGCAAGGACAGACAGCATGCTTTAAAGCCTCAAGCA 540
QY 541 GCCATCGACCAATTAATGGGAATGTGAACGGGTAATCGAGAGAGCAAGCAAAATTC 600
DB 541 GCCATCGACCAATTAATGGGAATGTGAACGGGTAATCGAGAGAGCAAGCAAAATTC 600
QY 601 CATCAATCGAAAGGAATTCCTCAGAGTAGAAGGAGAAATTCAGACCTCGAGAAATAC 660
DB 601 CATCAATCGAAAGGAATTCCTCAGAGTAGAAGGAGAAATTCAGACCTCGAGAAATAC 660
QY 661 GTTGAAGACACTAATATAGATCTCTGCTTACATGCGAGCTTCTTGTGCTCTGAG 720
DB 661 GTTGAAGACACTAATATAGATCTCTGCTTACATGCGAGCTTCTTGTGCTCTGAG 720
QY 721 AATCAATACATTAATGACTGTAGTCTGGAATGAACAAGCTGTTTGAAGAAACAGG 780
DB 721 AATCAATACATTAATGACTGTAGTCTGGAATGAACAAGCTGTTTGAAGAAACAGG 780
QY 781 AGGCACTGAGGGAATATGCTGAAGAGATGGCAATGTTGCTTCAAAATATACACAAA 840
DB 781 AGGCACTGAGGGAATATGCTGAAGAGATGGCAATGTTGCTTCAAAATATACACAAA 840
QY 841 TGTGACAGCGCTTGTATAGAGTCAATAGAAATGTACTATAGCCATGATGATACAGA 900
DB 841 TGTGACAGCGCTTGTATAGAGTCAATAGAAATGTACTATAGCCATGATGATACAGA 900
QY 901 GAGCAAGCATTAAGAACCGGTTTCAGATCAAAAGTGTGAAGTGAAGTCTGATACAAA 960
DB 901 GAGCAAGCATTAAGAACCGGTTTCAGATCAAAAGTGTGAAGTGAAGTCTGATACAAA 960
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QY 961 GACTGATCTGTGGATTCCTTGCCATATCATGCTTTTGGCTTTGTTGCTG 1020
DB 961 GACTGATCTGTGGATTCCTTGCCATATCATGCTTTTGGCTTTGTTGCTG 1020
QY 1021 GGGTTTCATCATGTGGGCTGCGACAGAGCAACATTTAGTCAACATTTGATGACTG 1080
DB 1021 GGGTTTCATCATGTGGGCTGCGACAGAGCAACATTTAGTCAACATTTGATGACTG 1080
QY 1081 TATTAGTAAATTAACACCCCTGTGTTCTG 1110
DB 1081 TATTAGTAAATTAACACCCCTGTGTTCTG 1110
```

RESULT 3

```
US-08-443-862-54
; Sequence 54, Application US/08443862
; GENERAL INFORMATION:
; APPLICANT: Yoshinobu OKUNO et al.
; TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,862
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,781
; FILING DATE: April 19, 1994
; APPLICATION NUMBER: 08/054,016
; FILING DATE: April 29, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1777 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: A2/A1ch1/2/68
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
```

Db 181 ATTGAAGTGAATGCTACTGAGCTAGTTCAGAGCTCCCTCAACGGGGAAAAATATGCAAC 240
OY 241 AATATGATACCTGATTTCTGATGATGATCACTCCAAATGGAAGCATTCCTCAATGACAG 300
Db 241 AATATGATACCTGATTTCTGATGATGATCACTCCAAATGGAAGCATTCCTCAATGACAG 300
OY 301 CCCTTTCAAAAGTAAACAGATCAATATGAGAGCATGCCCAAGTATGTTAAAGCAAAAC 360
Db 301 CCCTTTCAAAAGTAAACAGATCAATATGAGAGCATGCCCAAGTATGTTAAAGCAAAAC 360
OY 361 ACCCTGAAGTTGGCAGCAGGGATGGGGATGTACCAAGAAACAAATAGAGCCATATTC 420
Db 361 ACCCTGAAGTTGGCAGCAGGGATGGGGATGTACCAAGAAACAAATAGAGCCATATTC 420
OY 421 GGCGCAATAGCAGGTTTATAGAAATGGTTGGAGGGAATGATAGACGGTGGTGGT 480
Db 421 GGCGCAATAGCAGGTTTATAGAAATGGTTGGAGGGAATGATAGACGGTGGTGGT 480
OY 481 TTCAGGCATCAAAATTTCTGAGGGCAGAGCAAGCAGATCTTAAAGCACTCAAGCA 540
Db 481 TTCAGGCATCAAAATTTCTGAGGGCAGAGCAAGCAGATCTTAAAGCACTCAAGCA 540
OY 541 GCCATCGACCAATATGAGGGAATTTGAACAGGATATGAGAAGACGACGAGAAATTC 600
Db 541 GCCATCGACCAATATGAGGGAATTTGAACAGGATATGAGAAGACGACGAGAAATTC 600
OY 601 CATCAAAATCGAAAAAGAAATTTCTCAGAGTAGAAGGAGAAATTCAGAGCTCGAGAAATTC 660
Db 601 CATCAAAATCGAAAAAGAAATTTCTCAGAGTAGAAGGAGAAATTCAGAGCTCGAGAAATTC 660
OY 661 GTTGAAGACACTAAATATGATCTGTGCTTACAAATGCGAGACTTCTTCGCTCTGAG 720
Db 661 GTTGAAGACACTAAATATGATCTGTGCTTACAAATGCGAGACTTCTTCGCTCTGAG 720
OY 721 AATCAACATACATTTGACCTGACTGACTCGAAATGAGACACACTGTTTAAAAACAAAG 780
Db 721 AATCAACATACATTTGACCTGACTGACTCGAAATGAGACACACTGTTTAAAAACAAAG 780
OY 781 AGGCAACTGAGGAAAAATGCTGAAGAGATGGGCAATGTTGCTCAAAATATACCAAA 840
Db 781 AGGCAACTGAGGAAAAATGCTGAAGAGATGGGCAATGTTGCTCAAAATATACCAAA 840
OY 841 TGTGACAAAGCTTGTGATAGATCAATCAGAAATGTACTTATGACCATGATATACAGA 900
Db 841 TGTGACAAAGCTTGTGATAGATCAATCAGAAATGTACTTATGACCATGATATACAGA 900
OY 901 GACGAGATTAACAAACCGGTTTCAATCAAAAGGTGTTGAAGTGAAGTGTGATACAA 960
Db 901 GACGAGATTAACAAACCGGTTTCAATCAAAAGGTGTTGAAGTGAAGTGTGATACAA 960
OY 961 GACTGATCCTGTGATTTCTTTCCTTTCATCATGCTTTTCTTGTGTTGTTGCTG 1020
Db 961 GACTGATCCTGTGATTTCTTTCCTTTCATCATGCTTTTCTTGTGTTGTTGCTG 1020
OY 1021 GGGTTTCATCATGAGGCTGCGCAGAGAGCAACATTAAGTGCACATTTGATGAGTG 1080
Db 1021 GGGTTTCATCATGAGGCTGCGCAGAGAGCAACATTAAGTGCACATTTGATGAGTG 1080
OY 1081 TATTAGTATTAATAAACCCCTGTGTTCTG 1110
Db 1081 TATTAGTATTAATAAACCCCTGTGTTCTG 1110

RESULT 2

US-09-918-568-57

Sequence 57, Application US/09918568

GENERAL INFORMATION:

APPLICANT: Yoshinobu OKUNO et al.

TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING

NUMBER OF SEQUENCES: 38 ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.

STREET: 2033 K Street, N.W., #800
City: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Nordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/918,568
FILING DATE: 02-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/004,422
FILING DATE: January 8, 1998
APPLICATION NUMBER: 08/443,862
FILING DATE: May 22, 1995
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/054,016
FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 1110 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL: <Unknown>
ANTI-SENSE: <Unknown>
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
ORGANISM: A2/Aich1/2/68
STRAIN: <Unknown>
INDIVIDUAL ISOLATE: <Unknown>
DEVELOPMENTAL STAGE: <Unknown>
HAPLOTYPE: <Unknown>
TISSUE TYPE: <Unknown>
CELL TYPE: <Unknown>
CELL LINE: <Unknown>
ORGANELLE: <Unknown>
IMMEDIATE SOURCE:
LIBRARY: <Unknown>
CLONE: <Unknown>
POSITION IN GENOME:
CHROMOSOME/SEGMENT: <Unknown>
MAP POSITION: <Unknown>
UNITS: <Unknown>
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:

5 833.4 75.1 1765 50 US-10-311-581-7 Sequence 7, Appl
6 832 75.0 1764 50 US-10-311-581-21 Sequence 21, Appl
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8 645.2 58.1 666 5 US-08-013-415-1 Sequence 1, Appl
9 645.2 58.1 666 8 US-08-391-315-1 Sequence 1, Appl
10 642 57.8 666 4 US-07-837-773-3 Sequence 3, Appl
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ALIGNMENTS

RESULT 1
US-08-443-862-57 Application US/08443862
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKuno et al.
TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,862
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,781
FILING DATE: April 19, 1994
APPLICATION NUMBER: 08/034,016

FILING DATE: April 29, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 1110 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORGANISM: A2/Aichi/2/68
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-443-862-57
Query Match 100.0%; Score 1110; DB 9; Length 1110;
Best Local Similarity 100.0%; Pred. No. 1,5e+302; Indels 0; Gaps 0;
Matches 1110; Conservative 0; Mismatches 0;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 10, 2003, 02:11:24 ; Search time 2451.76 Seconds
(without alignments)
14835.212 Million cell updates/sec

Title: US-09-918-568-57
1110
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32997241 seqs, 16383922548 residues

Total number of hits satisfying chosen parameters: 65994482

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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2	1110	100.0	1110	38	US-09-918-568-57
3	868	78.2	1777	9	US-08-443-862-54
4	868	78.2	1777	38	US-09-918-568-54

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Tue Aug 12 10:28:32 2003

Job time : 129.277 secs

us-09-918-568-57.rnpn

Page 7

Best Local Similarity 56.2%; Pred. No. 0.012;
Matches 72: Conservative 1; Mismatches 55; Indels 0; Gaps 0;

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Db 197 CCAACCACTGGGAATTTGAGATGGGGAATCAAGACGAGACAAATCATGATCTT 138

OY 610 GAAAGGAATTCCTCAGTAGAAGGAGAAATTCGAGACCTCGAATACGTTGAAGAC 669

Db 137 CTGAAGGAATACAGTACACAGAAAGAGAGTAGAARCTAAAAACAGACCTTGGGGGA 78

OY 670 ACTAAAT 677

Db 77 ATACAAT 70

RESULT 7
US-60-485-450-38314/c

Sequence 38314, Application US/60485450

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C

TITLE OF INVENTION: VIRUS INFECTED SUBJECTS, METHODS OF DETECTION AND USES

FILE REFERENCE: C1001470

CURRENT APPLICATION NUMBER: US/60/485,450

CURRENT FILING DATE: 2003-07-09

NUMBER OF SEQ ID NOS: 47859

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 38314

LENGTH: 201

TYPE: DNA

ORGANISM: Homo sapiens

US-60-485-450-38314

Query Match 3.6%; Score 39.6; DB 7; Length 201;
Best Local Similarity 56.2%; Pred. No. 0.012;

Matches 72: Conservative 1; Mismatches 55; Indels 0; Gaps 0;

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OY 610 GAAAGGAATTCCTCAGTAGAAGGAGAAATTCGAGACCTCGAATACGTTGAAGAC 669

Db 137 CTGAAGGAATACAGTACACAGAAAGAGAGTAGAARCTAAAAACAGACCTTGGGGGA 78

OY 670 ACTAAAT 677

Db 77 ATACAAT 70

RESULT 8
US-10-286-897-5262

Sequence 5262, Application US/10286897

GENERAL INFORMATION:

APPLICANT: Hyseq Inc

TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides

FILE REFERENCE: 784FLEPCT

CURRENT APPLICATION NUMBER: US/10/286,897

CURRENT FILING DATE: 2002-11-01

PRIOR APPLICATION NUMBER: US/09/488,725

PRIOR FILING DATE: 2000-01-21

PRIOR APPLICATION NUMBER: US/09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US/09/598,042

PRIOR FILING DATE: 2000-06-20

PRIOR APPLICATION NUMBER: US/09/620,312

PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: US/09/653,450

PRIOR FILING DATE: 2000-08-31

PRIOR APPLICATION NUMBER: US/09/662,191

PRIOR FILING DATE: 2000-09-14

PRIOR APPLICATION NUMBER: US/09/693,036

PRIOR FILING DATE: 2000-10-19

PRIOR APPLICATION NUMBER: US/09/727,344

PRIOR FILING DATE: 2000-11-29

NUMBER OF SEQ ID NOS: 7143

SOFTWARE: PL_FL_genes_b Versions 1.0

SEQ ID NO 5262

LENGTH: 627

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)..(627)

OTHER INFORMATION: n = a,t,c or g

US-10-286-897-5262

Query Match 3.6%; Score 39.6; DB 6; Length 627;
Best Local Similarity 54.9%; Pred. No. 0.019;

Matches 78: Conservative 0; Mismatches 64; Indels 0; Gaps 0;

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Db 260 GAAATACGAGAGGAACTCCGAAATTCAGAGAGGAGGAGGAGATATGAGCTGAA 319

OY 640 ATTACGACCTCGGAAATACGTTGAGAGACGCTAAATAGATCTCTGCTTACATGC 699

Db 320 TTGGAGAGCGAGCTGCAACAATGAAACCGAAGACGACCTCTCGGAAATAC 379

OY 700 GAGCTCTTCTGCTGCTGAGAGA 721

Db 380 CGCCTTCGATGAGCTGGAANA 401

RESULT 9
US-10-286-897-1690

Sequence 1690, Application US/10286897

GENERAL INFORMATION:

APPLICANT: Hyseq Inc

TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides

FILE REFERENCE: 784FLEPCT

CURRENT APPLICATION NUMBER: US/10/286,897

CURRENT FILING DATE: 2002-11-01

PRIOR APPLICATION NUMBER: US/09/488,725

PRIOR FILING DATE: 2000-01-21

PRIOR APPLICATION NUMBER: US/09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US/09/598,042

PRIOR FILING DATE: 2000-06-20

PRIOR APPLICATION NUMBER: US/09/620,312

PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: US/09/653,450

PRIOR FILING DATE: 2000-08-31

PRIOR APPLICATION NUMBER: US/09/662,191

PRIOR FILING DATE: 2000-09-14

PRIOR APPLICATION NUMBER: US/09/693,036

PRIOR FILING DATE: 2000-10-19

PRIOR APPLICATION NUMBER: US/09/727,344

PRIOR FILING DATE: 2000-11-29

NUMBER OF SEQ ID NOS: 7143

SOFTWARE: PL_FL_genes_b Versions 1.0

SEQ ID NO 1690

LENGTH: 2051

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (146)..(1153)

US-10-286-897-1690

Query Match 3.6%; Score 39.6; DB 6; Length 2051;
Best Local Similarity 54.9%; Pred. No. 0.032;

[illegible]

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RESULT 2
US-60-470-920-19
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: GENERAL INFORMATION:
: APPLICANT: Luke, Catherine, J.
: APPLICANT: Vialta, Adrian
: APPLICANT: Wloch, Mary K.
: APPLICANT: Evans, Thomas G.
: APPLICANT: Geall, Andrew J.
: TITLE OF INVENTION: DNA Influenza Vaccine Compositions
: FILE REFERENCE: 1530.064000
: CURRENT APPLICATION NUMBER: US/60/470,920
: CURRENT FILING DATE: 2003-05-16
: NUMBER OF SEQ. ID NOS: 45
: SOFTWARE: patentIn version 3.2
: SEQ. ID NO 19
: LENGTH: 1741
: TYPE: DNA
: ORGANISM: Influenza A virus
: US-60-470-920-19

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OY	276 AAATGGAAGCATTCGCCAATGSCAACGCCCTTCAAAAGCTGAACAGATGCATATTGAGC	335		
Db	899 AATGGGGGCATTAACCTCTAGTAGTATGCCATTCCACAAATCACCCCCTCACCATGGGGA	958		
OY	336 ATGCCCCAGTATGTTAAGCAAACACCCCTGAAGTTGGCAACAGGAGTGGCAATATACC	395		
Db	959 ATCCCCCAATATGTGAAATCAACACAGATTAGTCTTGCGACGTGACTCAGAAATAACCC	1018		
OY	396 AGAGAA-----ACAACTAGAGCCCTATTGGGGCATATAGCAGCTTCATAGA	443		
Db	1019 TCAAAGGAGACGAATGAAAGAAAGAAGAGACTATTGGAGCTATACAGAGTTTTATAGA	1078		

OY	444	AAATGCTTGGAGGGAATGATAGACGGTTGGTACGGCTTTCAGAGATCAAAATTCMGAGG	503
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OY	564	ATTGAAACGGGTAAATCGAAGACGACGACGAAATTCATCAATTCGAAAGGAATCTC	623
Db	1199	GGTCACTCGATCATTTAACAAATATGACACTCAGTTTGGAGCCGTTGGAAAGGAAATTTAA	1258
OY	624	AGAAGTAGAAGGAGAAATTCAGGACCTTCGAAATACGTTGAAAGACATTAATAATAGATCT	683
Db	1259	TAACTTAGAAAGGAGAAATAGAGAAATTTAAACAGAAATGGAAAGCGATTCTTAGATGT	1318
OY	684	CTGGCTTACAAATGGGAGCTTCTTGTCGCTCTCGAGAAATCAACATCAATATGACCTGAC	743
Db	1319	CTGGACTTACATGCTGACACTTCTGGTTCTTCATGAAATATGAGAACTCTCGACTTCA	1378
OY	744	TGACTCGAAATGAACAAGCTGTTTGAATAAAACAGGAGCGCACTGAGGGGAAATGCTGA	803
Db	1379	TGACTCAAAATGTCAAGAACTTTTACGACAAAGGTCCGACTACAGCTTAGGGATATGCGAA	1438
OY	804	AGAGATGGGCAATGGTGCCTTCAAAATATACCAAAATGTGACAAACCTTCGATAGACTC	863
Db	1439	GGAACTGGGTATGGTGTGTTGCAATCTATACAAATATGATATATGAATATAGGAAG	1498
OY	864	AATCAGAAATGTACTATGACCAATGATGTATACAGAGAGCAAGACATTAACAAACCGGTT	923
Db	1499	TGTAAAAAAGCGAATGATGACTACCCGACGATATTTCAGAAAGAACGAACTAAACAGGA	1558
OY	924	TCAGATCAAGSGTGTAACTGAGAGTCTGGATACAAAGACTGGAATCTCTGGGATTT	979
Db	1559	GGAATATAGTGGATTAATTTGGAATCAATGGAACCTTACCAAAATTAAGTCTCAATTT	1614

```

RESULT 3
US-60-470-920-17
: Sequence 17, Application US/60470920
: GENERAL INFORMATION:
: APPLICANT: Luke, Catherine, J.
: APPLICANT: Vialta, Adrian
: APPLICANT: Wloch, Mary K.
: APPLICANT: Evans, Thomas G.
: APPLICANT: Geall, Andrew J.
: TITLE OF INVENTION: DNA Influenza Vaccine Compositions
: FILE REFERENCE: 1530.0640000
: CURRENT APPLICATION NUMBER: US/60/470,920
: CURRENT FILING DATE: 2003-05-16
: NUMBER OF SEQ ID NOS: 45
: SOFTWARE: Patentln version 3.2
: SEQ ID NO 17
: LENGTH: 1220
: TYPE: DNA
: ORGANISM: Influenza A virus
: US-60-470-920-17

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Query Match	11.2%	Score 124.8;	DB 7;	Length 1220;
Best Local Similarity	59.7%;	Pred. 2.5e-29;		
Matches 210;	Conservative 0;	Mismatches 142;	Indels 0;	Gaps 0;

OY	248	ATACCTGTATTTCGATGCATCTCCAAATGAGAACATTCACATGACAGACCCCTTTC	307
Db	869	ATGATTGTATACAGAGAGTGTCAAACACCCCATGTGCTATTAACACAGCATGCTCCCTTTCC	928
OY	308	AAAACGTAAMCAGATACATATGGACCATGCCCAAGTGTGTTAAAGCAAAACACCCCTGA	367
Db	929	AGAAATATACATCCAGTCATACATAGGACAGTCCCAAAATTCGTACGACGAGTACCAAAATTGA	988
OY	368	AGTTGGCACACAGGAGATCCGAATGTACACAGAAACAAATAGAGGCTTATTTCCGGCGCAA	427

